us-09-763-902b-1.rsp

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

Title: Perfect score:

US-09-763-902B-1 2459 1 MRFVVALVLINVAAAGAVPL......xIPLEKDERHQWIVLLSFQL 480 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 résidues Searched:

112892

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum.Match 100%. Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

-	Description	043493 homo sapien	rattu	P19246 mus musculu	P16884 rattus norv	P12036 homo sapien	clost			O9nzw4 homo sapien	077788 bos taurus	P41777 rattus norv	P07197 homo sapien	mus m	Q14978 homo sapien	mus n	Q28092 bos taurus	. P39653 streptococc		Q62598 rattus norv	Q9u7e0 caenorhabdi	P82179 canis famil	Q9ukj3 homo sapien		Q28820 oryctolagus		8	그	P54681 dictyosteli	25	88	-	52 bo	P46100 homo sapien
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S																																		
SUMMARIES	ID	TGN2_HUMAN	TGN3_RAT	NFH_MOUSE	NFH_RAT	NFH_HUMAN	SLP1_CLOTM	MRSP_STAAU	SR40_YEAST	DSPP_HUMAN	NFM_BOVIN	NP14_RAT	NEM_HUMAN	DSPP_MOUSE	NP14_HUMAN	DMP1_MOUSE	CYL2_BOVIN	DEXT_STRDO	DMP1_RAT	DSPP_RAT	ATRX_CAEEL	TRDN_CANFA	Y553_HUMAN	AMYH_YEAST	TRDN_RABIT	MLH_TETTH	TCOF_HUMAN	GAR2_SCHPO	RTOA_DICDI	AF4_HUMAN	NFM_RABIT	PPRB_HUMAN	CYL1_BOVIN	ATRX_HUMAN
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	Length	480	357	1087.	831	1020	1664	1637	406	1253	810	704	915	934	669	503	488	1337	489	687	1359	700	1089	1367	705	633	1411	200	400	1210	644	1581	299	2492
ď	Query	98.5	27.3						10.2				9.6		9.4	9.3			9.7		8.9		٠.	٠.	9.8	9 8	8.5	8.4	8.4	8.4	8.3	8.3	8.5	8.7
	Score	2421	672	306	286	272.5	259	257.5	251.5	250	245	241.5	236.5	234	232	227.5	226.5	226.5	226	221.5	219	21	216.5		212.5	211.5	. 208	207	. 902	205.5	202	204	202.5	202.5
	Result No.		7	რ	4.	ស	9		89	6	10	11	12	13	14	15	16	. 17	18	19	20	21	22	23			56	27	28	29	30	31	32	£.

JOINED. JOINED.

EMBL; AF029314; AAB96908.1; EMBL; AF029315; AAB96908.1;

AAB96908

EMBL; AF029316; EMBL; AF029313;

EMBL; AF027516; AAC39542.1; -.

homo sapien saccharomyc homo sapien culamydia t oryctolagus homo sapien homo sapien homo sapien saccharomyc saccharomyc drosophila
Q13061 P32334 Q03111 084419 P13666 P9567316 Q13116 P14907 P14907
•
TRDN HUMAN MSB2_YEAST BEAL_HUMAN PMPC_CHLTR SRCA_RABIT HT3_HUMAN CYL1_HUMAN CYL1_HUMAN MPI_HUMAN MSPI_YEAST TRP_DROME YEAST TRP_DROME
728 1306 559 1770 908 556 598 513 671 823 1275
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201.5 199.5 199.5 198.5 198.5 198.5 194.5 193.5 193.5
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## ALIGNMENTS

	RESULT 1	RESULT 1
	ביים ביים	LOUMAN STANDADD. DDT. 480 AA
	A A	3499: 043500: 015282: 09276
	D.	2001 (Rel. 40, Created)
	DŢ	(Rel.
	DŢ	update)
	DE:	Trans-Golgi network integral membrane protein 2 precursor (Trans-
	DE	51) (TGN46)
	Z 0	TGOLDS OF TGNSI OF TGN46.
	3 5	Chordata: Craniata: Vertebrata:
	88	Primates: Catarrhini; Hominidae;
	×o	)=9606;
	RN	
	a d	SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS OF TYR-430.
	Z Z	11330E=L1VE1, and Flacenta; MEDLINE=98086273: PubMed=9422759:
	RA	Kain R., Angata K., Keriaschki D., Fukuda M.;
	RŢ	"Molecular cloning and expression of a novel human trans-Golgi network
	RŢ	ein, TGN51, that contains
	$_{ m LI}$	motifs.";
	R.	J. Biol. Chem. 273:981-988(1998).
	X C	
	א מ ת	SEQUENCE FROM N.A. (150-CVA. 1170-4-6).
	RX X	MEDLINE=97063845: Pubmed=8907352:
	RA	Ponnambalam S., Girotti M., Yaspo ML., Owen C.E., Perry A.C.,
	RA	Suganuma T., Nilsson T., Fried M., Banting G., Warren G.;
	RT	"Primate homologues of rat TGN38: primary structure, expression and
	RI.	functional implications.";
	5 G	J. CELL SCI. 109:0/2-683(1998).
	36	-!- FUNCTION: MAY BE INVOLVED IN REGULATING MEMBRANE TRAFFIC TO AND FROM TRANS-COLOT NETWORK
	9 8	-:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. PRIMARILY IN TRANS-
	ပ္ပ	GOLGI NETWORK. CYCLES BETWEEN THE TRANS-GOLGI NETWORK AND THE CELL
	ပ္ပ	
	ပ္ပ	-!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; TGN46, TGN48 AND TGN51 (SHOWN
	2 5	HEKE); AKE FKOUNCED BI ALIERNALIVE SPLICING.
	3 5	
	ខ	IS BARELY EXPRESSED IN EMBRYONIC KIDNEY AND PROMYELOCYTIC CELLS.
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	ပ္ပ	This SWISS-PROT entry is copyright. It is produced through a collaboration
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	ງ ຍ	mounties and units sequence in the Tempoveu. Orage by and to commercial apprinties requires a license agreement (see bitto://www.ish.eib.ch/shnounce/
	88	or send an email to license@isb-sib.ch).
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	2	TOTOCOCK OFFICE TOTOCOCK

**QTPKDSPSKSSAEAQTPEDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTK** 

1 MREVVALVLINVAAAGAVPLLAATESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEP

240 240 300 360 360 420

241

ETDLISPPQEEVKSSEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSASSENREGTLS 

301

361

303

DSTGSEKDDLYPNGSGNGSAESSHFFAYLVTAAILVAVLYIAHHNKRKIIAFVLEGKRSK

421 VTRRPKASDYQRLDQKYVLILNVFPAPPKRSFLPQVLTEWYIPLEKDERHQWIVLLSFQL

KSGADGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGA

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                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
ENDOCYTOSIS SIGNAL (IN ISOFORM TGN46 AND
                                                                                                                                                                        ENDOCYTOSIS SIGNAL (IN ISOFORM TGN51).
ENDOCYTOSIS SIGNAL (IN ISOFORM TGN51).
14 X 14 AA TANDEM REPEATS.
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TRANS-GOLGI NETWORK INTEGRAL
                                                                                               Transmembrane; Glycoprotein; Repeat; Golgi stack;
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       AAB96906.1; JOINED
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                                    AF027515; AAC39541.1;
AF029316; AAB96907.1;
                             U62390; AAC39539.1;
                                                                          CAA64002.1;
                                                                                 HGNC:15450; TGOLN2
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SIGNAL 1, 2
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AF029316;
               AF029314;
AF029315;
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                                                          AF029314;
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                                    AF027515;
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                             EMBL;
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                                                           EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PRÖT entry is copyright. It is produced through a collaboration
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                          "Identification, sequencing and expression of an integral membrane protein of the trans-Golgi network (TGN38)."; Biochem. J. 270:97-102(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Trans-Golgi network integral membrane protein TGN38 precursor.
                                                                                                                                                                                                                                                                  STRAIN=Sprague-Dawley, TISSUE=Liver;
MEDLINE=90372941; PubMed=2204342;
Luzio J.P., Brake B., Banting G., Howell K.E., Bräghetta P.,
Stanley K.K.;
                                     357 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X53565; CAA37637.1;
                                       STANDARD;
                                                                                                                                                      Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S11468; S11468
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                         NCBI_TaxID=10116;
                                       TGN3_RAT
RESULT
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Gaps

. ..

Indels

Pred. No. 7.7e-98; 1; Mismatches 6

Conservative

Best Local Similarity Matches 473; Conserv

1 MRFVVALVLLNVAAAGAVPLLATESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEP

```
GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: March 4, 2003, 14:51:02; Search time 11.4899 Seconds

(without alignments)

1732.709 Million cell updates/sec
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Title: US-09-763-902B-1
Perfect score: 2459
Sequence: 1 MRFVYALVLLNVAAAGAVPL......YIPLEKDERHQWIVLLSFOL 480

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length:.0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of fesults predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score 2421	a Ω MA - 0	Length	DB 1	SUMMARIES ID TGN2_HUMAN	-71	Description 043493 homo saplen	sapien
100	672 306	27.3	357	יהה	TGN3_RAT			rattus norv mus musculu
4. ru	286		831		NFH_RAT	``.	4.9	rattus norv. homo sapien
92	259	,	1664	. <del></del>	SLP1_CLOTM MRSP_STAAU		2 4	clostridium staphylococ
დთ	· 251.5 250		1253		SR40_YEAST DSPP_HUMAN		P32583 sacche Q9nzw4 homo	saccharomyc homo sapien
10	245	10.0	810		NFM_BOVIN			bos taurus rattus norv
12		9.6	915	1	NFM_HUMAN		97	sapien
13	234	o o o o	 6 9 3 4 9 9 9 9	44	DSPP_MOUSE NP14_HUMAN		9 mus m 8 homo	musculu sapien
15	227.5	6.6	503	н,	DMP1_MOUSE		m snu g	musculu
17	226.5	9 9	1337		CYLZ_BOVIN		028092 bos ta P39653 strep	bos taurus streptococc
18.	226	9.5	489	٦	DMP1_RAT		~	s norv
13	221.5	00	1359		DSPP_RAT		Q62598 rattus nor O9u7e0 caenorhabd	s norv
21	217	8	700	· ~	TRDN_CANFA	•	_	canis famil
22	216,5	8.8	1089	Н	Y553_HUMAN		Q9ukj3 homo	homo sapien
23	214.5	8.7	1367	Н	AMYH_YEAST			saccharomyc
24	212.5.	9.8	-705	-	TRDN_RABIT		_	oryctolagus
25	211.5	9.8	633	Ä	MLH_TETTH		_	tetrahymena
56	208	.5	1411	7	TCOF_HUMAN		013428 homo	homo saplen
27	207	8.4	200	٦.	GAR2_SCHPO			schizosacch
28	506	<del>7</del>	400	Н,	RTOA_DICDI		dicty	1ctyostel1
53	205.5	80 ¢	1210	Η,	AF4_HUMAN	-		sapien
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	homo sapien	saccharomyc	homo sapien	chlamydia t	oryctolagus	homo sapien	homo sapien	homo sapien	saccharomyc	saccharomyc		schizosacch	
_	Q13061	P32334	203111	084419	P13666	09bw71	P35663	013316	012114.	P14907	P19334	010475	
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	TRDN_HUMAN	MSB2_YEAST	ENL_HUMAN	PMPC_CHLTR	SRCA_RABIT	HIR3_HUMAN	CYL1_HUMAN	DMP1_HUMAN	CHS5_YEAST	NSP1_YEAST	TRP_DROME	YDF3_SCHPO	
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	728	1306	559	1770	806	256	598	513	671	823	1275	1403	
	8.5	8.1	8.1	8	0 8	0.8	0 8	7.9	7.9	7.9	7.8	1.7	
	201.5	199.5	199	198.5	196	195.5	195.5	194.5	193.5	193.5	192.5	188.5	
	34	35	36	37	38	39	40	41	42	43	44	45	٠.

# ALIGNMENTS

	RESULT TGN2_H	RESULT 1 PGN2_HUMAN
	A D	HUMAN STANDAR 3; 043499; 043500
	古타	Creat Last
	28	ker. 41, Last annotation update) twork integral membrane protein
	e s	Golg1 network protein TGN51) (TGN46) (TGN48) (TGN38 homolog). TGOLN2 OR TGN51 OR TGN46.
	So	Homo sapiens (Human). Enkarvota: Metazoa: Chordata: Cranjata: Vertebrata: Euteleostom1:
	88	la; Primates; Catarrhini; Hominidae;
	S S	NCBI_TaxID=9606;
	8	A.
	2 %	TISSUE=Liver, and Fiacenta; MEDLINE=98086273; PubMed=9422759;
	RA.	., Kerjaschki D., Fukuda M.;
	r r	"Molecular cloning and expression of a novel human trans-Golgi network glycoprofein, TGN51, that contains multiple tyrosine-containing
	RT	
	RL	J. Biol. Chem. 273:981-988(1998).
	N. C.	SPOIDING BOOM N N (TEORODM MONAE)
	R P	ISSUE-Fetal liver, and Fetal thymus;
	RX	52;
	RA	lam S., Girotti M., Yaspo ML., Owen C.E., Pe
	A F	Suganuma I., Milsson I., Fried M., Banting G., Warren G.; "Drimate homologues of rat mon38. primary structure, expression and
	RT	in implications, ";
	RI.	(1996).
	ပ္ပင္ပ	-I-FUNCTION: MAY BE INVOLVED IN REGULATING MEMBRANE TRAFFIC TO AND
	3 8	TION: TYPE I
	ខូខ	BETWEEN THE TRANS-GOLGI NETWORK AND TH
•	ပ္ပ	ENDOSOMES.
	g'g	-:- ALTERNATIVE PRODUCTS: 3 ISOFORMS; TGN46, TGN46 AND TGN51 (SHOWN upper, and population by alternative collision
	ខ្ល	-I- TISSUE SPECIFICITY: ISOFORM TGN46 IS WIDELY EXPRESSED. ISOFORM
	ပ္ပ	TGN51 IS MORE ABUNDANT IN FETAL LUNG AND KIDNEY. ISOFORM TGN48
	ဗ	IS BARELY EXPRESSED IN EMBRYONIC KIDNEY AND PROMYELOCYTIC CELLS.
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	႘႘	or send an email to license@lsb-sib.ch).
	3.2	BL; AF027516;
	D.	AF029316; AAB96908.1;
	ž	
	DR	AF029315; AAB96908.1;

121

181 KSGADGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGA **EEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFKTESGE** ETDLISPPOEEVKSSEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSASSENREGTLS DSTGSEKDDLYPNGSGNGSAESSHFFAYLVTAAILVAVLYIAHHNKRKIIAFVLEGKRSK

241 181

241 301 301

DSTSKSHSELQTPKDSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPN

**QTPKDSPSKSSAEAQTPEDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTK** MRFVVALVLLNVAAAGAVPLLATESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEP

360

420

361 421

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus

Rattus norvegicus (Rat)

NCBI\_TaxID=10116;

01-FEB-1991 (Rel. 17, Created) 01-FEB-1991 (Rel. 17, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Trans-Golgi network integral membrane protein TGN38 precursor.

Identification, sequencing and expression of an integral membrane rotein of the trans-Golgi network (TGN38).";

protein of the trans-Golgi ne Biochem. J. 270:97-102(1990).

NTERACTION WITH NEURABIN-I AND NEURABIN-II, AND MUTAGENESIS

SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley, TISSUE-Liver;
MEDLINE-90372941; PubMed-2204342;
Luzio J.P., Brake B., Banting G., Howell K.E., Braghetta P.,
Stanley K.K.;

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PAPPKRSFLPQVLTEWYIPLEKDERHOWIVLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKRSFLPQVLTEWYIPLEKDERHQWIVLLS
                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
ENDOCYTOSIS SIGNAL (IN ISOFORM TGN46 AND ISOFORM TGN48).
ENDOCYTOSIS SIGNAL (IN ISOFORM TGN51).
ENDOCYTOSIS SIGNAL (IN ISOFORM TGN51).
14 X 14 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                           MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOL -> IFSPPSPNRMVYSSGKR (IN ISOFORM TGN48).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.5%; Score 2421; DB 1; Length 480; 98.5%; Pred. No. 7.7e-98; 1ve. 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                       FRANS-GOLGI NETWORK INTEGRAL
                                                                                                                                                                                                                                                         Signal; Transmembrane; Glycoprotein; Repeat; Golgi stack;
Alternative splicing, POTENTIAL.
SIGNAL 12 480 TRANS-GOLGI NETWORK INTEGRAL
                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
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-> Q (IN REF. 2).
-> A (IN REF. 2).
-> W (IN REF. 2).
-> E (IN REF. 2).
-> E (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L -> V (IN REF. AAB96908).
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FRANS-GOLGI
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91
103
105
158
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825
51006 MW;
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EMBL; X94333;
Genew; HGNC:15
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                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
DOMAIN
DOMAIN
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                                     EMBL;
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EMBL;
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MEDILINE-99445568; Pubbed-10514494; Stephens D.J., Banting G.; Stephens D.J., Banting G.; Stephens D.J., Banting G.; Disct. Interaction of the trans-Golgi network membrane protein, TGN38, with the F-actin binding protein, neurabin. ". J. Biol. Chem. 274:30080-30086(1999).

-I. SUBDINIT: INTERACTS WITH NEDRABIN'I AND NEURABIN-II. BINDS PREBENTIALLY TO THE DIMBRIC FORM OF NEURABIN-I.

-I. SUBCELLUIAR LOCATION: TRANS-GOLGI NETWORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
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PIR; S11468; S11468.
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Conservative

Best Local Similarity Matches 473; Conserv

MRFVVALVLLNVAAAGAVPLLATESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEP 60

us-09-763-902b-1.rsp

PubMed-3220257

MEDLINE-89121513;

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12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNLNLDDSKKHPE---TADAKLKETLQQLLPVD-PRQEKSGQKFTKDSGSPTGG---- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYPNKSGADGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 DSDNTTGGD------ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 KSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFKT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TGSDN------DKPTGGDSNKPTSKVPSNTETPKIDKVQLTEKGQKPTLISKT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESGE----ETDLISPPQEEVKSSEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSASS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENREGTLSDSTGSEKDDLYPNGSGNGSAESSHFFAYLVTAAILVAVLYIAHHNKRKIIAF 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRFVVALVLINVAAAGAVPLLATESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHP-- 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 QPSTPLPPGVDISQQVKTNRPT-----DQRLESDKEGQDKTVARTSASVSSGVESA 86
                                                          TRANS-GOLGI NETWORK INTEGRAL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                      NEURABIN-II BINDING.
MISSING: NO EFFECT ON NEURABIN-I AND
NEURABIN-II BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
                                                                                                                                                                      RETENTION SIGNALS.

6 X 8 AA TANDEM REPEATS.

N-LINKED (GLCNAC. . . ) (POTENTIAL).

S-AA, D. ABOLISHES NEURABIN-I AND NEURABIN-I BINDING.

Y->A: NO EFFECT ON NEURABIN-I AND
                                                                                                                                                CYTOPLASMIC TAIL, CONTAINS THE GOLG:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ul-AUG-1992 (Rel. 23, Last sequence update).
16-027-2001 (Rel. 40, Last annotation update)
Neurofilament triplet H protein (200 kDa neurofilament protein)
(Neurofilament heavy polypeptide) (NF-H).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.3%; Score 672; DB 1; Length 357; 40.1%; Pred. No. 6.1e-23; tive 48; Mismatches 122; Indels
   Repeat; Golgi stack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173B64C51CAD593B CRC64;
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                                                                                            PROTEIN TGN38
Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALEGKRSKVTRRPKASDYQRLNLK 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 AA; 38305 MW;
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                                                                                                                                                                                                                                                                                                                          147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357
   Transmembrane;
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SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                   348
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Matches 178;
                                                                                                                                                                                                                                                                                                                    CARBOHYD
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                                                                                                                  FRANSMEM
                                                                                                                                                                                                                                          ARBOHYD
Signal;
SIGNAL
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                                                                                                                                                   DOMAIN
                                                                                                                                                                                                           DOMAIN
                                                             CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF AXONAL CALIBER.

PTM: PHOSPHORVLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.

CAINLIARTY: BELOAS TO THE INTERMEDIATE FILAMENT FAMILY.

CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 534 TO 716 AND IS SHORTER DUE TO FRAMESHIFTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NF-H HAS AN IMPORTANT FUNCTION IN MATURE AXONS THAT IS NOT SUBSERVED BY THE TWO SMALLER NF PROTEINS.

FURNIT THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFH IS PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLU-RICH (ACIDIC).
50 X 6 AA TANDEM REPEATS OF K-S-P-A-E-A.
GLU/LYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M
AND H'WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
                         D., Grosveld
                                                                                                                                                                                                                                                                                                       (NF-H)
                                                                                      Sequence and structure of the mouse gene coding for the largest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfan; PF00038; filament; 1.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Neurone; Phosphorylation;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-89089138; PubMed-3145094;
Shneidman P.S., Carden M.J., Lees J.F., Lazzarini R.A.;
The structure of the largest murine neurofilament protein revealed by CDNA and genomic sequences.";
Brain Res. 464:217-231(1988).
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K -> QA (IN REF. 2 AND 3).

A -> AR (IN REF. 2 AND 3).

S -> T (IN REF. 2 AND 3).
            Julien J.-P., Cote F., Beaudet L., Sidky M., Flavell Mushynski W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COIL 1B.
LINKER 12.
COIL 2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LINKER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA39813.1; JOINED.
AAA39813.1; JOINED.
AAA39813.1; JOINED.
AAA39809.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Swiss Webster; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M24496; AAA39813.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M35131; AAA39809.1;
Z31012; CAA83229.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z31012; CAA83229.1;
PIR, JT0368; QPMSH.
PIR; A43778; A43778; MGD; MGI:97309; Nfh.
InterPro; IPR001664; IF.
                                                                                                                      neurofilament subunit.";
Gene 68:307-314(1988).
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                                                                                                                                                                                                                                                                                          559 EPKSPAEPKSPAEAKSPAEPKSPATVKSPGEAKSPSEAKSPAEAKSPAEA--KSPAEAKS 616
                                                                                                                                                                                                                                                                                                                          91 QKDSSN----KSGAEAKTQKGSTSKSGSEAQTTKDSTSKSHSELQTPKDSTGKSGAEAQT 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 37-831 FROM N.A. MEDINE-88309090; PubMed-2457365; Dautigny A., Pham-Dinh D., Roussel C., Felix J.M., Nussbaum J.L., Joiles P., "The large neurofilament subunit (NF-H) of the rat: cDNA cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Breen K.C., Robinson P.A., Wion D., Anderton B.H.; Partial sequence of the rat heavy neurofilament polypeptide (NF-H). Identification of putative phosphorylation sites.";
                                                                                                                                                                                                                                                                                                                                          DIRPPEQVKSPAKEKAK-SPEKEEAKTSEKVAPKKEEVKSPVKEEVKAKEPPKKVEEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVVPEQPSRKDHSKPISNPSDNK-------ELPKADT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1990 (Rel. 15, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet H protein (200 kDa neurofilament protein)
(Neurofilament heavy polypeptide) (NF-H) (Fragment)
                                                                                                                                                             75; Mismatches 138; Indels 138;
                                                                                                                            Score 306; DB 1; Length 1087; Pred. No. 8e-07;
                                              G -> A (IN REF. 3).
V -> M (IN REF. 2 AND 3).
T -> N (IN REF. 2 AND 3).
MW; 57BAC76A38EDICB9 CR664;
L -> G (IN REF. 2 AND 3)
P -> PREAKSP (IN REF. 3)
MISSING (IN REF. 3).
                                                                                                                                                                                             13 AAAGAVPLLATESVKOEEA---GVRPSAGNVSTHPSLSQRPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                831 AA
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MEDLINE-89065087; PubMed-3143606;
                                                                                                                              12.4%;
26.9%;
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                                                                                              116612
                                                                                                                                                             129; Conservative
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 492
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1087 AA;
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                                                                                                                                              Best Local Similarity
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P16884; Q63368;
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: THERE ARE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFH IS PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULYS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE OF AXONAL CALIBER.

PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT PUNCTION. SIMILARITY: BELONGS TO THE INTERMEDIATE PLAMENT FAMILY.

CAUTION: REP. 1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 783 ONWARD AND IS LONGER DUE TO A FRAMESHIFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coiled coil; Neurone; Phosphorylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 86:2463-2467(1989).
--I- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
NF-H HAS AN IMPORTANT FUNCTION IN MAIURE AXONS THAT IS NOT SUBSERVED BY THE TWO SMALLER NF PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                         neurotiliament peptide (NF-H): developmental and tissue expression the rat, and mapping of its human homologue to chromosomes 1 and 22.";
                                                                                                                                                 Abbinson P.A., Wion D., Anderton B.H.; Isolation of a cDNA for the rat heavy neurofilament polypeptide
                                                                                                                                                                                                                                                                                                                                                             Lieberburg I., Spinner N., Snyder S., Anderson J., Goldgaber D. Smulowitz M., Carroll Z., Emanuel B.S., Bretiner J., Rubin L.; "Cloning of a CDNA encoding the rat high molecular weight neurofilament peptide (NF-H); developmental and tissue expressi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEATS OF K-S-P
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... (IN REF. 2).

... (IN REF. 1 AND 4,

... (IN REF. 2 AND 4).

S. (IN REF. 2 AND 4).

T. (IN REF. 2 AND 4).

"IN REF. 2 AND 4).

"IN REF. 2 AND 4.
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-> P (IN REF. 2 AND 4).
1B0973C3F13EF768 CRC64;
                            Biophys. Res. Commun. 154:1099-1106(1988)
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EMBL; X13804; CAA32038.1; ALT_FRAME.
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                                        e. There are no restrictions on long as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A----DGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQ--GPID---- 233
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111780 MW; 1177C9DCB3DCF1D4 CRC64;
                             and the
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Pred. No. 2.1e-05;
66; Mismatches 185;
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                            Bioinformatics
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                                        the European Bioinformatics Institute. use by non-profit institutions as lo
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EMBL; X15307; CAA33366.1;
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Best Local Similarity 22.9
Matches 106; Conservative
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Pfam; PF00038; filament;
PROSITE; PS00226; IF; 1.
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Q06852;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                 MRSP_STAAU
P80544; Q9Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute as Institute by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Cell surface glycoprotein 1 precursor (Outer layer protein B) (S-layer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1094 PEEPIPTOTPSDEPTPSDEPTPSDEPTPSDEPTPSDEPTPSETPEEPIPTDTPSDEPTPS 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1154 DEPTPSDEPTPSDEPTPSDEPTPSETPEEPIPTDTPSDEPTPSDEPTPSDEPTPSDEPTP 1213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDEPTPSDEPTPSETPEEPIPTDTPSDEPTPS - DEPTPSDEPTPSDEPTPSDEPTPSET 1093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 VP----EQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFKTESGEE---TDL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 STHPSLSQRPGGS-TKSHPEP-OTPKDSPSKSSAEAQTPEDTPNKSGAEAKTQKDSSNKS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KD-------VPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNKV
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                                                                                                                                                                       Clostridium thermocellum,
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                            PERMINENCE TO SERVICE SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELL SURFACE GLYCOPROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBCELLULAR LOCATION: Cell wall.
-1- SIMILARITY: CONTAINS 4 S-LAYER HOMOLOGY (SLH) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62; Mismatches 178; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 SLH 4 (INCOMPLETE),
178194 MW; 5F396695BA9FE74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLY/PRO/SER/THR-RICH.
SLH 1 (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-layer; Signal; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00395; SLH; 3.
PROSITE; PS01072; SLH_DOMAIN; 2.
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1566 162
1626: 164
1664 AA;
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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                              NCBI_TaxID-1515;
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                                                                                                                 protein 1).
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1329 -TPSDEPTPSDEPTPSDEP--TPSDEPTPSDEPTPSDEPTPSDEPTPSETPEEPTFTTTP 1385
                                                                                          305 ISPPQEEVKSSEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSASSENREGTLSDSTG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein of Staphylococcus aureus.";
Eur. J. Biochem. 236:904-910(1996).
-!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Cell wall; Peptidoglycan-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPKDSPSKSSAEAQ 75
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141 X 2 AA TANDEM REPEATS OF D-[SAG].

LPXTG SORTING SIGNAL (POTENTIAL).

TSBE9ADB469BD309 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Savolainen K., Kuusela P., Paulin L., Korhonen T.K.;
"Pls, a large repeat-rich surface protein of methicillin resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHICILLIN-RESISTANT SURFACE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ilden P., Savolainen K., Tyynelae J., Vuento M., Kuusela P., Purification and characterisation of a plasmin-sensitive surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 257.5; DB 1;
; Pred. No. 0.00014;
70; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus.
Bacteria, Firmicutes, Bacillales, Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Methicillin-resistant surface protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1637 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001899; Gram_pos_anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGRFAMs; TIGR01167; LPXTG_anchor; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96270743; Pubmed-8665912;
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16-OCT-2001 (Rel. 40, Last seq
15-JUN-2002 (Rel. 41, Last ann
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                                                                                                                                                                                                                                                                                 1386 TPTPSTTPTSGSGGSGGS 1403
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21.6%;
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Best Local Similarity 21.6
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 624-628; 676 1199-1205 AND 1217-1224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ococcus aureus.
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                                                                                                                                                                                                                                                                                           1261 PNL---PEGETKVIPGKDGLKDPETGEIIEEPQDEVIIHGAKDDSDADSDSDADSDSDAD 1317
                                                                                                DADSDSDADSDSDSDSDSDSDSDSDSDSDSDSDSDADRDH--NDKTDKPNNKELPD-T 1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSASSENREGTLSDSTGSEKDDLYPNGS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Remacha M., Jimenez A., del Rey F., Ballesta J.P.G., Revuelta J.L.; "The complete sequence of a 15,820 bp segment of Saccharomyces cerevisiae chromosome XI contains the UBI2 and MPLI genes and three
                                                 TPEDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSKSHSELQTPKD
                                                                                                                                                     STGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGADGQTPKDGSSK
                                                                                                                                                                                                                                                         SGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNKVVPE
                                                                                                                                                                                                                                                                                                                                                          256 QPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFKTESGEETDLISPPQEEVKSS
                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
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-1- FUNCTION: NOT KNOWN; WEAK SUPPRESSOR OF A MUTANT OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT AC40 OF DNA DEPENDANT RNA POLYMERASE I AND III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lalo D., Carles C., Sentenac A., Thuriaux P., Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.
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8EA007695AF4BA1D
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(Rel. 29, Last sequence update)
(Rel. 36, Last annotation update)
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SRP40 OR YKR092C OR YKR412A.
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st 9:1349-1354(1993).
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STRAIN-ATCC 28583 / FL100;
Lalo D., Carles C., Senten
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Z28317; CAA82171.1;
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P32583;
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CONFLICT
SEQUENCE
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SR40_YEAST
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Q9NZM4; O95815;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Dentin stalophosphoproteth precursor [Contains: Dentin phosphoprotetin
(Dentin phosphophoryn) (DPP); Dentin sialoprotein (DSP)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254
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                                                             Gaps
                                                                                                                                                                                                                                            EDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSKSHSELQTPKDST 137
                                                                                                                                                                                                                                                                                                   GKSGAEAQTPEDSPNRSGAEAKTOK---DSPSKSGSEAQTTKDVPNKSGADGQTPKDGSS 194
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                                                                                                                       VPLLATESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEPQTPKDSPSKSSAEAQTP 77
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Xiao S., Yu C., Chou X., Yuan W., Wang Y., Bu L., Fu G., Qian M.,
Yang J., Shi Y., Hu L., Han B., Wang Z., Huang W., Liù J., Chen Z.,
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ur. J. Oral Sci. 106:1043-1047(1998).
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Zhang X., Zhao J., Li C., Gao S., Qiu C., Liu P., Wu G., Qiang i
Lo W.H.Y., Shen Y.;
"DSPP mutation in dentinogenesis imperfecta Shields type II.";
Nat. Genet. 27:151-152(2001).
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      Length 406;
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae, Homo
                                                          Indels
; Score 251.5; DB 1;
; Pred. No. 7.4e-05;
67; Mismatches 167;
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Gu K., Chang S.R., Slaven M.S., Clarkson B.H.,
Ritchie H.H.;
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                                                                                                                                                               11 VPKL---SVKEKEIEEKSSSSSSSSSSSS----
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   10.2%;
23.0%;
   Query Match 10.2
Best Local Similarity 23.0
Matches 82; Conservative
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DSPP_HUMAN
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NFM_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or.send an email to license@isb-sib.ch)
Nat. Genet. 27:201-204(2001).

-!- FUNCTION: DSP may be an important factor in dentinogenesis. DPP may be independent of calcium and facilitate initial mineralization of dentin matrix collagen as well as regulate the size and shape of the crystals.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed in teeth. DPP is synthesized by codontoblast and translently expressed by pre-ameloblasts.
-!- PTM: DSP is glycosylated.
-!- DISEASE: Defects in DSP are the cause of dentinogenesis imperfecta in DSP are the cause of dentinogenesis imperfects in DSP are the cause of dentinogenesis imperfects in DSP and the permanent teeth are affected in which both the primary and the permanent teeth are affected in which both the primary and the permanent teeth are affected in which with an incidence of 1:8000 live births. The teeth are amber and opalescent, the pulp chamber being obliterated by abnormal dentin. The enamel, although unaffected, tends to fracture, which makes dentin undergo rapid attrition, leading to shortening of the
                                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute. There are no restrictions on
by non'profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                teeth.
DISBASE: Defects in DSPP are the cause of autosomal dominant
DISBASE: Defects in DSPP are the cause of autosomal dominant
deafiness with dentinogenesis imperfecta 1 syndrome (DFNA39/DGI1
syndrome). Affected individuals present with DGI1 associated with
early onset progressive sensorineural high-frequency hearing loss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY CK1)
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V -> F (IN DFNA39/DG11)
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N-LINKED
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222
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336
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CARBOHYD
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PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM IS PHOSPHORYLATED ON A NUMBER OF THE SERINES. IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE OF AXONAL CALIBER (BY SIMILARITY).

PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The bovine neurofilament M subunit has a novel set of KSP repeats normally restricted to NF-H"; Submitted (SEP-198) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: NEUROFILAMENTS USBALLY COMTAIN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        884 DSSDSNESSNSSDSSDSSNSSDSSDSSNSSDSSNSSDSSSESSNSSDNSNSSDSSN 943
                                                                                                                                                                                                                                                                                                                                                                                                                                           81 PNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSKSHSELQTPKDSTGKS j40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 GAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKS----GADGQTPKDGSSKS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPOEEVKSSEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSASSENREGTLSDSTGSE 366
                                                                                                                                                                                                                                                                                                                                                                                 595 SSDSSNSSDSSDSSDSSDSSDSSDSKSDSSKSESD---SSDSDSKSDSSDSNSSDSS 651
                                                                                                                                                                                                                                                                                                                                 22 ATESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEPQTPKDSPSKS-SAEAQTPEDT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 PNKVVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFKTESGEETDL--IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNS---SDSSDSSNSSDSSDSSDSSDSSDSSNRSDSSNSSDSSDSSDSSDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea,
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament protein)
(Neurofilament medium polypeptide) (NF-M) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hill W.D., Zhang L., Balin B.J., Sprinkle T.J., Spicer K., Gearhart D.A.;
                                                                                                                                                 . R (IN REF. 2).
DAE240653904ED4A CRC64;
                                                                                                                                                                                                                                                                               71; Mismatches 203;
                                                                                                                                                                                                                          Score 250; DB 1;
Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              810 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
1065

80 1080

1095

1101

1132

126426 M
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                                                                                                                                                                                                Ouery Match
Best Local Similarity **...
78; Conservative
                                                             1095 109
1101 110
1104 110
1132 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEF3 OR NEFM OR NFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NFM_BOVIN
O77788;
           CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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us-09-763-902b-1.rsp

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norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 107; Conserv
                                                     NCBI_TaxID-10116,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                      SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSPHAFKTESGEETDLISPPQEEVKSSEPTEDVEP-----KEAEDDD---TGPEEGSPP 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 VVAAKKSPVKATAPELKEEEGEKEEEEGQEEEEEEEAAKSDQAEEGGSEKEGSSEKEEG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAQTIKDSTSKSHSELQTP--KDSTGKSGAEAQTPEDSPNRSGAEAKT-QKDSPSKSGSE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSPSKSSAEAQTPEDTPNKSGAEAKTQKDSSNKS-----GAEAKTQKGSTSKSG-S 114
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 VAAAGAVPLLAT-----ESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEPQTPK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nucleolar phosphoprotein pl30 (Nucleolar 130 kDa protein) (140 kDa nucleolar phosphoprotein) (Nopp140) (Nucleolar and coiled-body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQT -- TKDVPNKSGADGQTPKDGSSKSGAEDQTPKD-VPNKSGAEKQTPKDGSNKSGAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGPIDGPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-----
                                                                                                                                                                                                                                                                                                                                                                                                                                    84;
COINCIDENT WITH A CHANGE IN THE NEUROFILLAMENT FUNCTION (BY
                                                                                                                                                                                                                   Intermediate filament; Coiled coil; Neurone; Phosphorylation
                         SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                         Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                    10.0%; Score 2.0,
28.2%; Pred. No. 0.00026;
+ive 50; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKPKDVPEKKKAESPVKAESP--vKEEVP----AKPV-----
                                                                                                                                                                                                                                                                                                                                                     COIL 2B.
8 X 13 AA TANDEM REPEATS.
B8477D85560AC3F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      704 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340 KEE-KEKMSGSASSENREGTLSD----STGSEK 367
                                                                                                                                                                                                                                                                                                COIL 1B.
LINKER 12.
                                                                                                                                                                                                                                                                                                                           COIL 2A.
LINKER 2.
                                                                                                                                                                                                                                                                        COIL 1A.
LINKER 1
                                                                                                                                                               EMBL; AF091342; AAC36357.1; -.
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                                                                                                                                                                                         filament; 1.
                                                                                                                                                                                                                                                                                                                                                                    582
90799
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                            IPR001664; IF
                                                                                                                                                                                                                                                                        33
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphoprotein 1)
                                                                                                                                                                                                                                                                                                                                                                               810
                                                                                                                                                                                       Pfam; PF00038;
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01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP14_RAT
P41777;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                   NON_TER
                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                      This
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NP14_RAT
1D NP14_
AC P4177
DT 01-NC
DT 01-NC
DT 15-JU
DE NUCLE
DE phosp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289
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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
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or send an email to licensee(18b-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMON factor Nopple."

MAINTERANCE OF THE FUNDAMENTAL STRUCTURE OF THE FIBRILLAR CENTER AND LENGTION RELATED TO NUCLECUCGENESIS, MAY PLAY A ROLE IN THE MAINTERANCE OF THE FUNDAMENTAL STRUCTURE OF THE FIBRILLAR CENTER AND DENSE FIBRILLAR COMPONENT IN THE NUCLECLUGS. IT HAS INTRINSIC GTPASE AND ATPASE ACTIVITIES, MAY PLAY AN IMPORTANT ROLE IN TRANSCRIPTION CAPALYZED BY RNA POLYMERASE I (BY SIMILARIY).

-1. SUBGUIT: Interacts with Dkc1/Nap57, Nop5/Nap65 and fibrillarin.

-1. SUBGLIGLAR LOCATION: SHUTTLES ON CURVILINEAR TRACKS BETWEEN NUCLECLUGAR LOCATION. SHUTTLES ON CURVILINEAR TRACKS BETWEEN NUCLECLUGA AND CYTOPLASM. THESE TRACKS EXTEND FROM THE DENSE FIBRILLAR COMPONENT OF THE NUCLECLUGS ACROSS THE NUCLEOPLASM TO A LIMITED NUMBER OF NUCLEAR PORE COMPLEXES.

-1. PTW: THIS PROTEIN UNDERGOES RAPID AND MASSIVE PHOSPHORYLATION AND DEPHOSPHORYLATION ON CK-II AND PKC SITES. NOPPI40 IS ONE OF THE MOST PHOSPHORYLATED FROTEINS IN THE CELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 PE---PQTPKDSPSKSSAEAQTPEDT--PNKSGAEAKTQKDSSN-KSGAEAKTQKGSTSK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE-20143579; PubMed-10679015; Yang Y., Isaac C., Wang C., Dragon F., Pogacic V., Meier U.T.; Yang Y., Isaac Composition of mammalian box H/ACA and box C/D small nucleolar ribonucleoprotein particles and their interaction with the
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ion; Repeat; GTP-binding; ATP-bind
11 x 12 AA APPROXIMATE REPEATS OF
                                                                                                                                                                                                                                                      Meier U.T., Blobel G.; "Nopp140 shuttles on tracks between nucleolus and cytoplasm."; Cell 70:127-138(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 292-309 AND 563-601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14DF1BF2DE483EA3 CRC64
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ACIDIC SERINE CLUSTER 1
ACIDIC SERINE CLUSTER 2
ACIDIC SERINE CLUSTER 3
ACIDIC SERINE CLUSTER 5
ACIDIC SERINE CLUSTER 5
ACIDIC SERINE CLUSTER 6
ACIDIC SERINE CLUSTER 6
ACIDIC SERINE CLUSTER 6
ACIDIC SERINE CLUSTER 7
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SERINE CLUSTER 5
SERINE CLUSTER 6
SERINE CLUSTER 7
SERINE CLUSTER 7
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SERINE CLUSTER 1
SERINE CLUSTER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 67; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.8%; Score 241.5; DB 32.5%; Pred. No. 0.00032
                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH NOPS AND FIBRILLARIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein; Phosphorylation;
                                                                                                                                                                                                                    MEDLINE-92323542; PubMed-1623516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73562 MW;
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EMBL; M94288; AAA41719.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.58;
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16;

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PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM IS PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad., Sci. U.S.A. 85:1998-2002(1988).
-!- FUNCTION: NEUROPILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
                                                                                                                                                                                 TPAKPAPVKKKAESSS--DSSDSDSSEDEAPAKPVSATKSPLSKPAVTPKPPAAKAVATP 415
                                                                                                                                                                                                                                                                     473
                    | | | |:|:
238 DSEEEKKAAAPLKKTAPKKQVVAKAPVKVTAAPTQKSSSSEDSSSEEEEEQKKPMKKKAG 297
                                                                       -HSELQTPKDSTGKSGAEAQTPE-----DSPNRSGAEAKTQKDSPSKSGSEA 172
                                                                                                        357
                                                                                                                                                                                                                                                                                                          ADTNOLADKGKLS------PHAFKTESGEETDLISPPQEEVKSSEPTEDVEPKEAE 327
                                                                                                                                                                                                                                                                                                                                                   533
                                                                                                                                                                                                                            QGPIDGPSK------SGAEEQTS---KDSPNKVVPEQPSRKDHSKPISNPSDNKELPK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Identification of the major multiphosphorylation site in mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee V.M.-Y., Otvos L. Jr., Carden M.J., Hollosi M., Dietzschold B., Lazzarini R.A.;
                                                                                                                                                                                                                                                     298 PYSSVPPPSVSLSKKSVGAQSPKKAAAOTQPADSSADSSEESDSSSEEEKKTPAKTVVSK
                                                                                                                                                 173 OTTKDVPNKSGADGQTPKDGSSKSGAEDQTP-KDV-PNKSGAEKO--TPKDGSNKSGAEE
                                                                                                                                                                                                                                                                                                                                                 474 AGGDSSSDSESSSEEEKKTPPKPPAKKKAAGAAVPKPTPVKKAAAESSSSSSSSEDSSE
                                                                                                                                                                                                                                                                                                                                                                                          DDDTGPEEGSPPKEEKEKMSGSASSENREGTLSDSTGSEKDDLYPNGSGNGSAESS 383
                                                                                                                                                                                                                                                                                                                                                                                                                                587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schlaepfer W.W., Nelson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THELELES OF PHOSPHORILATION BEING ALTERED DEVELOPMENTALLY AND COLNCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION. SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1988 (Rel. 108, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet M. protein (160 kDa neurofilament protein)
(Neurofilament medium polypeptide) (NF-M) (Neurofilament 3).
                                                                                                                                                                                                                                                                                                                                                                                                                            534 EEKKKPKSKATPKPQAGKANGVPASON - GKAGKESEEEEDTEQNKKAAGTKPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJNE-87275853; PubMed-3608989; Myers M.W., Lazzarini R.A., Lee V.M.-Y., Schlaepfer W.W., Nels Myers M.W., Lazzarini R.A., Lee V.M.-Y., Schlaepfer W.W., Nels "The human mid-size neurofilament subunit: a repeated protein sequence and the relationship of its gene to the intermediate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1988 (Rel. 07,
01-AUG-1988 (Rel. 108,
16-OCT-2001 (Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEF3 OR NEFM OR NFM.
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PO7197;
112 SGSE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 KQTPKDGSNKSGAEEQG--PIDGPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSD 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            705 EKEVKEAPKEEKVEKKEEKP----KDVPEKKKAESPVKEEAVAEVVTITKSVKVHLEKET 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 KSHPEPQTPKDSPSKSSAEAQTPE-----DTPNKSGAEAKTQKDSSNKSGAEAKTQKGS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 TSKSGSEAQTIKDSTSKSHSELQIPKDSTGKSGAEAQIPEDSPNRSGAEAKTQKDSPSKS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKELPKADTNOLADKGKLSPHAFKTESGEETDLISPPQEEVKSSEPTEDVEPKEAEDDDT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          591 -SEEVATKEELVADAKVEKPEKAKSPVPKSPVEEKGKSPVPKSPVEEKGKSPVPKSPVEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Dentin sialophosphoprotein precursor (Dentin matrix protein-3) (DN
3) [Contains: Dentin phosphoprotein (Dentin phosphoprory)) (DPP);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   552 SEKEGS------AEAKEEKKVEEK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 GPEEGSPPKEEKEK-MSGSASSENREGTLSDSTGSEKDDLYPNGSGNGSAE 381
                                                                                                                                                                                                               coil; Neurone; Phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 x 13 AA TANDEM REPEATS.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.6%; Score 236.5; DB 1;
27.1%; Pred. No. 0.00066;
iive 47; Mismatches 150;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                 intermediate filament; Coiled
   modified and this statement entities requires a license
                                                                                                                                                                             Pfam; PF00038; filament; 1. PROSITE; PS00226; IF; 1.
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                                                                        EMBL; Y00067; CAA68276.1;
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                                                                                           PIR; A27864; A27864.
PIR; A30157; A30157.
Genew; HGNC:7734; NEF3.
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Best Local Similarity
Matches 95, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      915 AA;
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                                                                                                                                                                                                                                      Glycoprotein.
INIT_MET
                                                                                                                                              MIM; 162250;
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                                                                       Gu T.T.;
products
chromosome
                                                                                                                                                                                    MEDLINE-98211969; PubMed-9545272;
Feng J.O., Luan X., Wallace J., Jing D., Ohshima T., Kulkarni A.B.,
D'Souza R.N.; Kozak C.A., MacDougall M.;
"Genomic organization, chromosomal mapping, and promoter analysis of
the mouse dentif slatophosphoprotein (Dspp) gene, which codes for both
dentin staloprotein and dentin phosphoprotein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: DSP may be an important factor in dentinogenesis. DPP may bind high amount of calcium and facilitate initial mineralization of dentin matrix collagen as well as regulate the size and shape of the crystals.

SUBCELLULAR LOCATION: Secreted (By similarity).

TISSUE SPECIFICITY: Expressed in teeth, mainly in odontoblasts and pran: DSP is glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Dentinogenesis imperfecta 1 with or without progressive hearing loss is associated with distinct mutations in DSPP."; Nat. Genet, 27:201-204(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ritchie H.H., Berry J.E., Somerman M.J., Hanks C.T., Bronckers A.L., Hotton D., Papagerakis P., Berfall A., Butler W.T.; "Dentin sialoprotein (DSP) transcripts: developmentally-sustained expression in odontoblasts and transient expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S., Yu C., Chou X., Yuan W., Wang Y., Bu L., Fu G., Qian M., J., Shi Y., Hu L., Han B., Wang Z., Huang W., Liu J., Chen Z., G., Kong X.;
                                                                     MacDougall M., Simmons D., Luan X., Nydegger J., Feng J.O., "Dentin phosphoprotein and dentin sialoprotein are cleavage expressed from a single transcript coded by a gene on human 4. Dentin phosphoprotein DNA sequence determination."; J. Biol. Chem. 272:835-842(1997).
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAND-Liver; STRAIN-129/SVJ; TISSUE-Liver; Sfair C., Buller S., Lin E., George A., Veis A.; From mouse to zebrafish-dentin matrix proteins genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Stallc acid,
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                                                                                                                                                                                                                                                                                                                                                             characterization.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                         SEQUENCE FROM N.A., AND REVISIONS TO C-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SER/ASP-RICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ002141; CAA05208.1; ALT_SEQ
EMBL; AF135799; AAD42781.1; ALT_SEQ
                                          STRAIN-Swiss Webster; TISSUE-Molar; MEDLINE-97150835; PubMed-8995371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21096982; PubMed-11175790;
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98055479; PubMed-9395101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:109172; Dspp.
Signal; Extracellular matrix;
Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U67916; AAC12787.1; -..
                                                                                                                                                                          /SvJ; TISSUE-Liver
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934
451
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NCBI_TaxID=10090;
                            FROM
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Pai C.-Y., Chen H.-K., Sheu H.-L., Yeh N.-H.; "Cell-cycle-dependent alterations of a highly phosphorylated nucleolar protein pl30 are associated with nucleologenesis."; J. Cell Sci. 108:1911-1920(1995).
                                            (POTENTIAL).
(BY SIMILARITY).
(BY SIMILARITY).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DINOLADKGKLSPHAFKTESGEETDLISPPQEEVKSSEPTEDVEPKEAED-DDTGPEEGS
                               (POTENTIAL)
                                                                                                                             (POTENTIAL)
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                                                                                                           (POTENTIAL
                                                                                                                                                                                                           (POTENTIAL)
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sannotation update)
10-0CT-2001 (Rel. 40)
Nucleolar phosphoprotein plo (Nucleolar 130 kDa protein) (140
nucleolar phosphoprotein) (Noppl40) (Nucleolar and coiled-body
                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                              (POTENTIAL)
                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                         (POTENTIAL
                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                          .Length - 934;
                                                                                                                                                                                                                                                                       9.5%; Score 234; DB 1; Length 93
20.5%; Pred. No. 0.00086;
.ive 69; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 PPKEEKEKMSGSASSENREGTLSDSTGSEKDDLYPNGSGNGSAESS 383
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                                                                             CK1)
CK2)
CK2)
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N-LINKED (GLCNAC. . .) (P
A618789D8A57249A CRC64;
                                                                            PHOSPHORYLATION (BY C PHOSPHORYLATION (BY C PHOSPHORYLATION (BY C PHOSPHORYLATION (BY C
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                                                              PHOSPHORYLATION
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MEDLINE=95386590; PubMed=7657714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IISSUE-Bone marrow;
MEDLINE=96051387; PubMed=7584026;
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Mammalla; Eutheria; Primates;
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Homo sapiens (Human).
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934 AA;
                                                                                                                                                                                                                                                                                      Local Similarity
les 71; Conserv
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NOLC1 OR KIAA003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: SHUTTLES BETWEEN THE NUCLEOLUS AND THE CYTOPLASM. AT TELOPHASE IT BEGINS TO ASSEMBLE INTO GRANULAR-LIKE PRE-NUCLEOLAR BODIES WHICH ARE SUBSEQUENTLY RELOCATED TO NUCLEOLI AT THE EARLY G1-PHASE. ALTENATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                        Chen H.-K., Pai C.-Y., Huang J.-Y., Yeh N.-H.;

Chen H.-K., Pai C.-Y., Huang J.-Y., Yeh N.-H.;

"Human Noppl40, which interacts with RNA polymerase I: implications
for TRNA gene transcription and nucleolar structural organization.";

MOI. Cell. Biol. 19:8536-8546(1999)

-1- FUNCTION: RELATED TO NUCLEOLOGENESIS, MAY PLAY A ROLE IN THE
MAINTENNACO OF THE FUNDAMENTAL STRUCTURE OF THE FIBRILLAR CENTER
AND DENSE FIBRILLAR COMPONENT IN THE NUCLEOLUS. IT HAS INTRINSIC
GTPASE AND ATPASE ACTIVITIES. MAY PLAY AN IMPORTANT ROLE IN
TRANSCREPTION CATALIZED BY RNA POLYMERASE I.

-1- SUBUNIT: INTERACTS WITH NA POLYMERASE I 194 KDA SUBUNIT (RPA194)

AND WITH CASEIN KINASE-II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: THIS PROFIEIN UNDERGOES RAPID AND MASSIVE PHOSPHORYLATION AND DEPHOSPHORYLATION ON CK2 AND PKC SITES. THERE IS EVIDENCE SUGGESTING THAT CDC2 KINASE PHOSPHORYLATES P130 AT THE M-PHASE.
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                                                                                                                                                                                                                                                                                                 "The nucleolar phosphoprotein P130 is a GTPase/ATPase with intrinsic property to form large complexes triggered by F and Mg2+."; Biochem. Biophys. Res. Commun. 230:370-375(1997).
        Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
"Prediction of the coding sequences of unidentified human genes. I.
The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
analysis of randomly sampled cDNA clones from human immature myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear protein; Phosphorylation; Repeat; GTP-binding; ATP-binding;
                                                                                                                                                                 Pai C.-Y., Yeh N.-H.; "Cell proliferation described of two isoforms of the nucleolar phosphoprotein pl30."; Blochem. Blophys. Res. Commun. 221:581-587(1996).
Kawarabayasi Y.,
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NUCLEAR LOCALIZATION
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                                                                                                                                                                                                                                                      CHARACTERIZATION.
MEDLINE-97168979; PubMed-9016786;
                                                                                                                                 ALTERNATIVE SPLICING.
MEDLINE-96205319; PubMed-8630004;
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3336
436
529
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Res. 1:27-35(1994).
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Alternative splicing.
                                                                                                                                                                                                                                                                                        Chen H.-K., Yeh N.-H.;
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 Nomura N.,
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21;
            NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY CK2) (BY SIMILARITY).
K -> KVWTITSYARE (IN ISOFORM BETA).
D -> A (IN REF. 2).
R -> S (IN REF. 2).
X -> SV (IN REF. 2).
S -> P (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 KAAESSS--DSSDSDSSEDD---EAPSKPAG---TTKNSSNKPAVTTKSPAVKPAAPKQ 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409 PVGGGQKLLTRKADSSSSEEESSSSEEEKTKKMVATTK--PKATAKAALSLPAKQAPQGS 466
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                                                                                                                                                                                                                                                                             117 GKAAAKASESSSSEESRDDDDEEDQKKQPVQKGVKPQAKAAKAPPKKAKSSDSDSDSSSE 176
                                                                                                                                                                                                                                                                                                                                                                                  102 A---KT--QKGSTSKSGSEAQTT-----KDSTSKSHSELQ-------131
                                                                                                                                                                                                                                                                                                                ----EDTPNKSGAEAKTQKDSSNKSGAE 101
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MEDLINE-98184255; PubMed-9525343;
MCDOUGAIL M., Gu T.T., Luan X., Simmons D., Chen J.;
"Identification of a novel 1soform of mouse dentin matrix protein 1:
spatial expression in mineralized tissues.";
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                              GAVPLLATESVKQEEA-----SLSQRPGGST 54
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                 Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40) Last annotation update)
Dentin matrix acidic phosphoprotein 1 precursor (Dentin matrix
                                                                                                                                                                            Length 699;
                                                                                                                                             DFD4AD94EDF659FB CRC64;
INTERACTS WITH RPA194.
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                                                                                                                                                                                                               78; Mismatches 217;
                                                                                                                                                                              9.4%; Score 232; DB 1; 22.9%; Pred. No. 0.00081;
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                                                                                                                                                 73720 MW;
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Matches 119; Conservative
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699 AA;
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J. Bone Miner. Res. 13:422-431(1998)

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                                                                                                                                                                               TISSUE SPECIFICITY: EXPRESSED IN TOOTH PARTICURLARLY IN ODONTOBLAST, AMELOBLAST AND CEMENTOBLAST, ALSO EXPRESSED IN BONE PARTICULARLY IN OSTEOBLAST.
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DENTIN MATRIX ACIDIC PHOSPHOPROTEIN
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25.8%; Pred. No. 0.00095;
tive 54; Mismatches 172;
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                        STRAIN-129/SvJ; TISSUE-Spleen;
Feng J.Q., Tralanedes K., Luan X.,
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MGI:94910; Dmp1.
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SEQUENCE FROM N.A
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Search completed: March 4, 2003, 14:59:37

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RESULT 1
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    (without alignments)
    3007.543 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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	Description	096q12 homo sapien	Q95193 macaca fasc	. Q63575 rattus norv	Q62314 mus musculu	Q62313 mus musculu	Q932c5 staphylococ	Q99vj4 staphylococ	. 086476 staphylococ	Q53653 staphylococ	. 035482 rattus norv	Q9ki14 staphylococ	Q99r07 staphylococ	. Q28688 oryctolagus	Q28687 oryctolagus	Q96hf8 homo sapien	Q8sy55 drosophila	
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op	Query	90.1	73.6	27.6	.27.2	\$27.0	11.8	11.7	11.5	11.5	11.5	11.2	11.2	11,1	11.1	10.9	10.9	
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$\vdash$	Q95xw8 caenornabui Q9n973 leishmania	Q91803 xenopus lae	Q9vnx6, drosophila	Q8vbyl rattus norv	070022 staphylococ			. Q9bkv7 leishmania	Q9vel9 drosophila	S			ഗ	ന	Q9n435 caenorhabdi	Q9buv3 homo sapien	•	-		9	O	Obdyx7 mus musculu			drosc	Obj135 mus muscuin
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266.5 258.5	258 258	251	246	245	242.5	238.5	238.5	238.5	238.5	238	236.5	234.5	234.5	233.5	233.5	C	232	231.5	0	229.5	228	228	227.5	227.5	227.5	227
17	19	21	22	23	24	25	56	27	8	50	30	31	32	33	34	32	36	37	38	30	40	41	42	43	44	45

## ALIGNMENTS

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						,						Sđi	09	09	120	120	180	180	240	240
L2 L2 Q96QL2 PRELIMINARY; PRT; 437 AA.	. 19, Creat	01-DEC-2001 (TremBirel. 19, Last sequence update) 01-DEC-2001 (TremBirel. 19, Last annotation update)	Unknown (protein for MGC:14722).	Homo sapiens (Human). Enternata: Matazoa: Chordata: Craniata: Vertebrata: Euteleostomi;	Catarrhini; Hominidae;	NCBI_TaxID=9606;	SEQUENCE FROM N.A.	straight R :	Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.	EMBL; BCUUS401; AAHU0401.1; SEQUENCE 437 AA; 45865 MW; AA9734041CD74EFC CRC64;		BEST LOCAL SIMILATILY 33.3%; FIGU. NO. 3.26 113, Medels 0; Gaps Matches 434; Conservative 1; Mismatches 1; Indels 0; Gaps				61 QTPKDSPSKSSAEAQTPEDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTK 1	121 DSTSKSHSELQTPKDSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPN 1			181 KSGADGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGA 2
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	EEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFKTESGE 	ETDLISPQEEVKSSEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSASSENREGTLS 	DSTGSEKDDLYPNGSGNGSAESSHFFAXLVTAAILVAVLYIAHHNKRKIIAFVLEGKRSK	1795					precursor	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecidae; Macaca.		,	G.;	1	RAFFI	. PRIMARILY : NETWORK AND ().	ck.	POIENTIAL. TRANS-GOLGI NETWORK INTEGRAL MEMBRANE DEPOMENTAL MONTAL		SIMILARITY).			•				(POTENTIAL)
	ADKGK          	(EKMSG	HNKRK	IDNAKA				te)	0 / PN	ta; Edithec			arren	· }	RANE 1	N. PRI I NETW	Glycoprotein; Repeat; Golgi.stack	INTEG	EXTRACELLULAR (POTENTIAL) POTENTIAL	(AL). (BY SI							:: EE
	ADTNOI 	PPKEEF	VLYIAL					(TrEMBirel. 02, Created) (TrEMBirel. 02, Last sequence update) (TrEMBirel. 15, Last annotation update)	orn TG	tebra	•		G. C.E		MEMB	ROTEII -GOLG: ILARI	; Gole	TWORK	(POTE	LASMIC (POTENTIAL) YTOSIS SIGNAL (BY							 
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	SNPSDN           SNPSDN	SDDDTG 	AYLVTA			•	PRT;	Created) Last sequences	marane.	aniat			O M.L.	•	REGUI	MEMBH N THE MES (E	ein; F	NS-GOL	RACELL	CYTOPLASMIC ENDOCYTOSIS 15 X 14 AA A						. 6	N-LINKED
	HSKPI       HSKPI	EPKEA!	SSHFF				F.	Crea	ating	s, Cr		TISSUE=EFIDIDYMIS; MEDLINE=97063845; Pubmed=8907712;	Yasp ied M TGN38	. (96)	ED IN	YPE I ETWEEI NDOSOI	oprot(	TRAI	EXT	CYTC ENDC	4.4.	m' <del>∢</del> i	v. é. c.	805	1225	14.	Z Z
	PSRKD 	PTEDV	NGSAE	436	436		RY;	(TrEMBLrel. 02, C (TrEMBLrel. 02, I (TrEMBLrel. 15, I	Crab e	hordat rimate ca.		4ed=89	ct M., I., Fr Frat	18."; 585(19	INVOLV	ION: T	Glyc							•			
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	KDSPN               KDSPN	SPPQEI	EKDDL) 	VTRRPKASDYQRLDQK	KASDYO		PREI	(TrE	tcula	Eukaryota; Metazoa; Cho Mammalla; Eutheria; Pri Cercopithecinae; Macaca	N MON	63845 63845	S., N11	1mpli 109	N: MA	HECELLULAR LOCATION SIGI NETWORK, CYCLES REFACE RETURNING VI	Transmembrane	50.	390	411 438 54	88.00 68.00	200	124	152. 166	194 202 216	244	96
	EEQTS   - -  EEQTS	ETDLI       ETDLI	DSTGS        DSTGS	VTRRP	VTRRP	,	ന ന	B-199	og). afase	yota; 11a; P	NCE FF	1143=3 04-37	nbalam ıma T. ıte ho	lonal 11 Sci	NCTIC SOM TR	JBCELL SLGI N JRFACE	Tra		EM				٠			Q.	Z Q
	241	301	361		421	CT 2	Q95193 Q95193:	01-FEB-1997 01-FEB-1997 01-OCT-2000	homolog). Macaca fasci	Eukar Mamma Cerco	[1] SEQUENCE FROM N.A.	MEDLI	Ponna Sugan	funct. J. Cei	트립 -	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. PRIMARILY GOLGI NETWORK. CYCLES BETWEEN THE TRANS-GOLGI NETWORK AND SURFACE RETURNING VIA ENDOSOMES (BY SIMILARITY).	Signal;	CHAIN	DOMAIN TRANSMEM	DOMAIN DOMAIN DOMAIN	REPEAT REPEAT PEDEAT	REPEAT PEDEAT	REPEAT REPEAT	REPEAT REPEAT REPEAT	REPEAT REPEAT REPEAT	REPEAT REPEAT CARBOHYD	CARBOHYD
	Oy Dp	oy D	oy Oy	ò ,	<b>Q</b>	RESULT	-	5555		88,88	5 % d 2				•				FT		•						
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                                                                                                                                                                                                                                                                                                                                                                                 OM N.A.

GUE-DAWLEY, TISSUB-LIVER;
46851; PubMed-1575675;
Wilde A., Banting G.;
tion, molecular characterisation and immunolocalisation of
5t the trans-Golg1.network (TGN)-specific integral membrane
38.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    QTTKDVPNKSGADGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFKTESGEETDLISPPQEEVKSSEPTEDVERKEAEDDTGPEEGSPPKEEKEKM 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENREGTLSDSTGSEKDDLYPNGSGNGSAESSHFFAYLVTAAILVAVLYIAHHNK 406
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                                                                                                                                                                                                                            POTENTIAL.
TRANS GOLGI NETWORK
(TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN
TGN38.
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Wiberia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
network (TGN) specific integral membrane protein TGN38
                                           (POTENTIAL) (POTENTIAL) (POTENTIAL) (POTENTIAL)
                                                                                                                                                                             20;
                                                                                                                             73.6%; Score 1811; DB 6; Length 445; nilarity 80.9%; Pred. No. 3.8e-96; Conservative 26; Mismatches 40; Indels 2
194 N-LINKED (GLCNAC. .) (PC 216 N-LINKED (GLCNAC. .) (PC 230 N-LINKED (GLCNAC. .) (PC 289 N-LINKED (GLCNAC. .) (PC 385 N-LINKED (GLCNAC. .) (PC 46757 MW; C994B289A37DFAC4 CRC64;
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380
                                                         289
385
445 AA;
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FT DOMAIN 18 308 FT TRANSMEM 309 329 FT DOMAIN 330 329 FT SITE 356 359 FT SOMAIN 133 148 FT REPEAT 141 148 FT REPEAT 149 156 FT REPEAT 147 164 FT REPEAT 173 180 FT REPEAT 164 FT REPEAT 164 FT REPEAT 164 FT REPEAT 165 172 FT REPEAT 165 173 FT REPEAT 164 F	Query Match 27.2%; Best Local Similarity 39.7%; Matches 17.7; Conservative 4 OY 1 MREVVALVILINVAAAGAVPILAY Db 1 MREVVALLILISVAVARAL OY 61 OTPKDSPSKSSAEAQTPEDTPNI Db 32 QNPPNQPSKQSSTPLPPI	OY 115 EAQTTKDSTSKSHSELQTPKDS'  DB 87 GPPTAATDHSLGDSRRQPEK  OY 175 TKDVPNKSGADGQTPKDGSSKS(  131 TEDSGKPTGGNSGRPTGGD  OY 235 PSKSGAEEQTSKDSPNKVVPEQI  DD 163 PTEAGSNKATEDDSGK  OY 295 KTESGEETDLISPQEEVI	0 6 6 4 E	RESOLUT 3 062313 AC 062313 AC 062313 DT 01-NOV-1996 (TYEMBLEEL 01, DT 01-NOV-1996 (TYEMBLEEL 19, DE 01-DEC-2001 (TYEMBLEEL 19, DE Trans-9604g1 network protein 1) (T GN TYGNI.  OS MUS musculus (Mouse).  OC Eukaryota, Metazoa; Chordat OC Eukaryota; Eutheria; Rodenti OX NCBL_TAXID=10090;  RN (13) RN (11) RR SEQUENCE FROM N.A. RC STRAIN=ICR; TYSSUE-BRAIN; RX MEDLINE-95301533; Pubmed-75 RASAI K., TAKANASHI S., MUR RT "Strain-specific presence o
· · ·	· ·		·	
. 13;				
SEQUENCE   380 AA;   40990 MW;   B8DDC8C25E35B661 CRC64;	177 DVPNKSGADG 177 DVPNKSGADG 137 DSDNTTGGD- 237 KSGAEEQTSK 166TGS	213 ESGEKLA 353 ENREGTL 273 ENREGTL 273 ENGEGRE 413 VLEGKRS 11111 333 ALEGKRS SULT 4 2344	062314; 062314; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence 01-DEC-2001 (TrEMBLrel. 19, Last annotati Trans-golgi network integral membrane pro- golgi network protein 2) (TGN38 homolog). TGOLN2 OR TTGN2. Mus musculus (Mouse) Eukaryota Metazoa; Chordata; Craniata; V Mammalia; Eutheria; Rodentia; Sciurognath	RN [1]  RC STRAIN-ICR; TISSUE-BRAIN;  RX MEDLINE-95301533; PubMed-7540170;  RX MEDLINE-95301533; PubMed-7540170;  RX MEDLINE-95301533; PubMed-7540170;  RX MEDLINE-95301533; PubMed-7540170;  RY "Strain-specific presence of two TGN38 isoforms and absence of TGN41  RT "Strain-specific presence of two TGN38 isoforms and absence of TGN41  RY "Strain-specific presence of two TGN38 isoforms and absence of TGN41  RY "Strain-specific presence of two TGN38 isoforms and absence of TGN41  RY "STGNIL STORE TROUGHER TYPE IN TRANS-GCC TO TO THE TRANS-GCC TO TYPE IN TAXAS-TO TYPE
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1, Created)
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all membrane protein TGN38A precursor (Trans-(TGN38 homolog)
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urakami K., Nakayama K.;
of two TGN38 isoforms and absence of TGN41
                                                                                                                                                                                                                                                                                                                                                                                                      ATESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ta; Craniata; Vertebrata; Euteleostomi;
. a; Sciurognathi; Muridae; Murinae; Mus.
PROTEIN TGN38B.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
ENDOCYTOSIS SIGNAL (BY SIMILARITY).
7 x 8 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
2826FA9E958C5C27 CRC64;
                                                                                                                                                                                                                                                                                                                                                               94;
                                                                                                                                                                                                                                                                                                                        Length 363;
                                                                                                                                                                                                                                                                                                                        ; Score 668; DB 11; Length 36; Pred, No. 5.6e-31; 49; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||: |
||: |
||: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLDQK 436
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                                                                             Strausberg R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
FROM TRANS-GOLGI NETWORK.
SUBMITTED STATES INTROPER IN TYPE I MEMBRANE PROTEIN. PRIMARILY IN TRANS-GOLGI NETWORK. CYCLES BETWEEN THE TRANS-GOLGI NETWORK AND THE CELL SURFACE RETURNING VIA ENDOSOMES (BY SIMILARITY).
SURFACE RETURNING VIA ENDOSOMES (BY SIMILARITY).
SUBSCELLANEOUS: ALSO FOUND IN STRAINS BALB/C, C57BL/6 AND DBA/2.
EMBL; D50031; BAA085571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSENREGILSDSTGSEKDDLYPNGSGNGSAESSHFFAYLVTAAILVAVLYIAHHNKRKII 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTESGE----ETDLISPPQEEVKSSEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 KTESGETLAGDSDFSLKPEKGDKSSEPTEDVETKEIEEGDTEPEEGSPLEEENEKVPGPS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QTPKDSPSKSSAEAQTPEDTPNKSGAEAKT-----QKDSSNKSGAEAKTQKGSTSKSGS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAQTIKDSISKSHSELQIPKDSIGKSGAEAQIPEDSPNRSGAEAKIQKDSPSKSGSEAQI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKDVPNKSGADGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MREVVALVLLNVAAAGAVPLLATESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEP 60
                                                                                                                                                                                                                                                                                                                                                                                        TRANS-GOLGI NETWORK INTEGRAL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ONPPNOPSKOSS - - - - - TPLPSSNOVKTTRPTDGGGGKSDKKDQDKTTLAAVSSKAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 TEDSGKPTGGNSGKPTGGDSGK------PTEAGSNKAT-EDDSGKS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -------TKVDLDKPTSKISPDTETSKTDKVQPTEKGQKPTLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
ENDOCYTOSIS SIGNAL (BY SIMILARITY)
6 X 8 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..) (POTENTIAL) ...) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 664; DB 11; Length 353;
; Pred. No. 9.3e-31;
46; Mismatches 119; Indels 104;
                                                                                                                                                                                                                                                                                                                                           ransmembrane; Glycoprotein; Repeat; Golgi stack
                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (P
N-LINKED (GLCNAC. . .) (P
95C340C2F4A21EB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN TGN38A.
in mouse.";
J. Biol. Chem. 270:14471-14476(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFVLEGKRSKVTRRPKASDYQRLDQK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37848 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.0%;
                                                                                                                                                                                                                                                                               EMBL, BC009143; AAH09143.1;
MGD; MG1:105080; Ttgn1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRFQVALLLLSVAVARAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 39.7
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 AA;
                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                           MGD; MG
                                                                                                                                                                                                                                                                                                                                               Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411
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RESULT

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535 SGDGIDKPVVPEQPDEPGEIEPIPEDSDSDSPGSDSGSDSGSDSGSDSGSDSGSDSA 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDSDSASDSDSASDSDSASDSDSASDSDSASDSDSASDSD----SASDSDSASD 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGADGQTPKDGSSKSGAEDQTPKDVPNK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNP 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDNKELPKADTNQLADKGKLSPHAFKTESGEETDLISPPQEEVKS-SEPTEDVEPKEAED 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 AGNVSTHPSLSQRPG--GSTKSHPE-----PQTPKDSPSKSSAEAQTPEDTPNKSGAEAK 89
                                                                                                                                                                                                                                                                                                                                MEDLINE-21111952; PubMed-11418146; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Kuroda M., Ohta T., Uchiyama I., Baba T., Itan J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mulzutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekintzu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDTGPEEGSPPKEEKEKMS - - GSASSENREGTLSDSTGSEKDDLYPNGSGNGSAESS 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                       Staphylococcus aureus (strain Mu50 / ATCC 700699).
Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.8%; Score 289; DB 16; Length 935; 22.1%; Pred. No. 6.4e-09; ttive 83; Mismatches 181; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
SEQUENCE 935 AA: 96950 MW; DC5A2D92CE3BA91C CRC64;
                                                                                                    Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001515; BPD_transp.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR01167; LBYTG_anchor; 1.
TIGRRAMS; TIGR01164; VSIRK_signal; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Fibrinogen-binding protein A, clumping factor.
CLFA OR SA0742
                                                                             Last sequence update)
                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP003360; BAB56973.1; -.
                                         01-DEC-2001 (TrEMBLEL 19, 01-DEC-2001 (TREMBLEL 19, 01-JUN-2002 (TREMBLEL 21, Flbrinogen-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N. A.
                                                                                                                                                                                                                                                          NCBI_TaxID=158878;
                                                                                                                                                      FNB OR SAV0811
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Q99VJ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aureus.
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us-09-763-902b-1.rspt

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284 ADKGKLSPHAFKTESGEETDLISPPQEEVKSSEPTEDVEPKEAEDDDTGPEEGSPPKEEK 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 TQKGSTSKSGSEAQTTKDSTSKSHSELQTPKDSTGKSGAEAQTPEDSPNRSGAEAKTQKD 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 SGAEEQGPIDGPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 PSLSQRPGGSTKSHPEPQTPKDSPSKSSAEAQTPEDTPNKSGAEAKTQKDSSNKSGAEAK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McDevitt D., Francois P., Vaudaux P., Foster T.J.;
Molecular characterization of the clumping factor(fibrogen receptor
                                                       STRAIN-YERWMAN;
MI Eidhin D., Perkins S., Francois P., Vaudaux P.;
Clumping factor BCLifb), a new surface-located fibrinogen-binding
adhesin of Staphylococcus aureus.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ224764; CAA12115.1;
Interpro; IPRO01899; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor;
TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
TIGRFAMS; TIGR01168; YSIRK_Signal; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 SPSKSGSEAQTTKDVPNKSGADGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          850 KAPSNPKGEVNHSNKVSK---QHKTDALPETGDKSENTNATLFGAMM--ALLGSLLLF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 11.5%; Score 284; DB 2; Length 91:
Best Local Similarity 21.4%; Pred. No. 1.2e-08;
Matches 78; Conservative 76; Mismatches 191; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  CLUMPING FACTOR B. 38077C321F8D3E61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    933 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q53653 PRELIMINARY; PRT; Q53653; 01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94224142; Pubmed-8170386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Microbiol, 11:237-248(1994)
EMBL; Z18852; CAA79304.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000515; BPD_transp
                                                                                                                                                                                                                                                                                                                                                                                         44 PO
913 CL
97247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus
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45 9
913 AA;
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           [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus.
NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clumping factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-NEWMAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 802 SD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
Q53653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 SHSELQTPKDSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGAD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 GQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 KDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFKTESGEETDLI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPPQEEVKSSEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMS--GSASSENREGTLSDST 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 SPSKSSAEAQTPEDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  865 SDSESD---SDSDSDSDSDSASDSDSGSDSDSSSSDSDSTSDTGSDNDSDSDSDSDSES 921
                                                                                                                                                             MEDLINE-21311952; PubMed=11418146; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Curoda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y. Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M. Ogasawara N., Hayashi H., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 989;
Staphylococcus aureus (strain N315).
Bacteria: Firmicutés; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Foster T.J.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      989 AA; 102407 MW; DA6E807539623467 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP003131; BAB41975.1; -.
InterPro; IPR000315; BPD_transp.
InterPro; IPR01899; Gram_pos_anchor.
IGGRFAMs; TIGR01167; LPXTG_anchor; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.7%; Score 286.5; DB 16; 22.2%; Pred. No. 9.5e-09; Live 78; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       913 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 GSEKDDLYPNGSGNGSAESS 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          922 GSNNNVVPPNSPKNGTNASN 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-JUN-2002%(TrEMBLrel. 21, Clumping factor B precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Jancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 22.2% tes 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
SEQUENCE 989 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                               Staphylococcus.
WCBI_TaxID=158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus.
NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-NEWMAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       086476
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086476
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Gaps 28;

248

KSGAEDOTPK

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329 898 374

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Query Match

SOR

Best Loc Matches

535

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595 150 655 210 715 775

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AEEAASPEKETKSPVKEEAKSPAEAKS----PAEAKSP-AEAKSPAEVKSPAEVKSPAEA 550
                                                                                                                                                                                                                               KSHSELQIPKDSTGKSGAEAQIPED--SPN--RSGAEAKIQKD-----SPSKSGSEA 172
                                                                                                                                                                                                                                                                                                                                                             ---PAKLGVKEEAKPKEKA---EDAKAKEPSKPSEKEKPKKE 994
                                                                                                                                        KSSAEAQTPEDTPN----KSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTS 124
                                                                                                                                                                              KSPAEAKSPAEVKSPATVKSPAEAKSPAEA--KSPAEVKSP--ATVKSPGEAKSPAE--A 604
                                              AAAGAVPLLATESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEPQTPKD--SP--S 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in Staphylococcus
                                                                                                                                                                                                                                                            -- DIGPEEGSPPK-EEKEKMSGSASSENREGILSDSIGSEKDDLYPNG
                                                                                                                                                                                                                                                                                                                                                                                                                        -GPSKSGAEEQTSKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAKPPAEAKSPAEAKSPAEAKSPAEAKSPAEAKSPVEVKSPEKAKSPVKEGAKSLAEAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---TDLISPPQEEVKSSEPTEDVE----PKEAEDD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              941 PADIRSPEQVKSPAKEEAKSPEKEETRTEKVAPKKEEVKS--PVEEVKAKEPPKKVEEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KDSPGEAKKEEAKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGNGSAESSHFFAYLVTAAILVAVLYIAHHNKRKIIAFVLEGKRSKVTRRPKASDYQRLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wccrea K.W., Hartford O., Davis S., Ni Eidhin D., Lina G.
Speziale P., Foster T.J., Hook M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microbiology 146:1535-1546(2000).

EMBL; AF245041; AAF72509:1; -
Interpr.: IRPO/H601899; Gram_pos_anchor.

Pfam: PF00746; Gram_pos_anchor; 1.

PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.

SEQUENCE 1733 AA; 184720 WW; D8D652EA1692FD4E8 CRC64;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The serine-aspartate repeat (Sdr) protein family
  Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNKVVPEQPSRKDHSKPISNPSDNK-ELPKADTNQLADKGKL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 276.5; DB 2 Pred. No. 6.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                          D----VPNKSGAEKQTPKDGSN----KSGAEEQGPID--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        899 ТРАТРКТЕVКЕSККОЕАРКЕАОКРКАЕЕКЕРLTEKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435 OKYVLILNVEPAPPKRSFLPQVLTEWYIPLEK 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative cell-surface adhesin SdrF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20340957; PubMed-10878118;
    86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.2%; 22.0%;
                                                                                                                                                                                                                                                                                                                                   QTTKDVPNKSGADGQTPKDGSS
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SPHAFKTESGEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus.
NCBI_TaxID=1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epidermidis."
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    144;
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    Matches
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MEDLINE-91038277; PubMed-2230956;
Chin S.S., Liem R.K.;
"Transfected rat high-molecular-weight neurofilament (NF-H)
coassembles with vimentin in a predominantly nonphosphorylated form.";
J. Neurosci. 10:3714-3726(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSKSHSELQTPKDSTGKSGAEAQTPED 149
                                                                                                                                                                                                                                                                                                                                                                                                                            SPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGADGQTPKDGSSKSGAEDQTPKDVPNK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCDGIDKPVVPEQPDEPGEIEPIPEDSDSDPGSDSGSDSNSDSGSDSGSDSTSDSGSDSA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                    37 AGNVSTHPSLSQRPG--GSTKSHPE-----PQTPKDSPSKSSAEAQTPEDTPNKSGAEAK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKEAEDDDTGPEEGSPPKEEKEKMSGSASSENREGTLSDS-TGSEKDDLYPNGSGNGSAE
                                                                                                                                                                                                                                                                                                                                                                              SGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDNKELPKADTNQLADKGKLSPHAFKTESGEETDLISPPQEEVKS----SEPTEDVE
                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chin S.S.M.; Liem R.K.H.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                               Length 933;
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coil; Intermediate filament.
E 1072 AA; 115349 MW; 89A146D457A4D78B CRC64;
InterPro; IPR001899; Gram_pos_anchor.
TIGRRAMs; TIGR01167; LPXTG_anchor; L.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
PROSITE; PS000443; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 933 AA; 97058 MW; EB51A6DE2FF759F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                          11.5%; Score 284; DB 2; 1
22.1%; Pred. No. 1.2e-08;
ive 83; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 283; DB 11;
Pred. No. 1.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1072 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High molecular-weight neurofilament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.5%; 25.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00038; filament; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 19,
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00226; IF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1072 AA;
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Best Local Similarity
                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      884 SN 885
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Coiled

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PGGSTKSHPEPQTPKDSPSKSSAEAQTPEDTPNK-SGAEAKTQKDSSNKSGAEAKTQKGS 108
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J. Biol. Chem. 267:17354-17361(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M94316; AAA57153.1; -.
InterPro; IPR001386; Histone_H1/H5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-X/J; TISSUE-BRAIN;
MEDLINE-92381055; PubMed-1512270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55057 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         343 KEKMSGSASSENREGTL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --KSENTNATL 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0624; HISTONEHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 24.19
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  511 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                    176 KDVPNKSGADGQIPKDGSSKSGAEDQIPKDVPNKSGAEKQIPKDGSNKSGAEEQGPIDGP 235
                                                                                                                                                                                                                                                                                                                                                                                                          TESGEETDLISPPQEEVKS----SEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSA 350
                                                                                                                                   116 AQTTKDSTSKSHSELQTPKDSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 S-SENREGTLSDSTGSEKDDLYPNGSGNGSAESSHFFAYLVTAAILVAVLYIAHHNKRKI 409
                                            SHPEPQTPKDSPSKSSAEAQTPEDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-S. aureus (strain Mu50), and S.aureus (strain N315);
MEDLINE-21311952; PubMed-11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cul L., Oguchl A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekinizu K., Hirakawa H., Kubara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
                                                                                                                                                                                                                                                                                                                      SKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.2%; Score 274.5; DB 16; Length 877; 24.6%; Pred. No. 4.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3acteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            taphylococcus aureus (strain Mu50 / ATCC 700699), and
taphylococcus aureus (strain N315).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93649 MW; FOEF0A57AFDB357F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGRFAMS; TIGRO1167; LPXTG_anchor; 1.
IGRFAMS; TIGRO1168; YSIRK_Signal; 1.
PROSITE; PSO0343; GRAM_POS_ANCHORING; UNKNOWN_1
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP003366; BAB58792.1; -.
EMBL; AP003138; BAB43728.1; -.
InterPro; IPR001899; Gram_pos_anchor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JUN-2001 (TrEMBLrel. 17,
-JUN-2001 (TrEMBLrel. 17,
-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1717 LGALLLGRRRKKDNKEK 1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 IAFVLEGKRSKVTRRPK 426
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LFB OR SAV2630 OR SA2423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 24.6
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete | SEQUENCE
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                                            26
                                                                                                                                                                                1434
                                                                                                                                                                                                                                                                                                                                                                                                          296
Matches
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201 QTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPS----KSGAEEQTSKDSPNKVVPEQ 256
  612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 EAQTPE--DSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGADGQTPKDGSSKSGAED 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFKTESGEETDLISPPQEEVKSSE 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 EAKSPEKAKSPEKAKSPVKEEAKSPEKAKSPVEVKSPAEAKSPEKAKSPVKEEAKSPAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 TESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEPQTPKDSPSKSSAEAQTPEDTPN 82
                                                           TSKSGSEAQTTKDSTSKSHSELQTPKDSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKS
                                                                                                  GSEAQTTKDVPNKSGADGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEE
                                                                                                                                                                                                                                                                                                                                            289 LSPHAFKTESGEETD-LISPPQEEVKS-SEPTEDV----EPKEAEDDDTGPEEGSPPKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  554 PEPSPOPEPEP-TPDPEPSPOPEPSPDPDPDSDSDSDSGSDSGSDSGSDSGSDSDSDS
                                                                                                                                                                                                                                                                                       229 QGPIDGPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78; Mismatches 194; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soppet D.R., Beasley L.L., Willard M.B.; "Evidence for unequal crossing over in the evolution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FCAE02F7EA0509C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.1%; Score 273; DB 6; 24.1%; Pred. No. 2.9e-08;
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Search completed: March 4, 2003, 15:02:29 Job time : 36.8849 secs
                                           RESULT 15.
Q96HF8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKADTNQLADKGKLSPHAFKTESGEETDLISPPQEEVKSSEPTEDVEPKEAEDDD--TGP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 AKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSP 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ::|: : || |||::|| : :| ||||: : :| SPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 VPNKSGADGQTPKDGSS------KSGAEDQTPKDVPNKSGAEKQTPKDGSNKSG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 EEAKSPAEAKSPEKAKSPVKEEAKSPEKAKSPAEAKSPVKEEAKSPEKAKSPEKEEAKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 AEAKSPEKAKSPEKAKSPVEVKSPAEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEK 315
                                                                                                                                                                                               -KSPEKAKSPVKEEAKSPEKETPKKEEV-KV 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----KSGAEAKŢQKGSTSKSGSEAQŢTKDST 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 SKSHSELOTPKDSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPS-----KSGSEAQTTKD 177
374 GSGNGSAESSHFFAYLVTAAILVAVLYIAHHNKRKIIAFVLEGKRSKVTRRPKASDYQRL 433
                                                                   PTEDVEPKEA - - EDDDTGPEEG - SPPKEEKEKMSGSASSENREGTLSDSTGSEKDDLYPN 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 ESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEPQTPKDSPSKSSAEAQTPEDTPNK 83
                                                                                                             287 KAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPEKAKSPVKEEAKSPEKAKSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.1%; Score 273; DB 6; Length 606; 26.4%; Pred. No. 3.4e-08; tive 71; Mismatches 151; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurofilament-H (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                     -VEKDSK 407
                                                                                                                                                                                                                                                            434 DOKYVLILNVFPAPPKRSFLPQVLTEWYIPLEKDER 469
                                                                                                                                                                                                                                                                                                                                                                                                                          606 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-NEW ZEALAND WHITE; TISSUE-BRAIN;
MEDLINE-92381055; Pubmed-1512270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurofilament polypeptide H.";
J: Biol. Chem. 267:17354-17361(1992)
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PRINTS; PR00624; HISTONEH5.
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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EKAKSPVKEEAKSPEKAKSPVKE 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65260 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M94315; AAA57152
                                                                                                                                                                                                                                                                                                        386 KEPPKKVEETAPAPPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 SGAEAKTOKDSSN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         606 AA;
                                                                                                                                                                                                           347 KAKSPVKEEA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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EMBL; M
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PVKEEAKTPEKAKSPVKEEAKAPEKEIPKKEEVKSPVKEEEKPQEVKVKEPPKKAEEEKA 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAQTIKDSISKSHSELQIPKDSIGKSGAEAQIP----EDSPNRSGAEAKIQKDSPSKSGS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -EQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFKTESGEETDLISPPQEEVK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 КЕАРА-КУЕУКЕДАКРКЕКТЕУАККЕРДДАКАКЕРЅКРАЕККЕЛАРЕККД---ТКЕЕКАК 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 KSPAEAKSPVKEEAKSPAEVKSPEKAKSPTKEEAKSPEKA -- KSPEKAKSPEKEEAKSPE
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                                                                                                                                                        Euteleostomi;
Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 268; DB 4; Length 358;
; Pred. No. 3.8e-08;
60; Mismatches 148; Indels 54;
                                                                                                                                                                                                                                                                                               Strausberg R;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC008648; AAH08648.1;
NON TER
1
SEQUENCE 358 AA; 39275 MW; BOCCB4DBB94DF33A CRC64;
                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Unknown (Protein for IMAGE:3866238) (Fragment).
358 AA.
                                            Created
                                                                                                                                                                                                                                                                                                                                                                                                                                     10:9%;
                                          (TrEMBLrel. 19, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 26.09
Matches 92; Conservative
  PRELIMINARY;
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                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=EYE;
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ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 52, Application US/09978295A
Patent No. US20020156006A1
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RIOR APPLICATION NUMBER: 09/918585
RIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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Wood, William I.
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helton, David L.
tewart, Timothy
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Fong, Sherman
Gao, Wel-Qiang
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Soddard, Audrey
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Baker Kevin P.
Botstein, David
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Hillan, Kenneth
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Pan, James;
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936
1 MGILLGLLLGHLTVDTYGR......PLKATSTVKQSWDWTTDMDG 175
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/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                188354 segs, 42170167 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                            protein search, using sw model
                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sednence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence	· Sequence	Sequence	
US-10-176-757-28	US-10-176-913-28	US-10-180-552-28	US-10-180-557-28	US-09-906-838-213	US-09-907-613-213	US-09-907-942-213		US-10-174-572-28	US-10-174-579-28	US-10-174-582-28	174-	US-10-175-739-28	US-10-175-740-28	US-10-175-743-28	US-10-176-488-28	US-10-176-492-28	US-10-176-747-28	-01	US-10-176-985-28	US-10-176-987-28	US-10-176-991-28	US-10-176-992-28	US-10-176-993-28	-10-184-6	US-10-173-695-28	
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13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	.13.9	
130.5	130.5	130.5	130.5	130.5	130.5	130.5	130.5	130.5	130.5	130.5	130.5	130.5	130.5	130.5	130.5	130.5	.130,5	130.5	130.5	130.5	130.5	130.5	130.5	130.5	130.5	
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Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 QINNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                        Length 321;
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Pred. No. 1.1e-66;
0; Mismatches 1
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                    APPLICATION NUMBER: 60/085689
APPLICATION NUMBER: 60/085689
                                                                                   FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085579
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               60/085700
                                                                                                                                                                                                                                     PLICATION NUMBER: 60/085704
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20020169284A1
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Best Local Similarity 64.7%;
Matches 174; Conservative
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llvaroff, Ellen
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PLICATION NUMBER: 60/080194
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PLICATION NUMBER: 60/079923
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PLICATION NUMBER: 60/080327
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APPLICATION UNDRER: 60/081049
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081071
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PLICATION NUMBER: 60/079663
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APPLICATION NUMBER: 60/085338

ILING DATE: 1998-05-1

APPLICATION NUMBER: 60/084643

60/085339

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ING DATE: 1998-04-28
LICATION NUMBER: 60/083392.
ING DATE: 1998-04-29
LICATION NUMBER: 60/083495
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CATION NUMBER: 60/083545
S DATE: 1998-04-29
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PLICATION NUMBER: 60/083500
LING DATE: 1998-04-29
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APPLICATION NUMBER: 60/084414
FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/084441
FILING DATE: 1998-05-06
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084639
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APPLICATION NUMBER: 60/084640
FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
                                        APPLICATION NUMBER: 60/081203
FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/081952
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PLICATION NUMBER: 60/081838
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ICATION NUMBER: 60/082569
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CATION NUMBER: 60/082804
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LICATION NUMBER: 60/082797
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LICATION NUMBER: 60/083322
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LICATION NUMBER: 60/083499
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ING DATE: 1998-04-29
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PLICATION NUMBER: 60/083559
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APPLICATION NUMBER: 60/084366
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PLICATION NUMBER: 60/081955
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PLICATION NUMBER: 60/082704
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ON NUMBER: 60/081195
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                    998-04-08
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61 GSDPVTIFLENDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
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Pred. No. 1.1e-66;
0; Mismatches 1
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                           FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085323
FILING DATE: 1998-05-13
                                                                                                                                                                                           60/085580
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
                                                                        APPLICATION NUMBER: 60/085582
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APPLICATION NUMBER: 60/085579
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Conservative
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                                                                                                                   ILING DATE: 1998-05-1
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Desnoyers, Luc
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Baker Kevin P.
                                                                                                                                                                                              APPLICATION NUMBER:
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Best Local Similarity
Matches 174; Conserv
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PRIOR
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PILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081049
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081071
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081195

TLING DATE: 1998-04-08 PPLICATION NUMBER: 60/081203 LING DATE: 1998-04-15
PPLICATION NUMBER: 60/081817
LING DATE: 1998-04-15
PPLICATION NUMBER: 60/081819

LING DATE: 1998-04-09 PLICATION NUMBER: 60/081955

CATION NUMBER: 60/081229

998-04-09

PPLICATION NUMBER: 60/081952 LING DATE: 1998-04-15 PPLICATION NUMBER: 60/081838

998-04-1

LING DATE: 1998-04-21 PLICATION NUMBER: 60/082569

IG DATE: 1998-04-21 CATION NUMBER: 60/082704

LING DATE: 1998-04-15 PLICATION NUMBER: 60/082568 :LING DATE: 1998-04-22 PPLICATION NUMBER: 60/082804 ING DATE: 1998-04-22 LICATION NUMBER: 60/082796

998-04-2

ING DATE: 1998-04-23 LICATION:NUMBER: 60/083336 LICATION NUMBER: 60/083322

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TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same ILLE REFERENCE: P2630PIC9
URRENT APPLICATION NUMBER: US/09/978,192A
URRENT FILING DATE: 2001-10-15
                                                                                                               TREAT FILING DATE: 2001-10-15
XIOR APPLICATION NUMBER: 09/918585
XIOR FILING DATE: 2001-07-30
XIOR APPLICATION NUMBER: 60/062250
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APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079920
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NG DATE: 1997-11-03
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ATION NUMBER: 60/078936
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TION NUMBER: 60/078910
DATE: 1998-03-20
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DATE: 1998-03-20
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NG DATE: 1998-03-25

ICATION NUMBER: 60/079656
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LICATION NUMBER: 60/079664
ING DATE: 1998-03-27
LICATION NUMBER: 60/079689
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ICATION NUMBER: 60/079663
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LICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/080105
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Williams, P. Mickey Wood, William I.
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LING DATE: 1998-04-28
PLICATION NUMBER: 60/083392
LING DATE: 1998-04-29
PLICATION NUMBER: 60/083495

LING DATE: 1998-04-29 PLICATION NUMBER: 60/083499

LING DATE: 1998-04-29
PLICATION NUMBER: 60/083545
LING DATE: 1998-04-29
PLICATION NUMBER: 60/083554

ILING DATE: 1998-04-29 PPLICATION NUMBER: 60/083558

LING DATE: 1998-04-29 PLICATION NUMBER: 60/083559

LING DATE: 1998-04-29 PLICATION NUMBER: 60/083496 ILING DATE: 1998-04-29
PPLICATION NUMBER: 60/083500
ILING DATE: 1998-04-29
PPLICATION NUMBER: 60/083742

TLING DATE: 1998-04-30 PPLICATION NUMBER: 60/084366

60/084414

APPLICATION NUMBER: 60/084639

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181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
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                                                                                                                                                                                                                                                                                                                                                                                                              94;
                                                                                                                                                                                                                                                                                                                                                                     Length 321
                                                                                                                                                                                                                                                                                                                                                Score 870; DB 9; Length 32.
Pred. No. 1.1e-66;
                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                 PRIOR APPLICATION NUMBER: US/09/254,465 PRIOR FLILING DATE: 1999-03-05 PRIOR APPLICATION NUMBER: PCT/US98/24855 PRIOR PELING DATE: 1998-11-20 PRIOR FILING DATE: 1997-11-21 PRIOR PELING DATE: 1997-11-21 PRIOR APPLICATION NUMBER: US 60/056,364 PRIOR APPLICATION NUMBER: US 60/078,936
                                                                                                                                                           PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR FILING DATE: 1998-09-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 52, Application US/09999832A Publication No. US20020192706A1 GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                     92.9%;
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Filvaroff, Ellen
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Roy, Margaret An
Shelton, David L
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Desnoyers, Luc
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Kuo, Sophia S.
                                                                                                                                                                                                                                                                                                                                                                                                              Matches 174; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pong, Sherman
                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 30
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                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-09-953-499-2
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                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local:
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TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLOGYTOVLVKWLVOR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 870; DB 9;
Pred. No. 1.1e-66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 TEAPITMTYPLKAISTVKQSWDWTTDMDG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 TEAPTIMIYPLKAISTVKOSWDWTTDMDG 175
                               PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR APPLICATION NUMBER: 60/084627
PRIOR PLING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/085579
FILING DATE: 1998-05-15
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084598
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APPLICATION NUMBER: 60/085338
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/085582
                                                                                                                                                                                                                                                                                                                             FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085700
                                                                                                                                                                                                                                                                                                                                                                                       RIOR APPLICATION NUMBER: 60/085689 PRIOR FILING DATE: 1998-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085704
FILING DATE: 1998-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ION NUMBER: 60/085580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/085573
                                                                                                                                                                                                                                                                 RIOR APPLICATION NUMBER: 60/085323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/085697
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ilarity 64.7%;
Conservative
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APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGNQVVRDKITELRVQ----
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Wood, William I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gurney, Austin
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Matches 174;
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Best Local 3
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APPLICANT:
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Gaps

TE: 1998-04-09
ON NUMBER: 60/081229
TE: 1998-04-09
ON NUMBER: 60/081955
TE: 1998-04-15

998-04-

: 1998-04-21 NUMBER: 60/082704 : 1998-04-22

us-09-763-902b-6.rapb

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PELICATION NUMBER: 60/083336
LING DATE: 1998-04-27
PELICATION NUMBER: 60/083322
LING DATE: 1998-04-28
PELICATION NUMBER: 60/08392
LING DATE: 1998-04-29
LICATION NUMBER: 60/083495
LING DATE: 1998-04-29
PELICATION NUMBER: 60/083495
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PPLICATION NUMBER: 60/081195
LING DATE: 1998-04-08
PPLICATION NUMBER: 60/081203
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NG DATE: 1998-04-15
CCATION NUMBER: 60/081819
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ING DATE: 1998-04-15
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G DATE: 1998-04-22
CATION NUMBER: 60/082700
                                             G DATE: 1998-04-08
CATION NUMBER: 60/081071
G DATE: 1998-04-08
                                                                                                                                                                                                                                                                                        CATION NUMBER: 60/081952
G DATE: 1998-04-15
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ING DATE: 1998-04-21
LICATION NUMBER: 60/082569
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CATION NUMBER: 60/082797
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ICATION NUMBER: 60/082796
NG DATE: 1998-04-23
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CATION NUMBER: 60/083499
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ING DATE: 1998-05-06
LICATION NUMBER: 60/084441
ING DATE: 1998-05-06
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IG DATE: 1998-05-07
CATION NUMBER: 60/084639
                                        LICANT: Wood, William I.
LE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
LE OF INVENTION: Acids Encoding the Same
                                                                                                           ATION NUMBER: US/09/999,832A
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LING DATE: 1998-03-11
LING DATE: 1998-03-31
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LING DATE: 1998-03-31
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NW DATE: 1998-04-01
LICATION NUMBER: 60/080328
NW DATE: 1998-04-01
LICATION NUMBER: 60/080333
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18-03-25
                                                                                                                          G DATE: 2001-10-24
TION NUMBER: 09/918585
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ION NUMBER: 60/079786
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ATE: 1998-03-30
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NUMBER: 60/078939
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: 1998-03-27
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G DATE: 1998-03-31
CATION NUMBER: 60/080107
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IG DATE: 1998-03-30
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                         . P. Mickey
Timothy A.
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DATE: 1998-04-29 ATION NUMBER: 60/083545 DATE: 1998-04-29

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TLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                   REFERENCE: P2630PIC7
SNT APPLICATION NUMBER: US/09/978,189
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APPLICATION NUMBER: 09/918585
FILING DATE: 2001-07-30
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PLICATION NUMBER: 60/079656
LING DATE: 1998-03-26
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PPLICATION NUMBER: 60/079923
ILING DATE: 1998-03-30
PPLICATION NUMBER: 60/080105
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G DATE: 1998-03-20
CATION NUMBER: 60/078939
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ATE: 1998-03-20
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4G DATE: 1998-03-27
CATION NUMBER: 60/079689
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WG DATE: 1998-03-27
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ATE: 1998-03-27
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ICATION NUMBER: 60/077641
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                                                                                                                                               oy, Margaret Ann
helton, David L.
tewart, Timothy A.
                                                                                                                           aoni, Nicholas F
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Wood, William I
                                                                                    Wapier, Mary A.
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PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR APPLICATION NUMBER: 60/085689
PRIOR APPLICATION NUMBER: 60/085689
                                                                                                                                         PRIOR APPLICATION. ... 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR PILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
                                                                                                   APPLICATION NUMBER: 60/084643
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/085339
FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
               APPLICATION NUMBER: 60/084600
TILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084627
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PRIOR APPLICATION UNDRER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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Sequence 52, Application US/09978189

Publication No. US20030004102A1

; GENERAL INFORMATION:
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1998-05-07
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Matches 174;
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APPLICANT:
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998-03-3

Gerritsen, Mary

APPLICANT

Serber,

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RELLING DATE: 1998-04-01
RAPPLICATION NUMBER: 60/081070
RELING DATE: 1998-04-08
RELLING DATE: 1998-04-08
RELLING DATE: 1998-04-08
RAPPLICATION NUMBER: 60/081049
               ING DATE: 1998-04-01
LICATION NUMBER: 60/080328
ING DATE: 1998-04-01
                                                                                                                                                                                                                                                                                                                         ILING DATE: 1998-04-08
PPLICATION NUMBER: 60/081203
ILING DATE: 1998-04-09
PPLICATION NUMBER: 60/081229
                                                        FILING DATE: 1998-04-01
APPLICATION UNMERS: 60/080333
APPLICATION NUMBER: 60/080334
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PPLICATION NUMBER: 60/081817
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PLICATION NUMBER: 60/083336
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ING DATE: 1998-04-28
LICATION NUMBER: 60/083392
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LICATION NUMBER: 60/083495
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PLICATION NUMBER: 60/083496
LING DATE: 1998-04-29
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PPLICATION NUMBER: 60/083545
LING DATE: 1998-04-29
PPLICATION NUMBER: 60/083554
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PPLICATION NUMBER: 60/083558
ILING DATE: 1998-04-29
                                                                                                                                                                                                                                                                                LING DATE: 1998-04-08
PLICATION NUMBER: 60/081195
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PLICATION NUMBER: 60/081955
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PLICATION NUMBER: 60/081819
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CATION NUMBER: 60/081838
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LICATION NUMBER: 60/082568
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LICATION NUMBER: 60/082569
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CCATION NUMBER: 60/082804
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CATION NUMBER: 60/082700
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ICATION NUMBER: 60/082796
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ING DATE: 1998-04-29
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ION NUMBER: 60/080327
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61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
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Pred. No. 1.1e-66;
0; Mismatches 1; Indels 94;
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R APPLICATION NUMBER: 60/084637

R APPLICATION NUMBER: 60/084639

R FILING DATE: 1998-05-07

R FILING DATE: 1998-05-07

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R FILING DATE: 1998-05-07
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                                                                                                                                                                                                                           APPLICATION NUMBER: 60/084627
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084643
                                                                                                                                                                                                                                                                                                                                                                                                                          3 DATE: 1998-05-13
CATION NUMBER: 60/085582
                                                                                                                                                                                   APPLICATION NUMBER: 60/084600 FILING DATE: 1998-5-07
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APPLICATION NUMBER: 60/085339
                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085338
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APPLICATION NUMBER: 60/085323
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ATION NUMBER: 60/085700
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APPLICATION NUMBER: 60/085689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 92.9%;
Best Local Similarity 64.7%;
Matches 174; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Botstein, Dav
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Eaton, Dan

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LE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic LE OF INVENTION: Acids Encoding the Same
                                                                                                          ---TWOT 119
31 GPWKG-DVNLPC--TYDP-LOGYTQVLVKW--LVQRGSDP----VTIFLRDSS-GDHIQQ 79
                                                                                     80 AKYOGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEV-
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IRRENT APPLICATION NUMBER: US/09/902, 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLICATION NUMBER: PCT/US99/21090 (LING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICATION NUMBER: PCT/US99/20594
ILING DATE: 1999-09-08
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FILING DATE: 1999-09-13
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G DATE: 1999-11-29
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APPLICATION NUMBER: US 60/143,048
APPLICATION NUMBER: US 60/145,698
FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/145,698
APPLICATION NUMBER: US 60/145,698
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Publication No. US20020192659AI
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Godowski, Paul J.
Grimaldi, Christopher
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ljavin, Ivar J.
ather, Jennie P.
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ilvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soddard, A.
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173 PNG 175
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JRRENT FILING DATE: '2001-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/USOO/00219.
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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NOR FILING DATE: 1999-12-20
NOR APPLICATION NUMBER: PCT/US99/30999
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OR FILING DATE: 1999-12-02
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IOR APPLICATION NUMBER: PCT/US00/04414
IOR FILING DATE: 2000-02-22
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ING DATE: 1999-09-08
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ING DATE: 1999-07-28
                                                                                                                               odowski, Paul J.
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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                                                                      erber, Hanspeter
erritsen, Mary E
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                                                                                                                                                                        irney, Austin L.
                                                                                                                                                                                                                                     Jennie P
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                                                  Wel-Qlang
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; ORGANISM: Homo saptens
US-09-905-291A-213
                                                                                                                                                                                                                                                       James
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Best Local Similarity
Matches 52; Conserv
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120 PDG 122
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173 PNG 175
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Publication No.
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115 --YQGRVHLRQDKEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQS 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 GPWKG-DVNLPC--TYDP-LQGYTQVLVKW--LVQRGSDP----VTIFLRDSS-GDHIQQ 79
                                                                                                                                                                                                                                                                                                                                    69;
                                                                                                                                                                                                                                                                                               Length 360;
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PCT/US99/30095
                                                                                                          XIOR APPLICATION NUMBER: PCT/US00/00219
XIOR FILING DATE: 2000-01-05
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milarity 28.4%;
Conservative 2(
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                                                                                                                           PRIOR FILING DATE: 2000-
NUMBER OF SEQ ID NOS: 42
SEQ ID NO 213
LENGTH: 360
                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo Saplen
US-09-902-853-213
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Best Local Similarity
Matches 52; Conserv
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173 PNG 175
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1 MGLLLLVPLL--LLPGSYGLPFYNGFYXSNSANDQNLGNGHGKDLLNGVKLVVETPEETL 58
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Pred. No. 0.00086;
20; Mismatches 42
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PCT/US00/04414
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                                                                                                                                                                                                                                                                                                               ICATION NUMBER: PCT/US99/23089
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                                                                                          LING DATE: 1999-07-26
PLICATION NUMBER: US 60/146,222
LING DATE: 1999-07-28
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                                                                                                                                                                                           CATION NUMBER: PCT/US99/20944
                                        ON NUMBER: US 60/143,048
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Best Local Similarity 28.45
Matches 52; Conservative
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; ORGANISM: Homo Sapien
US-09-907-824-213
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us-09-763-902b-6.rapb

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NTION: Secreted and Transmembrane Polypeptides and Nucleic NTION: Acids Encoding the Same
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NG DATE: 1999-11-29
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NG DATE: 1999-09-15
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TE: 2000-02-22
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G DATE: 1999-07-26
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DATE: 1999-07-28
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ION NUMBER: 09/665,350
Application US/09904011
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wart, Timothy A
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Mather, Jennie P
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0.00086;
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URRENT FILING DATE: 2001-11-20
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LIOR REPLICATION NUMBER: US 60/143,048
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ILING DATE: 1999-09-08
PPLICATION NUMBER: PCT/US99/20944
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Wood, William, I.
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Best Local Similarity '28.4%;
Matches 52; Conservative 20
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ORGANISM: Homo sapiens
US-09-907-841-213
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PNG 175
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Oy 120 PDG 122 Db 173 PNG 175	\RESULT 13 US-10-176-758-28 ; Sequence 28, Application US/10176758 ; Publication No. US20030008353A1 ; GENERAL INFORMATION;	; APPLICANT: Baker, Kevin P. ; APPLICANT: Chen, Jian ; APPLICANT: Desnoyers, Luc ; APPLICANT: Goddard, Audrey	; APPLICANT: ; APPLICANT: ; APPLICANT: ; APPLICANT:	; APPLICANT: ; APPLICANT: ; APPLICANT: ; TITLE OF INV	4COD1	; Prior Application removed - See File Wrapper or Palm ; NUMBER OF SEQ ID NOS: 612 ; SEQ ID NO 28	; LENGTH: 360 ; TYPE: PRT ; ORGANISM: Homo Sapien US-10-176-758-28	Ouery Match 13.9%; Score 130.5; DB 9; Length 360; Best Local Similarity 28.4%; Pred. No. 0.00086; Matches 52; Conservative 20; Mismatches 42; Indels 68	QY 1 MGILLGLLIGHLTVDTYGRP	Qy 31.GPWKG-DVNLPCTYDP-LQGYTQVLVKWLVQRGSDPVTIFLRDSS-GDHIQQ ::	OY BO AKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQT	Qy 120 PDG 122 Qy 121 PDG 175 Dy 172 PMG 175	211 - 118 -	US-10-175-737-28 ; Sequence 28, Application US/10175737 ; Publication No. US20030013153A1 10; ; GENERAL INFORMATION:	APPLICANT: B APPLICANT: B APPLICANT: A APPLICANT: A APPLICANT: A APPLICANT:	; APPLICANT: ; APPLICANT: ; APPLICANT: ; APPLICANT:	, APPLICANT: , APPLICANT: : APPLICANT:
NUMBER OF SEQ ID NOS: 423 SEQ ID NO 213 LENGTH: 360 TYPE: PRT ORGANISM: Homo Saplen	US-09-904-011-213 Query Match Best Local Similarity 28.4%; Pred. No. 0.00086; Matches 52; Conservative 20; Mismatches 42; Indels 69; Gaps	OY 1 MGILLGLLLLGHLTVDTYGRP	Qy 31 GPWKG-DVNLPCTYDP-LQGYTQVLVKWLVQRGSDPVTIFLRDSS-GDHIQQ 79 ::	QY 80 AKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQT 119	Oy 120 PDG 122 	RESULT 12	Jointy-250-28 Sequence 28, Application US/10174590 Publication No. US20030008352A1 GENERAL INFORMATION:	APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc APPLICANT: Goddard, Audrey APPLICANT: Goddard, Audrey	Gurney, Austin Gurney, Austin Fau, James Smith, Victoria Smith, Dollin	Wood, William I. Shang, Zemin INVENTION SECRETE	REFERENCE: P3430R1C42 NT APPLICATION NUMBER: NT FILING DATE: 2002-C	Prior application removed - See File Wrapper or Palm UMDER OF SEQ ID NOS: 612 SEQ ID NO 28 LENGTH: 360	; TYPE: PRT: ; ORGANISM: Homo Sapien US-10-174-590-28	Query Match 13.9%; Score 130.5; DB 9; Length 360; Best Local Similarity 28.4%; Pred. No. 0.00086; Matches 52; Conservative 20; Mismatches 42; Indels 69; Gaps		OY 31 GPWKG-DVNLPCTYDP-LQGYTQVLVKWLVQRGSDPVTIFLRDSS-GDHIQQ 79 ::	Qy 80 AKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQT 119

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Search completed: March
Job time : 6.18902 secs
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FILE REFERENCE: P3430R1C50
CURRENT APPLICATION NUMBER: U5
CURRENT FILING DATE: 2002-06-
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ORGANISM: Homo Saplen
US-10-175-737-28
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LING DATE: 1999-07-28
FLICATION NUMBER: PCT/US99/20594
FLICATION NUMBER: PCT/US99/20944
                                                                                                                        ING DATE: 1999-09-15
LICATION NUMBER: PCT/US99/23089
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                                                           LING DATE: 1999-09-13
PLICATION NUMBER: PCT
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Best Local Similarity 28.4
Matches 52; Conservative
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; ORGANISM: Homo Sapien
US-09-906-742-213
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homo sapten

plasmodium homo sapien placopecten

063731 rattus norv 19nj22 aequipecten

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09p216 043241 08wza3 014980 075033

homo sapien

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PGPNWKLKVSNLKMVLRSLVEYSQDVLAHPVSEEHLPDVSLIGEFSDPAELGKLLQLVLG 120
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MEDLINE-99126435; Pubmed-9927460;
Kramar H., Phistry M.;
"Genetic analysis of hook, a gene required for endocytic trafficking
in Drosophila.";
Genetics 151:675-684(1999).,
EMBL: AF044924; AACO9299.1; -
SEQUENCE 719 AA; 83163 MW; 2E14C6B1435CE96C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Last annotation update)
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Pred. No. 1.1e-163;
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Local Similarity 99.9%;
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09by13 homo sapien
060561 homo sapien
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1 MSVDKAELCGSLLTWLQTFH.....SRRGPLGRLASLNLRPTDKH 719
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             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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Length 719; Indels

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SEEAEEGDELQQRCLDLERQLMLLSEEKQSLAQENAGLRERMGRPEGEGTPGLTAKKLLL
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Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
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EMBL; BC012443; AAH12443.1; -
EMBL; BC012443; AAH12443.1; -
EMBL; BC012443; AAH12443.1; -
EMBL; BC012443; AAH12443.1; -
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Pred. No. 9.4e-163;
0; Mismatches 1;
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Matches 716;
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LOSQLEQLQEENFRLESGREDERLRCAELEREVAELQHRNQALTSLAQEAQALKDEMDEL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Pred. No. 8.4e-139;
17; Mismatches 53; Indels
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Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the Err.,
Submitted (DEC-2001) to the Err.,
BMBL; BC019486.1; -.
Hypothetical protein.
Hypothetical protein.
T16 AA; 83366 MW; 313333ABFBC6AA50 CRC64;
T16 AA; B3366 MW; 113333ABFBC6AA50 CRC64;
T16 AA; B3366 MW; INC. Score 3102.5; DB 11; L6
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 83.4 kba protein.
Mus musculus (Mouse).
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            181 SEEVEEGDHLQQHYLDLERQLLLISEEKQNLAQENAALRERVGRSEVESAPGLTAKKLLL
                                               LOSQLEQLOEENFRLESGREDERLRCAELEREVAELQHRNQALTSLAQEAQALKDEMDEL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC002226; AAH02226.1;...
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01-JUN-2001 (TIEMBLICEL. 17, Last sequence update)
01-DEC-2001 (TIEMBLICEL. 19, Last annotation update)
similar to hook2 protein (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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RDSLREANEELRCAQLOPRGLTQADPSLDPTSTPVDNLAAEILPAELRETLLRLQLENKR
                                       LCROEAADRERQEELORHLEDANRARHGLETQHRLNQQQLSELRAQVEDLQKALQEQGGK
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                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                      473;
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S
                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.3%; Score 2048.5; DB 11; Length 86.8%; Pred. No. 2.5e-89; ive 28; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: #E0266609; AAH26609.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  55950 MW; C035938BD9B106D5 CRC64;
                                                                                                                                                                                                                                                                                         21, Created)
21, Last sequence update)
21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                       Similar to hook2 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 86.8 Matches 413; Conservative
                                                                                                                                                                                                                                                                       PRELIMINARY;
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01-JUN-2002 (TrEMBLrel:
01-JUN-2002 (TrEMBLrel:
                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                  473 AA;
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Q8R347;
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                family
604 VDKARMVMQTMEPKQRPAAGAPPELHSLRTQLRERDVRIRHLEMDFEKSRSQREQEEKLL
                                                                         419 ISAWYSMGMALEHRAGEEHAPAHAOSFLAQORLATNARRGPLGRQA-LSLRPTDKH 473
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                                                            ISAWYNWGMALQQRAGEERAPAHAQSFLAQQRLATNSRRGPLGRLASLNLRPTDKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 718;
                                                                                                                                                                                                                                                                                                                                                                                            novel
                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                          Walenta J.H., Didier A.J., Liu X., Kramer H.;
"The Golgi-associated hook3 protein is a member of a nimicrotubula-binding proteins";
J. Cell Biol. 152:923-934(2001).
EMBL. AF241830; AAK29204.1...
PRINTS: PRO1608; BACINVASINC.
EXQUENCE. 718 AA; 83125 WW; 9528EC9C854D39FA CRC64;
                                                                                                                                                                                                                  01-JUN-2001 (TIEMBLIEL. 17, Last sequence update) 01-JUN-2002 (TIEMBLIEL. 21, Last annotation update) Golgi-associated microtubule-binding protein HOOK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
48.3%; Score 1758; DB 4;
Best Local Similarity 49.9%; Pred. No. 1.8e-75;
Matches 360; Conservative 158; Mismatches 187;
                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21135884; PubMed-11238449;
                                                                                                                                                                      PRELIMINARY;
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Q9BY13;
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                                                                                                                      70
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kramer H., Phistry M.;
"Genetic analysis of hook, a gene required for endocytic trafficking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 KAELCGSLLTWIQTFHVPSPCASPQDLSSGLAVAYVLNQIDPSWFNEAWLQGISEDPGPN
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              REQEEKLLISAWYNMGMALOORAGEER - - APAHAOSFLAOORLATNSRRGPLGRLASLNL
 SILLKRKLEEHLQKLHEADLELQRKREYIEELEPPTDSSTARRIEELQHNLQKKDADLRA
                                                    MEERYRRYVDKARMVMQTMEPKQRPAAGAPPELHSLRTQLRERDVRIRHLEMDFEKSRSQ
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 728;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E35CA91F2BB89B3E CRC64;
                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1667; DB 4;
Pred. No. 3.6e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the EMBL/GenBank/DDBJ
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84647 MW;
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AL035416; CAB52263.1;
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HOOK1 OR DJ782L23.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-581 FROM N.A
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                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                    060561, 09UJC3)
01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (JUL-2001)
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SEQUENCE 728 AA; 8
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Matches 347; Conserv
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NCBI_TaxID=7227
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Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
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Best Local Similarity 31.6%; Pred. No. 2.3e-33;
Matches 230; Conservative 155; Mismatches 255; Indels 88; Gaps
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251 QLQLEQLQEENFRLEAAKDDYRVHCEELEKQLIEFQHRNDELTSLAEETRALKDEIDVLR
                                                                                                                                                                                                                                                                                                                                                                            RQEELQRHLEDANRARHGLETQHRLNQQQLSELRAQVEDLQKALQEQGGKTEDAISILLK
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                                                                       OSSERAGOLEATLTSCRRRLGELRELRROVROLEERNAGHAERTROLEDELRRAGSLRAQ
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF044926; AAC09301.1; -
FlyBase; FRO0024376; Dvirkhook.
SEQUENCE 678 AA; 77198 WW; 1B8535E80F06C673 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Itolt R.A., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A corge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
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Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
A. Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                  468 NKRLCRQEAADRERQEELQRHLEDAN-RARHGLETQHRLNQQQLSELRAQVEDLQKALQE
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                                      239 LGPIQAGSVRYNELRRQLELVKEELLQSEGAREDLKIKAQQQGETDLLHMQQRIDELMKST
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                                                                                                                                 288 QEAQALKDEMDELRQSSERAGQLEATLTSCRRRLGELRELRRQVRQLEERNAGHAERTRQ
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Last annotation update)
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Haris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalail M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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T.The genome sequence of Drosophila melanogaster.";
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
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6.7e-33;
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Kramer H., Phistry M.;
"Muttations in the Drosophila hook gene inhibit endocytosis of the boss
transmembrane ligand into multivesicular bodies.";
J. Cell Biol. 133:1205-1215(1996).
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                                                                                           -- EAVTQSTSLQCKVTQL 562
                                                                                                                                                                  QHNLQKKDADLRAMEERYRRYVDKARWVMQTMEPKQRPAAGAPPELHSLRTQLRERDVRI 642
                                                                                                                                                                                                      FINESAREQEILVYDAKYRKCVEKAKEVIKSIDPRIASA-----LDASVLEKSADL 613
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EAENKALREGOGG----QTALAQLLDDANKRCENLREQLKTANERILSLSHASQSDDPIL 522
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                   RHLEMDFEKSRSQREQEEKLLISAWYNMGMALQQRAGEERAP---AHAQSFLAQQR 695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phistry M., Sunio A., Kramer H.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ
BEBL; 048352; AAC47261.1; -
EMBL; AF044925, AAC99300.1; -
                                                                                                                   KESEFGKQ-----IKQLMELNEQK----TLQLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-96281964; PubMed-8682859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flybase; FBgn0001202; hk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 01, C
(TrEMBLrel. 01, I
(TrEMBLrel. 16, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227;
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01-NOV-1996 (
01-MAR-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HK OR HOOK
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Rawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Arawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R., Saito T., Okacaki Y., Ashburner M., Batalov S., Casavant T., Radeta K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ruehl P., Lewis S., Matsud Y., Nikaido I., Fesole G., Quackenbush J., Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Anoo H., Balakelli R., Barsh G., Black J., Bult C., Fletcher C., Fujita M., Gariboldi M., Rodstincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchonni L., Mashina J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Ruzuki H., Toyo-oka K., Wang K. H., Weltz C., Whitteker C., Wilming L., Hasselman P., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                    523 KESEFGKQ-----IKQLMELNEGK----TLQLE-----EAVTQSTSLQCKVTQL 562
                         QLENKRICRQEAADRERQEELQRHLEDANRARHGLETQHR-LNQQQLSELRAQVEDLQKA 523
                                                                                                                                                                                                            EAENKALREGGG----QTALAQLLDDANKRCENLREQLKTANERILSLSHASQSDDPIL 522
                                                                                                                                                                                                                                                                                                                                                                   OHNLOKKDADLRAMEERYRRYVDKARMVMOTMEPKORPAAGAPPELHSLRTQLRERDVRI 642
345 TRQLEDELRRAGSLRAQLEAQRRQVQELQGQRQEEAMKAEKWLFECRNLEEKYESVTKEK
                                                                                       405 ERLLAERDSLREANEELRCAQLQPRGLTQADPSLDPTSTPVDNLAAEILPAELRETLLRL
                                                                                                                                        ----TALTGTTVSRELQPSATVEKLQRL
                                                                                                                                                                                                                                                                            LQEQGGKTEDAISILLKRKLEEHLQKLHEADLELQRKREYIEELEPPTDSSTAR-RIEEL
                                                                                                                                                                                                                                                                                                                                                                                                             ETNLSAREQEILVYDAKYRKCVEKAKEVIKSIDPRIASA------LDASVLEKSADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     643 RHLEMDFEKSRSQREQEEKLLISAWYNMGMALQQRAGEERAP---AHAQSFLAQQR 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 AA; 29278 MW; 3AB6C1F2E1F85354 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 AA.
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01-JUN-2001 (TrEMBLrel. 17, Last seq
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4EDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4930033L17R1k protein (Fragment).
                                                                                                                   EMBL; AK020924; BAB32257,1; -. MGD; MGI:1925213; A930033L17R1k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel
01-JUN-2001 (TrEMBLrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                us musculus (Mouse)
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SEQUENCE
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                                                                                                                                      418
                                                                                                                                                                                     465
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                                                                                                                                                                                                                                                                            524
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Q9CTN6
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128 KQDHIQRIMTLEESYQHVVMEAIQELMTKDTPDSLSPETYGNFDSQSRR-YYFLSEEAEE 186
                                                                                                                                                    127 KKQDHIQRIMTLEESVQHVVMEAIQELMTKDTPDSLSPETYGN---FDSQSRRYYFLSEE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 NLKMVLRSLVEYSQDVLAHPVSEEHLPDVSLIGE--FSDPA--ELGKLLQLVIGCAISCE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 DIE-PLLKNMALHLKRLIDERDEHSETIIELSEERDGLHFLPHASSSAQSPCGSPGMKRT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 ------TAKKILILQSQLEQLQEENFRLESGREDERLRCAELEREVAELQHRNQ 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 ESROHLSVELADAKAKIRRLRQELEEKTEQ--LLDCKQELE----QMEIELKRLQQENM 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 AERTROLEDELR--RAGS------LRAQL-----EAGRROVQELGGGRQEEA 380
14 LCDSLIIWLQTFKTASPCQDVKQLTNGVTMAQVLHQIDVAWFSESWLSRIKDDVGDNWRI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 LETKTMLEDQLEGTRARSDKLHELEKENLQLKAKLHDMEMERDMDRKKIEELMEENMTLE 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                      68 KVSNLKMVLRSLVEYSQDVLAHPVSEEHLPDVSLIGEFSDPAELGKLLQLVLGCAISCEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Differential expression of 3-7 gene in functionally distinct ME-1
                                                                                                                                                                                                          187 GDELQQRCLDLERQLMLLSEEKOSLAQENAGLRERMGRPEG--EGTPGLTAKKLLLLQSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 KKEEFIERIQGLDFDTKAAVAAHIQEV-----THNQENVFDLQWMEVTDMSQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 AEEGDELQQRCLDLERQLMLLSEEKQS---LAQENAGL----RERMGRPEGEGTPGL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 ALTSLAQEAQALKDEMDELRQSSERAGQLEATLTSCRRRLGELRELRRQVRQLEERNAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.6%; Score 385:5; DB 4; Length 709; Best Local Similarity 23.6%; Pred. No. 8.2e-11; Matches 165; Conservative 141; Mismatches 248; Indels 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         709 AA
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PRINTS; PR01608; BACINVASINC.
PRINTS; PR00042; LEUZIPPRFOS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3-7 gene product (Fragment)
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Submitted (JUN-1995) to the
EMBL; D64159; BAA21515.1;
HSSP; P03069; 1GCL.
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3; Gaps

8 LCGSLLTWLQTFHVPSPCASPQDLSSGLAVAYVLNQIDPSWFNEAWLQGISEDPGPNWKL

Best Local Similarity 48.0% Matches 118; Conservative

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													26;					,
381 MKAEKWLFECRNLEEKYESUTKEKERLLAERDSL-REANEELRCAOLOPRGLTOAD 435	436 PSLDPTSTPVDNLAAEILPAELRETLLRLOLENKRL	521 QKALOBOGGKTEDAISILLKRKLEBHLQKLHEADLELQRKREYIEELEPPT 571	572 DSSTARRIEELQHNLQKKDADLRAMEERYRRYVDKARWYMOTWEPKQRPAAGAP 625 572 DSKITNLKITCEKIEALEQENSELERENRKLKKTLDSFKNLTFQLESLEKENSQLD 625	626 PELHSLRTQLRERDVRIRHLEMDFEKSRSQREQEEK 661 	LT 13	.01 091101 PRELIMINARY; PRT; 742 AA. 0911101.	-2000 (7 -2000 (7 -2002 (7 etical E	Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;	ENCE FROM N.A. JE-HYPOTHALAWUS; J., Jiang C., Huang C	Y., Fu G., vel gene ex tted (DEC-)	112218; AAF1/20b.1; 3069; IGCL. PRO1608; BACINVASINC. 1cal protein.	742 AA; 87326 MW; F54FC3E5BZD0B4EZ CR	Query Match 10.6%; Score 385.5; DB 4; Length /42; Best Local Similarity 23.6%; Pred. No. 8.6e-11; Matches 165; Conservative 141; Mismatches 248; Indels 145; Gaps	71 NLKMVLRSLVEYSQDVLAHPVSEEHLPDVSLIGEFSDPAELGKLLQLVLGCAISCE 126				
Oy Db	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	. 20 . 20	. & Q	20 d	RESULT	090101	82228	8888	R R B R	RT R	Z C C Z	တ္တ	OME	8 8	8 6 E	ç d	\$ 6	ð

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61 PGP-----NWK----LKVSNLKMVLRSLVEYSQDVLAHPVSEEHLPDVSLIGEFS 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 ESKNGLEQMKTLLTLLGAAVQCPNKELFIARIKELDLETQHAIVGLIKQVTDSHSLVLT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LD40094p.
CG12734.
CG12734.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                              476 AAD------RERQEELQRHLEDANRARHGLETQHRLNQQQLSELRAQVEDL 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  453 SKDLMKEKAQLEKTIETLRENSERQIKILEQEN--EHLNOTVSSLRORSQISAEARVKDI 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               521 Q---KALQEQGGKTEDAISIL-----LKRKLEEHLQKLHEADLELQRKREYIEELEPPT 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S11 EKENKILHESIKETSSKLSKIEFEKROIKKELBHYKEKGERAE-ELENELHLEKENELL 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   572 DSS-----TARRIEELQHNLQKKDADLRAMEERYRRYVDKARWVMQTWEPKQRPAAGAP 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          570 QKKIINLKIICEKIEA----LEQENSELERENRKLKKYLLDSFKNLIFQLESLEKENSQLD 625
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                                                                                                                                                                       381 MKAEKWLFECRNLEEKYESVTKEKERLLAERDSL-REANE----ELRCAQLQPRGLTQAD 435
                                                                                                                                                                                                                                                                                                                               1 MSVDKAELCGSLLTWLQTFHVPSPCASPQDLSSGLAVAYVLNQIDPSWFNEAWLQGISED 60
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                                                                                                          282 LETKTMLEDQLEGTRARSDKLHELEKENLOLKAKLHDMEMERDMDRKKIEELMEENWTLE 341
                                                                                                                                                                                                           142 MAQKQSMDESLHLGWELEQISRTSELSEAPQKSLGHEVNELTSSKLKLEMENQSLKTV 401
                                                                                                                                                                                                                                                                                              --CRQE 475
222 NLLSDARSARMYRDELDALREKAVRVDKLESEVSRYKERLHDIEFYKARVEELKEDNQVL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BERKELEY;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Paclèb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              626 PELHSLR---TQLRERDVRIRHLEMDFEKSRSQREQEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1235 AA.
                                                                                                                                                                                                                                                                                                    436 PSLDPTSTPVDNLAAEILPAELRETLLRLOLENKRL
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                                                                      342 AERTROLEDELR--RAGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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600 ELEQYLEKSRQYELTKQKLYEIEARVSTYERENASLLKEVSKLKEGSEQKSVQLDDSINR 659
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                                                173 EDSLERLTPQS------MYTHILRLTKERDVMYLKWID-----LACVETEMTASDN 217
                                                                                                                                                  218 LVECGOGVSVTRSPSNGTATSTPSSSSNSESNHLAVECADLRSKNRKLRQELEEKSENLL 277
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156 KDTPDSLSPETYGNFDSQSRRYYFLSEEAEEGDELQQRCLDLERQLMLLSEEKQSLAQEN
                                                                                                                                                                                                254 RLESGREDERLRCAELEREVAELQHRNQALTSLAQEAQALKDEMDELRQSSERAGQLEAT
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                          331 VOKYREKLGDSDFYKSRVEELREDNRVLLESKEMLEEQLQR----
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Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Meoptera; Endopterygota; Diptera;
Pterygotda; Drosophilldae; Drosophila.
NCBI_TaxID-7227;
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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.W., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Bodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Doubin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gang F., Garrell J.H., Gu Z., Guan P., Harris M.,
Alatia N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyam C.,
RA Alalal M., Kalush F., Karpen G.H., Ke Z., Kennison J., Ketchum K.A.,
RA Liasko P., Lei Y., Levitsky A.A., Lij J., Lil Z., Liang Y., Lin X.,
A Lu X., Mattel B.E., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G. Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Relnert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Shie B.C., Saden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shie B.C., Saden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shein S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Lens R.A., Myers E.W., Rulin G.M., Venter J.C.;
RT The genome sequence of Drosophila melanogaster.",
REMBL, AE003477; AAR47730.1; ---
REMBL, REMBL, REMONS REMA, Relance C.,
Reman Relance C., Reminger C., Remerter J.C.;
REMBL, REMBL, REMONS REMA, Relance C., Remons Reman Relance C.,
Reman Relance C., Reminger C., Remons Reman Relance C.,
Reman Relance C., Reminger C., Remons Reman Relance C.,
Reman Relance C., Remons 
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InterPro; IPR002017; Spectrin.
SEQUENCE 1381 AA; 157512 MW;
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QQ	427	427 IMDLDKSFSENEDDCNSGDNSLSEQLINNAQTRALKLELENRRLTAALEQLKESSFHEST 486	486
λo	486	486 ORHLE-DANRARHGLE-TQHRLNQOQLSELRAQVEDLOKALQEGGGKTEDAISILLKRKL 543	543
q	487	487 SKMLELEKEKKKLSLKIEQMQENINRLTQQNVELEGVFKNALEENKKLQDAVDNRQKSYD 546	546
ογ	544	544 EEHLOKLHEADLE-LORKREYIEELEPPTDSSTARRIEELOHNLOKKDADLRAMEE 598	. 865
. QQ	547	547 RQSLEREADRQKLSDAEQHVETLNKEKQRIQTLNESIQRRADDLERLAESKTK 599	299
ολ	599	599 RYRRYVDKARMVMQTMEPKQRPAAGAPPELHSLRTQLRERDVRIRH 644	644
q	900	600 ELEQYLEKSRQYELTRQKLYEIEARVSTYERENASLLKEVSKLKEGSEQKSVQLDDSINR 659	629

9 Q

Search completed: March 4, 2003, 15:02:39 Job time : 53.2588 secs

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us-09-763-902b-3.rsp

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

March 4, 2003, 14:51:02; Search time 12.4234 Seconds (without alignments) 1732.709 Million cell updates/sec Run on:

US-09-763-902B-3 2620 1 MAABREPPPLGDGKPTDFED.....TQQQLIKYWEAFLPEAKAIA 519

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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SUMMARIES	OI.	SNX2_HUMAN	SNX2_MOUSE	SNX1_RAT	SNX1_MOUSE	SNX1_HUMAN	VPS5_YEAST	SNX5_HUMAN	SNAD_MOUSE	SNA/ HOMAN	SNX6 HUMAN	SNX4_YEAST	SNX4_HUMAN	SNX8_HUMAN	SNX9_HUMAN	SNX3_HUMAN	SNX3_MOUSE	SNXC_HUMAN	MVP1_YEAST	CENE_HUMAN	YM92_CAEEL	1	SNXJ_HUMAN	PCP1_SCHPO	NUF1_YEAST	TAC2_MOUSE	- 1	- 1	YN48_YEAST	MLP1_YEAST	SNXI_HUMAN	MYH6_HUMAN		
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## ALIGNMENTS

BRT; 519 AA.  SNX2_HUMAN SYANDARD; PRT; 519 AA.  G00741; G103650; P82862; Q9BTS8; G16-CCT-2001 (Rel. 40, Last sequence update) G17-CCT-2002 (Rel. 41, Last annotation update) G17-CCT-2002 (Rel. 41, Last annotation update) G18-CCT-2002 (Rel. 40, Last sequence (Leptana) G19-CCT-2002 (Rel. 40, Last sequence (Leptana) G11 (Leptana) G11 (Leptana) G11 (Leptana) G12 (Leptana) G13 (Leptana) G13 (Leptana) G14 (Leptana) G15 (Leptana) G15 (Leptana) G16 (Leptana) G17-CCT-2003 (Leptana) G17-CCT-200	DR EMBL; AF03482; AACI,1421.1;  DR EMBL; BC03382; AAH03382.1;  DR Genew; HGNC:11173; SNX2.  DR HGNC:11173; SNX2.  DR INTERPO: IPR001683; PX.  DR INTERPO: IPR003329; Sorting_nexin.  DR Pfam; PF07370; Sorting_nexin.  DR Pfam; PF03700; Sorting_nexin; 1.  DR SMART; SM00312; PX; 119_nexin; 1.  KW Transport; Protein transport.  FT DOMAIN 140 269 PX.
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Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Radawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

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Ruchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuchi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
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                                                                                                 PVIFDRSREE1EEEANGDIFDIE1GVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                   ;
0
                                           Length 519;
                                                                Indels
F -> V (IN REF. 3).
S -> A (IN REF. 3).
897DA7E15935C3A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2612; DB 1;
Pred. No. 1.1e-131;
1; Mismatches 1;
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331 331 8
384 384 5
519 AA; 58535 MW;
                                            99.78;
                                                     Local Similarity ...
les 517; Conservative
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CONFLICT
CONFLICT
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                                             Query Match
                                                       Best Loca
Matches
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                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RYLQRTVKHPTLLQDPDLRQFLESSELPRAVNTQALSGAGILRMVNKAADAVNKMTIKMN 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.; Kawaishi K., Hasegawa Y., Rawaji H., Kohtsuki S., Nature 409:685-690(2001).
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    -!- FUNCTION: May be involved in several stages of intracellular

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BAB27035).
CRC64;
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                                                                                                                                                                                                                                                                                             -i - SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY -i - SIMILARITY: CONTAINS 1 PX DOMAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R -> I (IN REF. 1;
R -> P (IN REF. 1;
55DD0BB74E82CD82
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Pred. No. 3.8e-129;
3; Mismatches 7;
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InterPro; IPR005329; Sorting_nexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam. PF00787; PX: 1.
Pfam. PF00787; PX: 1.
Pfam: PF00310; Sorting_nexin; 1.
SMART: SM00312; PX: 1.
PR0031E; PS50195; PX: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AK002692; BAB22287.1; -. EMBL; AK005470; BAB24060.1; -. EMBL; AK010572; BAB27035.1; -.
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Best Local Similarity 98.18;
Matches 509; Conservative
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                                                                                                                                                                                                                                                                  trafficking.
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MGD; MGI:1928395; Snx1
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SUXI MOUSE

Q9WV80; Q9EQZ9;

16-OCT-2001 (Rel. 4

15-JUN-2002 (Rel. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 DISANSNGPKPTEVVLDDDRE--DLFAEATEEVSLDSPEREPILSSEPSPAVTPVTFTL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 IAPRIESKSMSAPVIFDRSREEIEEEANGDIFDIEIGVSDPEKVGDGMNAYMAYRVTTKT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - HPTQEATNSPKP---QPSYEELEEEEQCFDLTVGIIDPEKIGDGMNAYVAYKVITQT 171
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                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epidermal growth factor receptor.";
J. Biol. Chem. 276;7069-7078(2001).
-1- FUNCTION: MAY BE INVOLVED IN SPERAL STAGES OF INTRACELLULAR TRAFFICKING. PLAYS A ROLE IN TARGETING LIGAND-ACTIVATED EGFR THE LYSOSOMES FOR DEGRADATION AFTER ENDOCYTOSIS FROM THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLFPIRNGSKENGIHEEQDQEPQDLFADATVELSLDSTQNNQ--KTMPGKTLIP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interacts with sorting Nexin 1 and regulates degradation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 59.7%; Score 1564.5; DB 1; Length 522; Best Local Similarity 59.9%; Pred. No. 3.5e-76; Matches 318; Conservative 74; Mismatches 108; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F0F05664087E4D24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SURFACE AND RELEASE FROM THE GOLGI.
SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
SIMILARITY: CONTAINS I PX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L.S., Raynor M.C., Wei X., Chen H.Q., Li L.;
              41, Last sequence update)
41, Last annotation update)
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DOMAIN 143 272.
SEQUENCE 522 AA; 59044 MW; F0F05664087
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IPR005329; Sorting_nexin.
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Pfam; PF03700; Sorting_nexin; 1.
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                                                                                                                                                                                                                          Created)
                                                                                                                                                                               STANDARD;
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15-JUN-2002 (Rel.
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                                                                                                                     RESULT 3
SNX1_RAT
LD CON NO. C
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                                                                                                                                                                                                            408
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                                                                       ADAVNKMTIKMNESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKELSANTAAFAKSA 348
                                                                                                           292 IDAVSKMTIKMNESDIWFEEKLQEVECEEQRLRKLHAVVETLVNHRKELALNTALFAKSL 351
                                                                                                                                                                                                                                            409 HRMKCWOKWEDAQITLLKKREAEAKWWYANKPDKIQQAKNEIREWEAKVQQGERDFEQIS 468
232 AEFLEKRRAALERYLQRIVNHPTMLQDPDVREFLEKEELPRAVGTQALSGAGLLKMFNKA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakamura N., Wada Y., Futai M.;
Nakae Sorting nexin 1.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: MAY BE INVOLVED IN SEVERAL STAGES OF INTRACELLULAR TRAFFICKING. PLAYS A ROLE IN TARGETING LIGAND-ACTIVATED EGFR THE LYSOSOMES FOR DEGRADATION AFTER ENDOCYTOSIS FROM THE CELL SURFACE AND RELEASE FROM THE SOLGI.
-!-SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
                                                                                                                                                                                                        349 AMLGNSEDHTALSRALSQLAEVEEKIDQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469 KTIRKEVGRFEKERVKDFKTVIIKYLESLVQTQQQLIKYWEAFLPEAKAIA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takahara T. Omatsu Y., Maeda Y., Shimoyama S., Inaba K. "Complete sequence of mouse sorting nexin 1 (Snx1) cDNA. Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40, Created)
40, Last sequence update)
41, Last annotation update)
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Interpro; IPR005329; Sorting_nexin.
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Pfan; PF03700; Sorting_nexin; 1.
SMART; SM00312; PX; 1.
PROSITE; PS50195; PX; 1.
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                                                                                                                                     DISANSNGPKPTEVVLDDDRE--DLFAEATEEVSLDSPEREPILSSEPSPAVTPVTFTL 108
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                                                                                                                                                                                                                                                                           232 AEFLEKRRAALERYLQRIVNHPTMLQDPDVREFLEKEELPRAVGTQALSGAGLLKMFNKA 291
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Kurten R.C.; Cadena D.L., Gill G.N.;
"Enhanced degradation of EGF receptors by a sorting nexin, SNX1.";
Science 272:1008-1010(1996).
                                                                                                                                                                                                                                IAPRIESKSMSAPVIFDRSREEIEEEANGDIFDIEIGVSDPEKVGDGMNAYMAYRTTKT
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Mammalla, Eutherla, Primates, Catarrhini, Hominidae, Homo.
                                                    DB 1; Length 522;
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MEDLINE-99038232; PubMed-9819414;
Haft C.R., de la Luz Sierra M., Barr V.A., Haft D.H., Taylor
"Identification of a family of sorting nexin molecules and
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
S -> C (IN REF. 2).
MISSING (IN REF. 2).
S -> F (IN REF. 2).
: lefc06B3EA551311 CRC64;
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                                                                         108;
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15-UNN-2002 (Rel. 41, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
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                                                   59.4%; Score 1557.5; 59.7%; Pred. No. 8.3e
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124 S
138 M3
389 S
58952 MW;
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Q13596; 060750;
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                                                                         Matches 317;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                        -1- FUNCTION: MAY BE INVOIVED IN SEVERAL STAGES OF INTRACELLULAR TRAFFICKING. PLAYS A ROLE IN TARGETING LIGAND-ACTIVATED EGER THE LIYOSOMES FOR DEGRADATION AFTER ENDOCYTOSIS FROM THE CELL. SURFACE AND RELEASE FROM THE GOLG!.

-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 1A; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
-1- SIMILARITY: CONTAINS 1 PX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Golgi stack; Alternative splicing
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Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
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P -> S (IN REF. 2).
P -> S (IN REF. 2).
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.nterPro; IPR005329; Sorting_nexin.
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fam; PF03700; Sorting_nexin; 1.
sMART; SM0312; PX; 1.
sROSITE; PS50195; PX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97279235; PubMed-9133743; Valens M., Bohn C., Dalgnan-Fornter B., Dang V., Bolotin-Fukuhara M.; The sequence of a 54.7 kb fragment of yeast chromosome XV reveals the presence of two tRNAs and 24 new open reading frames."; Yeast 13:379-390(1997).
forms, a complex with Vps17p and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1- FUNCTION: REQUIRED FOR RETENTION OF LATE GOLGI MEMBRANE PROTEINS AND VACUOLAR BIOGENESIS.
1- SUBUNIT: INTERACTS WITH VPS17.
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As sorting nexin.1 homologue, Vps5p, forms.a complex with Vps17p ar
is required for recycling the vacuolar protein-sorting receptor.";
Mol. Biol. Cell 8:1529-1541(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          juired for localizing membrane proteins to the late Golgi."; Cell Sci. 110:1063-1072(1997).
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Horazdovsky B.F., Davies B.A., Seaman M.N.J., McLaughlin S.A.,
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- CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
                                                                                                           QISKTIRKEVGRFEKERVKDFKTVIIKYLESLVQTQQQLIKYWEAFLPEAKAIA
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XXXXII 279 394 PX
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"The yeast VPSS/GRD2 gene encodes a sorting nexin-1-like required for localizing membrane proteins to the late on
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- PTM: PHOSPHORYLATED ON SERINE RESIDUE(S):
- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
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VPS5. OR GRD2 OR YOR069W OR YOR29-20.
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15-JUN-2002 (Rel. 41, Last annotation update)
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01-NOV-1997 (Rel. 35, Last sequ
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Q92331; Q08483;
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                                                                                                                                                                                                                                                                                             157 PRILFDSARAQRNSKRNHSLKAKRTTASDDTIKTPFTDPLKKAEKENEFVEEPLDDRNER 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 KKICQDPVLQKDKDFLLFLTSDDFSSESKKRAFLTGSGAINDSNDLSEVRISEIQLLGAE 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNEIREWEAKVQQGERDFEQISKTIRKEVGRFEKERVKDFKTVIIKYLESLVQTQQQLIK 506
                                                                                                                                                                                                                                                                                                                                                        -- DREDLFAEATEEVSLDSPEREPILSSEPSPAVTPVTPTTLIAP-RIESKSMSAPVIFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----MVNKAADAVNK---MTI-----KMNESDAWFEEKQOQFENLDQQLRKLHVSVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRRAALERYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVCHRKELSANTAAFA - - - KSAAMLGNSEDHTALSRALSQLAEVEEKIDQLHQEQAFADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 YMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEAKMMVANKPDKIQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             606 RKEFOTLERRYNLTKKOWQAVGDKIKDEFQGFSTDKIREFRNGMEISLEAAIESQKECIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDTSRNTLAASTEEFSSMVETLASLNVSEPNSEL---LNNFADVHKSIKSSLERSSLQET
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"A large family of endosome-localized proteins related to sorting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Exkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
      Length 675;
14.7%; Score 386; DB 1; Length 67!
llarity 23.3%; Pred. No. 1.4e-13;
Conservative 114; Mismatches 220; Indels
                                                                                                               EPPPLGDGKPTDFEDL --- EDGEDLFTSTVS----TLESSPSSPEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 QRTVKHPTLLQDPDLRQFLESSELPRAVNTQA-LSGAGILR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                404
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MEDLINE-21378165; Pubmed-11485546;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09Y5X3; Q9BWPO;
16-007-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. J. 358:7-16(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
Query Match
Best Local Similarity
Matches 141; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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                  A Jones M., Stavrides G., Almeda J.P., Babbage A.K., Bagguley C.L., Ra Balley J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Bearley J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Basley J., Barlow K.F., Barkey S.E., Bridgeman A.M., Brown A.J., Buck D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., R. Coulson A., Covilier R.E., Connor R.E., Corby N.R., A. Elington A.G., Frankland J.A., Fraser A., French L., Garner P., Billington A.G., Frankland J.M., Fraser A., French L., Garner P., A. Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Ray M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachle L.J., McLay K., McMurray A., A. Huntesh W.J.F., McConnachle L.J., McLay K., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peeck A.I., Stockt C.E., Sehra H.K., Shownkeen R., Sims S., Stuce C.D., Smith M.L., Sockt C.E., Sehra H.K., Shownkeen R., Sims S., Stuce C.D., Smith M.L., Sockt C.E., Sehra H.K., Shownkeen R., Tromans A.C., Vaudin M., Wall IN, Wall IN, Walliams S.A., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Williams L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., A. Williams J., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Seeck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Ovarian carcinoma;

TISSUE-Ovarian carcinoma;

Signal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikama T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,

Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,

Tanai H., Yamanoto J., Wakamatsu A., Nakamura Y., Nagahari K.,

Masuho Y., Kanehori K.,

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V -> L (IN REF. 3).
87A85620AF827EC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
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11.8%; Score 308.5; DB 1;
Best Local Similarity 26.4%; Pred. No. 9.2e-10;
Matches 111; Conservative 79; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:14969; SNX5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transport; Protein transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF121855; AAD27828.1;
EMBL; AL121585; CAC00471.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AK001793; BAA91914.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00312; PX; 1.
PROSITE; PS50195; PX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; PX; 1.
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SOLITI WE BERREAD BY A STREET OF STR
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-Pancreas;

MIDINE-21085660; Pubmed-11217851;

MAZAWA T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J.; Shinagawa A., Shibata K., Konoo H., Adachi J., Fukuda S.,

A Azawa K., Tazwa M., Nishik K., Kiyosawa H., Kondo S., Yamanaka I.,

A Saito T., Okazaki Y., Gojobori T., Bonoo H., Rasukawa T., Saito R.,

R Saito T., Okazaki Y., Ashburner M., Batalov S., Casavant T.,

A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Kadota K., Matsudo Y., Nikaido I., Pesole G., Quackenbush J.,

A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washlo T.,

A Sakai K., Okido T., Füruno M., Aono H., Baldarelli R., Barsh G.,

B Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,

A Brownstein M.J., Bult C., Pletcher C., Fulita M., Gariboldi M.,

RA Brownstein M.J., Mashima J., Mamazarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Sizuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Sizuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Sizuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Sizuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Sizuki H., Rodriguez L., Sakamata H., Rohrsuki S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342
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DRSR-EEIEEEBANGD----IFDIEIGVSDPEKVGDGMNAYMAYRAYTKTSLSMFSKSEFSV 180
                                             14 DRSKLRSVSVDLNVDPSLQIDIPDALSERDKV-----KFTVHTKTTLPTFQSPEFSV 65
                                                                                                                                                                                                                  --- DKARLKSKDVKLAEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                 185 GFFKSVVKSADEVLFTGVK--EVDDFFEQEKNFLINYYNRIKDSCVKADKMTRSHKNVAD
                                                                                                                                                                                                                                                                                                                                                                            --ANTAAFAKSAAMLGNSEDHTALSRALSQLAEVEEKIDQLHQEQAFADFYMFSELLSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397 IRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEAKMWVANKPDKIQQAKNEIREWEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               457 VQQGERDFEQISKTIRKEVGRFEKERVKDFKTVIIKYLE-----SLVQTQQQLIK
                                                                                           KRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVG-----MTKVKVGKEDSSSTEFVEKR
                                                                                                                                                                                                                                                                                   280 GILRMVNKAADAVNKMTIKMNESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKELS-
                                                                                                                                                                                          -- AALERYLORTVKHPTLLQDPDLRQFLESSE--LPRAVNTQALSGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Sorting nexin 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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Q9D8U8;
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Indels

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J. 358:7-16(2001)
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SMART; SM00312; PX; 1.
PROSITE; PS50195; PX; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Senew; HGNC:14971;
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                      ISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ransport;
     Biochem.
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                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRSR-BEIBEBEANGD---IFDIEIGVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 KRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVG-----MTKVKVGKEDSSSTEFVEKR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -AALERYLORTVKHPTLLQDPDLRQFLESSE--LPRAVNTQALSGA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 QELEABYLAVFKKTVSTHEVFLQRLSSHPVLSKDRNFHVFLEYDQDLSVRRKNTKEMFG- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GILRMVNKAADAVNKMTIKMNESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKELS- 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 GFFKSVVKSADEVLFSGVK--EVDDFFEQEKNFLINYYNRIKDSCAKADKMTRSHKNVAD 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- ANTAAFAKSAAMLGNSEDHTALSRALSQLAEVEEKIDQLHQEQAFADFYMFSELLSDY 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEAKMMVANKPDKIQQAKNEIREWEAK 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- DKARLKSKDVKLAETH 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21378165; PubMed-11485546; TeasGale R.D:, Loci D., Houghton F., Karlsson L., Gleeson P.A.; A large family of endosome-localized proteins related to sorting nexin l.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C24D8C78F753FAFC CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.7%; Score 305.5; DB 1; 26.2%; Pred. No. 1.3e-09; Live 78; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               457 VQQGERDFEQISKTIRKEVGRFEKERVKDFKTVIIKYLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387 AA
SIMILARITY: CONTAINS 1 PX DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLNIEAAKDLLYRRTKALIDYENSNKAL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 172 P. 404 AA; 46797 MW;
                                                                                                                                                                                                                                                                EMBL; AK007676; BAB25180.1; -
EMBL; BC002242; AAH02242.1; -
                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00787; PX; 1.
SMART: SM00312; PX; 1.
PROSITE; PS50195; PX; 1.
Transport; Protein transport.
ODMAIN 25 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 26.28 Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                               IPR001683; PX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                        MGD; MGI:1916428; Snx5
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Q9UNH6; Q91
                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
SNX7_HUMAN
ID SNX7_HI
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DT 16-0CT
DT 1
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SPER PRESCOCIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKVKVGKEDSSSTEFVEKRRAALERYLQRTVKHPTLLQDPDLRQFLESSELPRAVNTQAL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LHV----SVEALVCHRKELSANTAAFAKSAAMLGNSEDHTALSRALSQLA 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 SGAGILRMYNKAADAVNKMT-----IKMNESDAWFEEKQQQFENLDQQLRK--- 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- MGVMKRRDQI-QAELDSKVEVLTYK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAEAKMM----VANKPDKIQQAKNEIR-EWEAKVQQGERDFEQISKTIRKEVGRFEKERVK 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NQIKFEDEPDLKDLFITVDEPESHVTTI 46
Duesterhoeft A., Lauber J., Mewes H.-W., Gassenhuber J., Wiemann S., Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                             Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 387;
                                                                                                                                                                                                                                        trafficking. - SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M -> I (IN REF. 2).
S -> P (IN REF. 3).
M -> T (IN REF. 2).
F -> G (IN REF. 2).
F -> L (IN REF. 2).
E703B3EC6013DC1F C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 YFDEMKEYGPIHILWSASEEDLVDTLKDVASCIDRCCK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.5%; Score 300.5; sal Similarity 23.4%; Pred. No. 2.3. 105; Conservative
                                                                                                                                                                                                                                                                                                   - SIMILARITY: CONTAINS 1 PX DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF121857; AAD27830.1; -.
EMBL; AL049989; CAB43229.1; ALT_INIT
EMBL; BC010349; AAH10349.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KADTDLLPEEIGKLEDKVECANNALKADWE
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/60; TISSUE-Embryonic liver;

K Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

K Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

R Arakawa T., Hara A., Eukunishi Y., Konno H., Adachi J., Fukuda S.,

A lzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

K Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

R Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

R Ruchi P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,

R Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofman M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Bordonebach M., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Buzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Havasaki J., Warshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,

Havasaki H., Saka
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: May be involved in several stages of intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; resource, ....
DOMAIN 30 151 PX
CEPRIENCE 387 AA; 45000 MW; SED78D359CD32A1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             trafficking (By similarity).
SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
SIMILARITY: CONTAINS 1 PX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.18; Score 291.5; DB 1; 23.6%; Pred. No. 6.9e-09; tive 76; Mismatches 149;
                                                                                                                                                                                         [5-JUN-2002 (Rel. 41, Created)
[5-JUN-2002 (Rel. 41, Last sequence update)
[5-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                               387 AA.
485 DFKTVIIKYLESLVQTQQQLIKYWEAFL 512
                                      344 DIKLAFTDMAEENIHYYEQCLATWESFL 371
                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK011015; BAB27333.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nterPro: IPR001683; PX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001)
                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50195; PX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:1923811; Snx7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00787; PX; 1.
                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00312; PX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090
                                                                                                                                                                                                                                                            Sorting nexin 7.
                                                                                                                                                   SNX7_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
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"Sorting nexin 6, a novel SNX, interacts with the transforming growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 LAEVEEKIDQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLK 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     427 KREAEAKMM----VANKPDKIQQAKNEIR-EWEAKVQQGERDFEQISKTIRKEVGRFEKER 482
                                                                                                                                                                                                                                                               275 ALSGAGILRMVNKAADAVNKMT------IKMNESDAWFEEKQQQFENLDQQLRK-- 322
                                                                                                                                                                                                                                                                                                        -----RWKONM 341
                                     103 ----KGMVERFNDDFIETRRKALHKFLNRIADHPTLTFNEDFKVELTAQAEEL----SSY 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 RDYFDEMKEYGPIHILWSASEEELVDTLKGMAGCIEQCCKA----TEKRMAGLSEAL-- 267
157 NAYMAYRVTTKTSLSMFSKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGM 216
                                                                                                                              TKVKVGKEDSSSTEFVEKRRAALERYLQRTVKHPTLLQDPDLRQFL--ESSELPRAVNTQ 274
                                                                                                                                                                                                                                                                                                                                                                                                 ------LHV----SVEALVCHRKELSANTAAFAKSAAMLGNSEDHTALSRALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21378165; PubMed-11485546;
Teasdale R.D., Loci D., Houghton F., Karlsson L., Gleeson P.A.;
"A large family of endosome-localized proteins related to sorting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor beta family of receptor serine-threonine Kinases.";
J. Biol. Chem: 276:19332-19339(2001).
-!- FUNCTION: May be involved in several stages of intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and for
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: Interacts with TGFB receptors.
-!- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
-!- SIMILARITY: CONTAINS 1 PX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Sorting nexin 6 (TRAF4-associated factor 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 YKKADIDLLTEEIGKLEDKVECANNALKADWE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            483 VKDFKTVIIKYLESLVQTQQQLIKYWEAFL 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 KNDLRSAFTDTAEQNIRYYEQCLATWESFL 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21276432; PubMed=11279102;
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Biochem. J. 358:7-16(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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Q9UNH7; Q9Y4
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                                                                                                                                                                                                                                                                                                                                                                                                    323
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17;

119;

Indels

97 SPAVTPVTPTTLIAPRIESKSMSAPVIFDRSREEIEEEANGDIFDIEIGVSDPEKVGDGM 156

16;

Conservative

SP-MMPTSPLSMI

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---NOIKFEDGPDLKDLFITVDAPESHVTTI 46

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Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNX4_HUMAN
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167
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 entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch),
                                                                                                                                                                                                                                                                                                                                             ALER------YLORTVKHPTLLQDPDLRQFLESSELPRAVNTQALSGAG-- 280
                                                                                                                                                                                                                                                                                                                                                                                                                         RKELSANTAAFAKSAAMIGNSEDHTALSRALSQLAEVEEKIDQLHQEQAFADFYMFSELL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                        DRSREEIEEEANGDI----FDIEIGVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSVK 181
                                                                                                                                                                                                                                                                            RRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGK----EDSSSTEFVEKRRA 237
                                                                                                                                                                                                                                                                                                RQHEEFIWLHDSFVENEDYAGYIIPPAPPRDFDASREKLQKLGEGEGSWTKEEFTKMKQ 127
                                                                                                                                                                                                                                                                                                                                                                           281 -----ILRMVNKAADAVNKMTIKMNESDAWFEEKQQQFENLDQQLRKLHVSVEALVCH 333
                                                                                                                                                                                                                                                                                                                                                                                                180 KKEKLEDFFKNMVKSADGVIVSGVK--DVDDFFEHERTFLLEYHNRVKDASAKSDRMTRS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEAKMWYANKPDKIQQAKNEIREW 453
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                           99
                                                                                                                                                                                   Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFT IN POSITION 404.
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Pohl T.M., Aljinovic G.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY. -!- SIMILARITY: CONTAINS 1 PX DOMAIN.
                                                                                                                                                        E3659DB19C59E1BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAKVQQGERDFEQISKTIRKEVGRFEKERVKDFKTVIIKYLE 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | | : ||:||:||: |: |: || |: ::: |
ETSQLCCQKFEKISESAKQELIDFKTRRVAAFRKNLVELAE 382
                                                                                                                                                                               9.5%; Score 248; DB 1; I
22.9%; Pred. No. 1.5e-06;
11ve 74; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P47057; Q06794;
01-FEB-1996 (Rel. 33, Created)
1-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sora S., Tiboni O., Sanangelantoni A.;
                                              EMBL; U83194; AAD24202.1; ALT_INIT
Genew; HGNC:14970; SNX6.
                                                                                                                                             PX.
                                                                                                                                                        SEQUENCE 406 AA; 46648 MW;
                                                                                                                               Transport; Protein transport.
DOMAIN 26 173
                                 EMBL; AF121856; AAD27829.1;
                                                                                                                                                                                          Local Similarity 22.99 tes 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorting nexin 4.
SNX4 OR YJL036W OR J1244.
                                                                              InterPro; IPR001683; PX. Pfam; PF00787; PX; 1. SMART; SM00312; PX; 1. PROSITE; PS50195; PX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                      MIM; 606098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNX4_YEAST
P47057; 00
                                                                                                                                                                               Query Match
                                                                                                                                                                                                        fatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --QPNKDEVTDAEMNAFKTVHKQNEE---FTEIREKSDKLDRTVTKIDKLFHKVVKKNDS 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 MSEDYTKLGSNLQELQELVTGENEELAAKLKIF-----NEGVTQLSYGLQDLTKYL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- EVEEKIDQLHQ----- EQAFADFYMFSELLSDYI-----RLIAAVKGV 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 DYEYIVDLKDLEHYIDSMRÖLIKLKDOKQIDY----EELSDYLTRSIKEKNNLISGYGG- 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 DRSREEI----EEEANGD----IFDIEIGVSDPEK-VGD--GMNAYMAYRVTTKTSLSMF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 -----SKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKS----IVGMTKVKVGK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDHRMKCWQKWEDAQITLLKKREAEAKMMVANKPDKIQQAKNEIREWEAKVQQGERDFEQ 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDSSSTEFVEKRRAALERYLORTVKHPTLLODPDLRQFLESS--ELPRAVNTQALSGAGI 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----SNFFANKLEELAGINQEASRREKINKLEGKITSLTGELENAKKVADG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLIKLKDQKQIDY -> PDQIERPETDRL (IN REF 2).
10964322A1A22F16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --EALVCHRKELSANTAAFAKSAAMLGNSEDHTALSRALSQLA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 8.7%; Score 228; DB 1; Length 423; Local Similarity 23.1%; Pred. No. 1.8e-05; les 107; Conservative 76; Mismatches 154; Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 YDNRGDPESIIVVHRRYSDLLLLHDILLNRF--PTCIIPPLPDKKVFQYIAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Butharia; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                     EMBL; Z49311; CAA89327.1; -.
EMBL; Z48229; CAA88260.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΡX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423 AA; 49002 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transport, Protein transport.
DOMAIN 29 157
                                                                                                                                                                                                                                                                                                     SGD; S0007467; SNX4.
InterPro; IPR001683; PX
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PROSITE; PS50195; PX; 1
                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00787; PX; 1.
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40,
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16-OCT-2001 (Rel.
15-JUN-2002 (Rel.
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SAIEKEWGDGLQSAGHHMDVYASSIDDILEDEEHYAD-----QLKEYLFYAEALRAVCR:319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 KHELMQYDLEMAAQDLASKKQQCEELVTGTVRTFSLKGMTTKLFGQETPEOREARIKVLE 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 -IFDIEIGVSDPEKVGDGMNA-----YMAYRVTTKTSLSWFSKSEF--SVKRRFSDFLG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPILCRDKIFYLFLTQEGNWKETVNE-----TGFQLKADSRLKALN-ATFRVKNPDKRFT
                                S.I.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 AEVEEKI-----DQLHQEQAFADFYMFSELLSDYIRLIAAVKGVF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEIREWEAKVOOGERDFEQISKTIRKEVGRFEKERVKDFKTVIIKYLESLVQTQQQLIKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 PERO----LOPAPLEPLGSPDAGLGAAVGKEAEGAG------EESSGVDTMTHNNF
                                                                                                                                                      nitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
FUNCTION: May be involved in several stages of intracellular
trafflicking.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 PEREPILSSEPSPAVTPVTPTLIAPRIESKSMSAPVIFDRSREEIEEEANGD---
SEQUENCE FROM N.A.
MEDLINE-99038232; PubMed-9819414;
Haft C.R., de la Luz Sierra M., Barr V.A., Haft D.H., Taylor
"Identification of a family of sorting nexin molecules and
"Intercirization of their association with receptors.";
Mol. Cell. Biol. 18:7278-7287(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3D5B52AC52A07686 CRC64;
                                                                                                                                                                                                                           THE SORTING NEXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 221; DB 1;
Pred. No. 4.6e-05;
                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE SORTIN SIMILARITY: CONTAINS 1 PX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF065485; AAC83149.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         BC018762; AAH18762.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interPro; IPR001683; PX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50195; PX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGNC:11175; SNX4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00787; PX; 1.
                                                                                                                                                          Strausberg R.;
Submitted (DEC-2001)
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                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 IEEEANGDIFDIEIGVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSVKRRFSDFLGL 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SFSGSDVQNKLKESAQCVGDEFLNCKLATRAKDFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P.A.;
sorting
                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: May be involved in several stages of intracellular trafficking (By similarity).
-i- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
-i- SIMILARITY: CONTAINS 1 PX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 194; Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Teasdale R.D., Loci D., Houghton F., Karlsson L., Gleeson "A large family of endosome-localized proteins related to next 1 "."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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90C5EDB761C31E88 CRC64;
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Pred. No. 0.00011;
                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                465 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-21378165; Pubmed-11485546;
                                                                                · PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88;
                                                                                                                         09Y5X2; 096I67;
16-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last sequ
15-0TW-2002 (Rel. 41, Last anno
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                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF121858; AAD27831.1; -
EMBL; BC007785; AAH07785.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE OF 4-465 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nexin 1.";
Biochem. J. 358:7-16(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:14972; SNX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00312; PX; 1 PROSITE; PS50195; PX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001683;
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nes 99; Conserv
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                                                                                         SNX8 HUMAN
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RESULT 14
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OY 301 -ESDAWFEEKOOOFENLDOOLKKLHVSVEA  Db 212 ADIOAOFAISRELINIYNSPHKLRDRAEN  Oy 353NSEDHTALSRALSOLAEVEE  Db 372 SWAALMSSTWGSIKGALKGLSVEFALLAD  OY 401 AA-VKGVFDHRMKCWGWWEDAOITLIKKRE  OY 400 AA-VKGVFDHRMKCWGWWEDAOITLIKKRE  OY 512 IDEAKAI 518  Db 437 RPKLSCL 443  RESULT 15  SNX9_HUMAN  OY 512 IDEAKAI 518  DD 512 IDEAKAI 518  DT 16-OCT-2001 (Rel 40, Last annotati)  DT 16-OCT-2001 (Rel 40, Last sequence  DT 16-OCT-2001 (Rel 40, Last annotati)  DE POCT-101 (Rel 40, Last annotati)  DE SNX9_HUMAN  SNY 90 S SH3PX1.  I 16-OCT-2001 (Rel 40, Last annotati)  E SOTTING NA. A.  RESULT 15  SOTTING NA. A.  RESULT 15  SOTTING SH3PX1.  I 10-OCT-2001 (Rel 40, Last sequence  DT 16-OCT-2001 (Rel 40)  SNY 90 S SH3PX1.  I 10-OCT-2001 (Rel 40)  SNY 90 S SH3PX1.

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(See http://www.isb-sib.ch/announce,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.6%; Score 200; DB 1; Length 595; Best Local Similarity 20.1%; Pred. No. 0.00085; Matches 103; Conservative 81; Mismatches 213; Indels 1.
                                                                                     This SWISS-PROT entry is copyright. It is produced through
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                                                                                                                      the Swiss Institute of Bioinformatics
                                                                                                                                                                          use by non-profit institutions as long a modified and this statement is not removed.
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or send an email to license@isb-sib.ch)
                                                                                                                                                 the European Bioinformatics Institute.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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EMBL; AF076957; AAD43001
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nterPro; IPR001452; SH3
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PROSITE; PS50002; SH3; 1
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544 MSYALQAEMNHFHSNRIYDYNSVIRLYLEQQVQ 576 qq

Search completed: March 4, 2003, 14:59:40 Job time : 14.4234 secs

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

March 4, 2003, 14:55:07; Search time 6.06686 Seconds (Without alignments) 848.711 Million cell updates/sec

US-09-763-902B-6 936 1 MGILLGLLLLGHLTVDTYGR......PLKATSTVKQSWDWTTDMDG 175 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched:

262574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_AA Database :

chance to have a result being printed, Pred. No. is the number of results predicted by chance to becore greater than or equal to the score of the result being and is derived by analysis of the total score distribution.

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## SUMMARIES

· ·	Appli Appl	Appi Appli Appli	Appl ppli	201 201 201 201	Appl Appl Appl Appl	Appl Appl Appl Appli Appli Appli	App
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9	-09-254-465 -08-597-495 -09-068-051	09-346-356 09-254-465 08-225-477 -US95-0435	9-254-4 8-979-4 9-272-4	US-09-651-200-; US-08-456-104-, US-08-479-744A US-08-280-757B	-205-697 -702-525 -651-200 595-0257	-08-205-697 -08-702-525 T-US95-0257 -08-724-394 -08-928-383 -09-462-270	JS-09-188-930
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US-09-462-270-2 US-09-254-465A-1 US-07-870-029-2	US-08-233-005-2 US-08-428-943-2	US-09-016-649-2 PCT-US95-04858-2	5260223-1	US-08-642-406A-22	US-09-199-534-22	US-09-199-534-22	US-08-434-000A-2	US-09-312-157-2	US-08-985-950-2	US-08-928-383B-23	US-08-928-383B-24	US-08-928-383B-26	US-09-404-879A-393	
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## ALIGNMENTS

RESULT 1

US-09-254-465A-2
; Sequence 2, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napler, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1216R1(US)
CURRENT APPLICATION NUMBER: US/09/254,465A
; CURRENT FILING DATE: 1999-03-05
, PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 2
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-465A-2

121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180 94; Gaps 1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60 Score 870; DB 4; Length 321; Pred. No. 9.9e-84; ); Mismatches 1; Indels 9 ö Query Match 92.9%; Best Local Similarity 64.7%; Matches 174; Conservative 61 121 ò g ŏ g δ

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PPLICANT: Tumas, Daniel PPLICANT: Wood, William I. SPLICANT: Wood, William I. COMPOSITIONS AND METHODS FOR THE TREATM! IIILE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS IIILE OF INVENTION: OF DISEASES
                                                                                                                                                                    TLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT TLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS ILE REFERENCE: P1216R1(US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 RDSSGDHIQQAKYQGRLHVSHKV-PGDVSLQLSTLEMDDRSHYTCEVTWQTP-DGNQVVR 127
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FILING DATE: 1998-11-20
APPLICATION NUMBER: US 60/066,364
                                                                                                                                                                                                                                      FILE REFERENCE: FILLOWARDS US/09/254,465A CURRENT APPLICATION NUMBER: US/09/254,465A LILING DATE: 1999-03-05
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Ashkenazi, Avi J
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Napier, Mary A.
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Goddard, Audrey
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-06
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PRIOR APPLICATION NUMBER:
                                                                                         , Sherman
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US-09-254-465A-24
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11arity 29.1%; Pred. No. 0.0083;
Conservative 21; Mismatches 52;
                                                                                                                                                               E: St. Onge Steward Johnston & Reens
986 Bedford Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             terson, B., and Yamada, Y.
Link protein cDNA sequence reveals
tandemly repeated protein sequence.
                                                           APPLICANT: Susan Hockfield
APPLICANT: Diane M. Jaworski
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: Incoman-Binding Protein
TITLE OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: St. Onge Steward Johnston & Ree
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 MD diskette
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    functional domains
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
RIOR APPLICATION DATA:
                               Application PC/TUS9504353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rat link protein
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/225
FILING DATE: API11 8, 1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                              SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                                                                                    Word Processor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION AUTHORS: Doege, K...
                                                                                                                                                                                                                                                  United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mary M. Krinsky
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ. ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 37; Conserva
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Score 95.5;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                    155 YPL----KATSTVKQSWDWTTDM 173
                                                                                                                                                                                                                                                                                                                                                       169 LPLOYEWOKLSDSOKMPTSWLAEM 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.2%;
26.0%;
                                                         Best Local Similarity 26.0 Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2:0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
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Best Local Similarity
Matches 53; Conserv
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US-09-651-200-23
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         US-08-979-424-3
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                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                  13 LTVDTYGRPILEVPESVTGPWKG-DVNLPCTYDPLQGYTQVLVKW--LVQRGSDPVTIFL 69
                                                                                                                                                                                                                                                                                       Length 273;
                                                                                                                                                                                             10.8%; Score 101.5; DB 4; Length 27.8%; Pred. No. 0.0082; tive 25; Mismatches 57; Indels
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SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lal, Preeti
APPLICANT: Cofley, Neil C.
TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN
UNMER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Incyte Pharmaceuticals, Inc
PRIOR APPLICATION NUMBER: US 60/078,936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: PCT/US98/19437
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 26
SEQ ID NO 26
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Filed Herewith
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REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
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Best Local Similarity 27.8%
55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 650-855-05:
TELEFAX: 650-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIOR APPLICATION DATA: APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                            ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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                                                                                                                                                              US-09-254-465A-26
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                                                                                                          LENGTH: 273
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US-08-979-424-3
                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                               55 --IEWLISPADNOKVDQVIILY---SGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTN 109
                                                                                                                                                                                                                                                                                                                                                                             103 LEMDDRSHYTCEVTWQTPDGNQ----VVRDKITELRVQKHSSKLL----KTKTEAPTTMT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                         110 LQLSDIGTYQCKVKKAPGVANKKIHLVVLVKPSGARCYVDGSEEIGSDFKIKČE-PKEGS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 VLVKWLVQRGS----DPVTIFLRDSSGDHIQQAKY---QGRLHVSHK--VPGDVSLQLST 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 --IEWLISPADNOKVDOVIILY---SGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTN 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 LEMDDRSHYTCEVTWQTPDGNQ----VVRDKITELRVQKHSSKLL----KTKTEAPTTMT 154
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                                                                                                                                                                 APPLICANT: DeGregori, James
TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes
FILE REFERENCE: 90-98
CURRENT APPLICATION NUMBER: US/09/272,496
CURRENT FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: US 60/092782
EARLIER FILING DATE: 1998-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MALLLCFVLL--CGVVDFARSLSITTPEEMIEKAKGETAYLPCKFTLSPEDGGPLD---- 54
                                                                                                                         1 MGILLGLLLLGHLTVDTYGRPI-LEVPESVTGPWKGD-VNLPCTY-----DPLQGYTQ 51
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                                                              43;
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DB 2; Length 365;
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                                                              Indels
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0.054;
ches 80;
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TITLE OF INVENTION:
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59 QRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQ 118
                                                                                                                                                                                                                                                                                                                                                                        60 QOKLVLYBHYLGTEKLDSV-NAKYLGRTSFDR---NNWTLRLHNVQIKDMGSYDCFIQKK 115
                                                                                                                                                                                                                                                                                       7 MGLAILIFVIV-----LLISDAVSVETQAYFNGTAYLPCPFTKAQNISLSELVVFWQD 59
                                                                                                                                                                                                  Indels 18; Gaps
                                                                                                                                                                                                                                              5 LGLLLLGHLTVDTYGRPILEVPESVT----GPWKGDVNLPCTYDPLQ--GYTQVLVKWLV 58
                                                                                                                                                   Length 309;
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                                                                                                                                                                                                                                                                                                                                                                                                                             119 TPDGNQVVRDKITELRVQKHSSKLLKTKTEAPITMTYPLKATSTVKQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 92; DB 2; Len
Pred. No. 0.099;
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APPLICATION NUMBER: US/08/479,744A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                  33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: LAHIVE & COCKFIELD, LLP 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3, Application US/08479744A 6084067
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APPLICATION WUMBER: 08/147,773
FILING DATE: 3-NOV-1993
TTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Freeman, Gordon J. APPLICANT: Nadler, Lee M. APPLICANT: Gray, Gary, S. TITLE OF INVENTION: No. 6084067 TITLE OF INVENTION: Uses Theref CORDERCES: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
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                                                                                                                                                      Query Match 9.8%;
Best Local Similarity 24.0%;
Matches 40; Conservative 3
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amino acid
                       : 309 amino acids
amino acid
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SEQUENCE CHARACTERISTICS
                                                                                ) MOLECULE TYPE: protein US-08-456-104-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
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APPLICATION NUMBER:
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APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 QRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQ 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGLAILIFVTV-----LLISDAVSVETQAYFNGTAYLPCPFTKAQNISLSELVVFWQD 53
                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.8%; Score 92; DB 4; Length 303; Best Local Similarity 24.0%; Pred. No. 0.096; Matches 40; Conservative 33; Mismatches 76; Indels
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  NCE: 15966-562 (CURA-62)
LICATION NUMBER: US/09/651,200
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60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,104
                                                     1999-09-03
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RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
                                                                                                              60/172909
                                         CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60,1523
PRIOR PELING DATE: 1999-03
PRIOR APPLICATION NUMBER: 60,71729
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 25
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                  ; Score 92; DB 3; Length 309;
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33; Mismatches 76; Indels
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REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP2
FELECOMMUNICATION:
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APPLICATION NUMBER: US/08/280,757B
FILING DATE: 26-JUL-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08280757B
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PPLICATION NUMBER: 08/109,393
TLING DATE: 19-AUG-1993
PPLICATION NUMBER: 08/147,773.
TLING DATE: 3-NOV-1993
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                                                            Best Local Similarity 24.0 Matches 40; Conservative
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MEDIUM TYPE: Floppy
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Human, protein transport molecule, PTAM; diagnosis, cytostatic; antiarthritic; antiasthmatic; immunosuppressant; antiarteriosclerotic; antiallergic; antidiabetic; antilipaemic; antirheumatic; osteopathic; dermatological; antidiamemic; antipsoriatic; hepatotropic; antigout;
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Baughn MR, Patterson C;
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                             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Perfect score:
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molecules (PTAMS) given in AAN92317 to AAN82324. The PTAMS have cytostatic, antiarthritic, antialergic, antidiabetic, antilarpressant, antiarthritic, antiallergic, antidiabetic, antilipaemic, antirheumatic, osteopathic, dermatological, antianaemic, antipaemic, contropic, antigout, antialiarmatory and antiary activities, and protection transport. PTAM proteins and antagonists are useful for expression or activity of PTAM. PTAM polynucleotides are useful for expression or activity of PTAM. PTAM polynucleotides are useful for compression or activity of PTAM. PTAM polynucleotides are useful for complex, proposed with decreased or increased diagnosing conditions associated with PTAM, comprising detecting PTAM by comprising detecting pram by biological sample. Diseases prevented, treated or diagnosed include cell proliferative disorders such as cancers, immune disorders, secretory treated or disorders and other conditions associated with abnormal vestice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trafficking, such as allergies, asthma, urticaria and autoimmune haemolytic anaemia. Anti-PTAM antibodies may be used as autoimmune a targeting or delivery mechanism for bringing pharmaceutical agents into cells or tissues expressing PTAM and for diagnosis of PTAM, red advisor and sor screening using libraries of compounds. PTAM, and the screening wing libraries of compounds. PTAM polynucleotides are useful for generating hybridisation proposed.
                                                                                                    New human protein transport-associated polypeptide and polynucleotide useful for diagnosis, prevention and treatment of cell proliferative and secretory disorders such as leukemia, cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for generating hybridisation probes useful in mapping the naturally occurring genomic sequences.
                                                                                                                                                                                                                                                                              encode the human protein
                                                                                                                                                                                                            Claim 1; Page 60-61; 75pp; English.
                              2000-256642/22
                           WPI; 2000-256642,
N-PSDB; AAA08035
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480 AA Seguence

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OTPKDSPSKSSAEAOTPEDTPNKSGAEAKTOKDSSNKSGAEAKTQKGSTSKSGSEAOTTK 120
                                                                                                 DSTSKSHSELQTPKDSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPN 180
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Ouery Match
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Best Local Similarity 100.0%; Pred. No. 1.7e-154;
Matches 480; Conservative 0; Mismatches 0;
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RESULT

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The present invention describes a human trans-Golgi network protein designated hTGN48-iso. hTGN48-iso is expressed in tissue near liver cancer cells. Also described are methods for the preparation and detection of the hTGN480iso protein and nucleotide sequences. The present sequence represents the human hTGN48 protein which is used in comparison with the hTGN48-iso protein in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNKVVPEQPSRKDH 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 SKPISNPSDNKELPKADINQLADKGKLSPHAFKTESGEETDLISPPOEEVKSSEPTEDVE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHFFAYLVTAAILVAVLYIAHHNKRKIIAFVLEGKRSKVTRRPKASDYQRLDQKYVLILN 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human trans-Golgi network protein isomer and its coded sequence
                                                                                                                             Human; hTGN48-iso; hTGN48; TGN; trans-Golgi network; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                           (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1205.5; DB
Pred. No. 4.4e-72;
1; Mismatches 4
   standard; Protein; 251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 18; 20pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB57023 standard; Protein; 1072
                                                                                             Human hTGN48 protein sequence.
                                                                                                                                                                                                                                                                                            11-APR-2000; 2000CN-0115366.
                                                                                                                                                                                                                                                              11-APR-2000; 2000CN-0115366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.0%;
95.2%;
                                                           22-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-183594/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VF-PAPPKR 450
                                                                                                                                                                                                                                                                                                                                                           Xiao H, . Qian B,
                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                            CN1272541-A.
AAB74607
                                 AAB74607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB57023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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ABB57023
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AKSPMKEGAKPPEKAKPLDVKSPEAQTPVQEEANDPTDIRPPEQVKSPAKEKAK-SPEKE. 853

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19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               737 AKSPAEAKSPIEVKSPEKAKTPVKEGAKSPAEAKSPEKA--KSPVKEDIKPPAEAKSPEK 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 SKSGSEAQTTKDSTSKSHSELQTPKDSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        621 AEAKSPÄEAKSPAEAKSPAEAKSP--ATVKSPGEAKSPSEAKSPAEAKSPAEAKSPAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 SEAQTIKDVPNKSGADGQIPKDGSS----KSGAEDQIPKDVPNKSGAEKQIPKDGSN--- 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --NOLADKGKLSPHAF 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 TKSHPEPQTPKDSPSKSSAEAQTPEDTPN----KSGAEAKTQKDSSNKSGAEAKTQKGST 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563 AKSPAEPKSPAE--PKSPAEAKSPAEPKSPATVKSPGEAKSPSEAKSPAEAKSPAEAKSP 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.4%; Score 304; DB 23; Length 1072; Best Local Similarity 25.6%; Pred. No. 6.8e-12; Matches 117; Conservative 82; Mismatches 148; Indels 110;
Mouse ischaemic condition related protein sequence SEQ ID NO:9
                                                                           Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ishii Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 AAAGAVPLLATESVKQEEA---GVRPSAGNVST----HPSLSQRPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 72-76; 2690pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asai S, Takahashi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                     8-MAY-2001; 2001WO-JP04192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .8-MAY-2000; 2000JP-0145977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-034733/04.
N-PSDB; ABI99206.
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                                                                                                                                                                                                                                                              WO200188188-A2.
                                                                                                                                                                                           Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ishikawa K,
                                                                                                                                                                                                                                                                                                                                          22-NOV-2001
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pheumoniae, Pseudomonas aeruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. Programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation is wide variety of organisms. The present sequence represents an
                      Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at format directly trom MIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus cellular proliferation protein #251
                                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wall D,
                                                                        340 K-----EEKEKMSGSASSENREGTLSDSTGSEKD 368
                                                                                                           914 KVEEKKETPTEKPKDSTAEAKKEEAGEKKKAVASEEE 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq ID No 5471; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohlsen KL, Zyskind JW,
Xu HH;
                                                                                                                                                                                                                AAU33975 standard; Protein; 1021 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        essential prokaryotic cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-253625P
2000US-257931P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6-FEB-2001; 2001US-269308P
                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-611495/70.
N-PSDB; AAS51834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200170955-A2
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27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                              14-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3-MAY-2000
6-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001
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                                                                                                                                                                                                                                                       AAU33975;
                                                                                                                                                                         RESULT 4
                                                                                                                                                                                               AAU33975
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us-09-763-902b-1.rag

antibiotics, comprise sequences of antisense nucleic acids

Example 3; Seq ID No 12544; 511pp;

inhibitors English,

to antisense

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75 OTPEDTPNKSGAEAKTOKDSSNKSGAEAKTOKGSTSKSGSEAQTTKDSTSKSHSELQTPK 134
                                                                                                                                                                                                       135 DSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGADGQTPKDGSS 194
                                                                                                                                                                                                                                                             255 EQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFKTESGEETDLISPPQEEVKS 314
                                                                                                                                                                                                                                                                                                                             ---SA 896
                                                                                                                                                                                                                                                                                                                                                                            SDSDSGSDSDSASDSDSGSDSDSSSSDSDSASDSTSDTESDNDSDSESDSNSDSDSGSN 956
                                                                                                                                                                                                                                                                                                                                                          ----TGSE 366
                                                                             ATESVKQEEAGVRPSAGNVSTHPSLSQRPGGS-----TKSHPEPQTPKDSPSKSSAEA
                                                                                                                                                   195 KSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNKVVP
                                                          24;
                                Length 1021;
                       846 ESDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSASDSDSGSDSD---
                                                                                                                                                                                                                                                                                                                                                SEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSAS---SENRECTLSDS-
                                                                                                                                                                                                                                                                                                                                                                                                                            57 NNVVPPNSPKNGTNASN 973
                                                                                                                                                                                                                                                                                                                                                                                                        367 KDDLYPNGSGNGSAESS 383
                                                       Conservative
 1021 AA;
                                        Similarity
                                                    84;
 Sequence
                          Query Match
Best Local
                                        Best Loca
Matches
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prokaryotic cellular proliferation, their use in identifying the genes their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruqinosa and Entercoccus faecalis. The form of a also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an avide variety of organisms.

of the printed specification, but was obtained in electronic format directly from WIPO at

tp.wipo.int/pub/published\_pct\_sequences

1021 AA;

Seguence Query Match

essential prokaryotić cellular proliferation protein

Length 1021;

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Staphylococcus aureus cellular proliferation protein #1121
                                                                                                                                     Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
AAU36951 standard; Protein; 1021 AA.
                                                                                                                                                                                                                                                                                                                                             20000S-206848P.
                                                                                                                                                                                                                                                                                                                                                                               2000US-242578P.
2000US-253625P.
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                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                      Staphylococcus aureus
                                                                                                                                                                                                                      WO200170955-A2
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27-NOV-2000;
22-DEC-2000;
                                                                       14-FEB-2002
                                                                                                                                                                                                                                                                                                                             21-MAR-2000;
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                                                                                                                                                                                                                                                          27-SEP-2001
                                   AAU36951;
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Trawick JD, . Carr GJ;

Wall D,

Zyskind JW,

KĽ,

Ohlsen F Xu HH;

Haselbeck R, Yamamoto RI,

WPI; 2001-611495/70. N-PSDB; AAS54810.

polynucleotides for the identification and development of

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OTPEDTPNKSGAEAKTOKDSSNKSGAEAKTOKGSTSKSGSEAOTTKDSTSKSHSELOTPK 134
                                                                                                                                                             DSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGADGQTPKDGSS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                       SDSDSGSDSDSDSDSDSDSDSDSDSDSDSTESDTESDNSDSDSGSN 956
                                                                                                                                                                                                                                                                                  254
                                                                    22 ATESVKQEEAGVRPSAGNVSTHPSLSQRPGGS-----TKSHPEPQTPKDSPSKSSAEA 74
                                                                                                                                                                                                                                                                                                                                                                                                           SEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSAS---SENREGTLSDS----TGSE
                                                                                                     195 KSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNKVVP
                                                                                                                                                                                                                                                                                                EQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAPKTESGEETDLISPPQEEVKS
                                                                                                                                                                                                                                                                                                                                                                 SdrF; SdrG; SdrH; coagulase negative; staphylococcus; scepticemia; osteomyelitis; endocarditis; immune response; vaccine; graft; stent; intravenous catheter; heart valve; cardiac.
                                      Indels 24;
12.3%; Score 302; DB 22; 22.3%; Pred. No. 8.8e-12; ive 81; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY83170 standard; Protein; 1802 AA.
                 Best Local Similarity 22.38
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDDLYPNGSGNGSAESS 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNVVPPNSPKNGTNASN 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Recombinant or synthetic proteins from coagulase-negative staphylococciseful for prevention, treatment and diagnosis of staphylococcal infections bind soluble and immobilized fibrinogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHPEPQTPKDSPSKSSAEAQTPEDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 AQTIKDSTSKSHSELQIPKDSTGKSGAEAQIPEDSPNRSGAEAKIQKDSPSKSGSEAQIT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 SKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated Staphylococcus Sdr cell wall proteins which bind both soluble and immobilized fibrinogen are useful for treating or preventing coagulase-negative staphylococcal infection such as scepticemia, osteomyelitis or endocarditis, and for inducing immune responses in patients. The cell wall proteins are also useful for reducing coagulase-negative staphylococci infection of induciling medical devices such as vascular grafts, vascular stents, intravenous catheters, artificial heart valves and cardiac assist devices. The cell wall associated proteins are able to inhibit cells present on the surface of implanted biomaterials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N1 Eldhin D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 KDVPNKSGADGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1802;
                                                                                                                                                                                                                                                                       /note= "Position encoded by TAA stop codon" 1800
                                                                                                                                                                                                                                                                                                                                            'note= "Position encoded by TGA stop codon"
                                                                                            'note- "Position encoded by TAA stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 11.6%; Score 285.5; DB 21; Length Best Local Similarity 22.0%; Pred. No. 2e-10; Matches 93; Conservative 84; Mismatches 209; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hartford O, McCrea K,
                                                                                                                                                                                             by TAG stop
                                                                                                                                            by TAA stop
                                                                                                                                                                                                                                                stop
                                                                                                                                                                                                                                              by TGA
                                                                                                                                            note- "Position encoded
                                                                                                                                                                                             'note- "Position encoded
                                                                                                                                                                                                                                              encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN (TEXA) UNIV TEXAS A & M SYSTEM.
                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                              note- "Position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Davis S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0098443.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              claim 2; Figure 2; 104pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-256637/22.
N-PSDB; AA293533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Poster IJ, Hook M,
                                                                                                                                                                      Misc-difference 177
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Staphylococcus sp
                                                                                                                                                                                                                                                                          Misc-difference
                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                             W0200012689-A1
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25-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAR-2000
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                                  TESGEETDLISPPQEEVKS----SEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSA 350
                                                                       S-SENREGTLSDSTGSEKDDLYPNGSGNGSAESSHFFAYLVTAAILVAVLYIAHHNKRKI 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition used for generating immune response or for inhibiting microbial colonization in an animal comprises antibodies that bind collagen binding protein fibrinogen binding protein governoment fibrinogen binding protein and, optionally, fibronectin binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microbial surface components recognising adhesive matrix molecules; collagen binding protein; CBP; CNA; fibrinogen binding protein; CBP; CLumping factor B; ClBP; FNBP; Clumping factor A; ClFA; Clumping factor B; ClFB; FNBP; fibronectin binding protein; Staphylococcus infection; serine-aspartate regeat region protein; SDR protein; SdrF.
                                                                                                                                                IAFVLEGKRSKVTRRPKASDYQRLDQKYVLILNVFPAPPKRSFLPQVLTEWYIPLEKDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multicomponent vaccine; immunostimulatory; antibacterial; MSCRAMM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staph. epidermidis serine-aspartate repeat region protein SdrF
                                                                                                             --GTLLGTLFAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Encoded by in-frame stop codon TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note- "Encoded by in-frame stop codon
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                                                                                                    SDSDSDSDSDSDKNAKDKL-PDTGANEDHDSK---
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(QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
12
                                                                                                                                                                                                                                                                                                                                                    AAY70119 standard; Protein; 1802 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Fig 3; 115pp; English
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                                                                                                                                                                       : :| |:| | : | CALLLGRRRKKDNKEKX---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INHI-) INHIBITEX INC
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N-PSDB; AAZ51201.
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                                                                                                                                                                                                                                                             1800 XVW 1802
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                                                                                                                                                                                                                         HQW 472
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combinations of bacterial binding proteins termed MSCRAMM (microbial surface components recognising adhesive matrix molecules) or their antibodies. A vaccine composition is provided that includes collagen binding protein or peptide, e.g. CNA, a fibrinogen binding protein or peptide, e.g. CNA, a fibrinogen binding protein composition is provided that includes collagen binding protein or peptide, e.g. CNA, a fibrinogen binding protein continually a fibromectin binding protein e.g. Febra, and optionally a fibromectin binding protein e.g. Febra, The vaccines are useful for imparting protection against a broad spectrum of Staphylococcus aureus, in an animal. The combinations can also be used to select donor blood pools for the present sequence is a serine-asparate repeat region protein, sdrf from Staphylococcus enidermidie
                                                                                                                                                                                                                                                                                           protein, SdrF from Staphylococcus epidermidis. The Sdr protein is useful in vaccine preparation in combination with specific bacterial binding proteins. These vaccines can be used to treat a broad spectrum of bacterial infections, including those arising from both coagulase-positive and coagulase-negative bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 SHPEPQTPKDSPSKSSAEAQTPEDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 AQTTKDSTSKSHSELQTPKDSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTT 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-SENREGILSDSTGSEKDDLYPNGSGNGSAESSHFFAYLVTAAILVAVLYIAHHNKRKI 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 IAFVLEGKRSKVTRRPKASDYQRLDQKYVLILINVFPAPPKRSFLPQVLTEWYIPLEKDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.6%; Score 285.5; DB 21; Length 1802; 22.0%; Pred. No. 2e-10; Live 84; Mismatches 209; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ClfA; fibrinogen binding protein; bacterial colonisation; indwelling medical device; staphylococcal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus fibrinogen binding ClfA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY58435 standard; Protein; 933 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 22.0%
les 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          1802 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1800 XVW 1802
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                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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ID AAY
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fibringgen binding protein, Ciff. Ciff is an important receptor anolyed in S. aureus colonisation of indwelling medical devices (e.g., catheters, artificial heart valves). Shortly after implantation, the surfaces of medical devices become coated with host plasma and matrix proteins such as fibringoen and fibronectin, and there is considerable evidence to suppose that bacterial adherence to fibringoen/fibring is important in the initiation of device-related infection. The fibringoen-binding region of Ciff is thought to reside between residues important in the initiation of Ciff is thought to reside between residues of fibringoen-binding region of Ciff is thought to reside between residues repeated region (region R) comprising 154 repeats of the dipeptide cremains contains a repeated region (region R) comprising 154 repeats of the dipeptide cremains of other Gram positive bacteria that are responsible for anchoring the protein to the cell wall and cell membrane. Ciff, or its framments, may be used to block S. aureus colonisation of wounds, to provent adherence of S. aureus to indwelling medical devices, as vaccines to protect against S. aureus infection (e.g., mastitis in runnants), to raise specific antibodies, and for diagnosis (by runnants).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                      560.867
/note= "Region R"
896.900
/note= "Gram positive wall-associated consensus motif"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      535 SGDGIDKPVVPEQPDEPGEIEPIPEDSDSDPGSDSGSDSNSDSGSDSGSDSTSDSGSDSA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 AGNVSTHPSLSQRPG--GSTKSHPE-----PQTPKDSPSKSSAEAQTPEDTPNKSGAEAK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adhesion of S. aureus and for diagnosis. Nucleotides encoding ClfA its fragments may be used as diagnostic probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPNRSGAEAKTOKDSPSKSGSEAOTTKDVPNKSGADGOTPKDGSSKSGAEDOTPKDVPNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding the fibrinogen-binding protein of saureus, useful for treatment or prevention of infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agglutination or immunoassay). The specific antibodies are used for passive immunisation, to block infection
                                                                                                                                   332. 550
/note- "Fibrinogen-binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents the Staphylococcus aureus
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; Pred. No. 1.2e-10;
83; Mismatches 173;
                                                "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELIZABETH COLLEGE DUBLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2A-1-4; 35pp; English
Location/Qualifiers
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J..559
∵re= "Region A"
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Conservative 8
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                                                                                                               note-
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Best Local Similarity
Matches 80; Conserv
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Peptide
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ΐ,

Staphylococcus aureus

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binding protein. It is useful as a vaccine to protect against human and animal infections caused by S.aureus, such as against mastilis, to block S.aureus from colonising and infecting a wound, to block adherence of S.aureus to indwelling medical devices such as catheters, replacement heart valves and cardiac assist devices. The protein can be used to diagnose batterial infections. Polyclonal and monoclonal antibodies raised against the fibrinogen binding protein are useful for passively immunising against infections caused by S.aureus, to prevent infection of a wound and to diagnose bacterial infections.
                                                                                                                                                                   --SSDSDSESDSNSDSESGSNNNVVPPNSPKNGTNA 883
                                                                                               towel Staphylococcus aureus fibrinogen binding protein useful as raccine to prevent infection, promote wound healing, block adherence indwelling medical devices and for diagnosing staphylococcus aureus
SCAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNP 269
                                 774
                                                                     SDNKELPKADTNQLADKGKLSPHAFKTESGEETDLISPPQEEVKS-----SEPTEDVE 322
                                                                                                                                             PKEAEDDDTGPEEGSPPKEEKEKMSGSASSENREGTLSDS-TGSEKDDLYPNGSGNGSAE 381
                      The present sequence is a novel Staphylococcus aureus fibrinogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ibrinogen binding protein; bacterial infection; mastitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 284; DB 22;
Pred. No. 1.2e-10;
3; Mismatches 173;
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                                                                                                                                                                                                                                                                                                                                         AAB69508 standard; Protein; 933 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      staphylococcus aureus ClfA protein.
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llarity 22.1%;
Conservative 83
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                                                                                                                                                                                SDSASDSDSGSDSDS---
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N-PSDB; AAF58593.
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SN 885
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                                                                                                                                                                                                                SS 383
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Best Local S
Matches 80
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210
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AGNVSTHPSLSQRPG--GSTKSHPE-----PQTPKDSPSKSSAEAQTPEDTPNKSGAEAK 89

83;

1 Similarity 80; Conserv

37

Indels 26;

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Fibrinogen-binding protein; alpha chain; beta chain; ClfB; SdrC; SdrD; SdrE; fibrinogen; medical device; competitive inhibitor; pharmaceutical. treatment; infection; septicemia; osteomyelitis; mastitis: endocarditis extracellular matrix; vagcular graft; vascular stent; vaccine;
                                                                                                      209
                                                                                                                                                                269
                                                                                                                                                                                                                        SDNKELPKADTNQLADKGKLSPHAFKTESGEETDLISPPQEEVKS-----SEPTEDVE 322
                                                                                                                                                                                                                                                                                  PKEAEDDDTGPEEGSPPKEEKEKMSGSASSENREGTLSDS-TGSEKDDLYPNGSGNGSAE 381
                                                                                                                                                                                                                                                                                                   654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ar matrix; vascular graft; vascular stent; vaccine;
catheter; artificial heart valve; cardiac assist device;
                                                                                                                       90 TOKDSSNKSGAEAKTOKGSTSKSGSEAQTIKDSTSKSHSELQTPKDSTGKSGAEAQTPED
                                                               SPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGADGQTPKDGSSKSGAEDQTPKDVPNK
                                                                                                                                                                SGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNP
                                                                                                                                                                                                                                                    Staphylococcus aureus fibrinogen-binding proteins for treating septicemia, osteomyelitis, mastitis or endocarditis
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FORFAS T/A BIORESEARCH IRELAND.
FOSTER T J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment; infection; septicemia; extracellular matrix; vascular gra
                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; 918
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JOSEFSSON E.
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PERKINS S E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-357844/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOOK M A O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY08640 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibacterial
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26-NOV-1997;
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Perkins SE;
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                                                                                                                                                                                                                                                                                                                                               SS 383
                                                                                                                                                                                                                                                                                                                                                                               885
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884 SN
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FORF-)
FOST/)
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skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome.

Staphylococcus aureus

EP786519-A2 10-JUL-1997

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Sure). Staphylococcus aucusus is thought to utilize fibrinogen to adhere to medical devices binding proteins that bind both the alpha and beta fibrinogen chains (clfb, SdrC, SdrD and SdrE) can therefore be used as competitive inhibitors to block this binding. Antibodies against clfb, SdrC, SdrD and SdrE mediated binding. The proteins of the invention can be used in a pharmaceutical composition for the treatment of Staphylococcus aureus infection e.g. septicemia, osteomyelitis, mastitis or endocarditis or to inhibit the binding of S. aureus to the extracellular matrix. The proteins or their fragments may be used to coat a medical device to reduce the S. aureus infection of an indwelling medical device, especially where the medical device is selected from the group consisting of vascular grafts, vascular stents, intravence at partificial heart valves, and cardiac assist devices. Clfb, SdrC, SdrD, SdrE, or an active fragment, subdomman or encoding gene may be used as a vaccine. The DS (appartate serine) repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region or a gene encoding it may be used as an identifying probe for the identification of genes and encoding proteins from Staphylococcus aureus (other than CIEA), S. hemolyticus, S. lugdenensis, and S. schleriferi. The proteins of the invention have antibacterial activity.
                                                                                            Staphylococcus aureus fibrinogen-binding
                                                                                                                                                      (and their encoding nucleic acids are ClfB, SdrC, SdrD and
                                                                                   This invention describes novel Staphylococcus aureus fibrinoc proteins that bind both the alpha and beta fibrinogen chains
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918 AA; Sequence

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99 GAEAKTOKGSTSKSGSEAQTTKDSTSKSHSELQTPKDSTGKSGAEAQTPEDSPNRSGAEA 158
                                                                           KTQKDSPSKSGSEAQTTKDVPNKSGADGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPK 218
                                                                                                                                                                                                                                                                                                                              PKEEKEKMSGSASSENREGTLSDSTGSEKDDLYPNGSGNGSAESSHFFAYLVTAAILVAV 398
                                                                                                                                                                                                                                                                                                                                                  PNNEQKAPSNPKGEVNHSNKVSK---QHKTDALPETGDKSENTNATLFGAMM--ALLGSL
                                                                                                                                                                            DGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKA
                                                                                                                        DTNQLADKGKLSPHAFKTESGEETDLISPPQEEVKSSEPTEDVEPKEAEDDDTGPEEGSP
                                                                                                                                                                                                                                                                                                  28;
  Length 918;
50 PGGSTKSHPEPQTPKDSPSKSSAEAQTPEDTPNK---
              Best Local Similarity 21.6
Matches 80; Conservative
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 Query Match
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skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the 5191 S aureus DNA sequences contained on the computer readable medium.

936 AA;

Sequence

This sequence represents a Staphylococcus aureus protein sequence of the invention. The DNA sequences encoding the S.aureus proteins are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, for polysoning, osteomyelitis, skin and surgical wound infections, scaled in a sample of the surface of the standard with the second of the standard with the second of the standard with the second of the standard of the standard of the standard of the second of the standard of

Staphylococcus aureus in the production of

Polynucleotide(s) and proteins derived from stored on computer readable medium and used

WPI; 1997-374922/35.

anti-S.aureus vaccines Polynucleotide(s) and

Claim 23; Page 3255-3258; 3271pp; English.

Kunsch CA;

Fannon MR,

Chol GH, Dillon PJ,

Barash SC, Rosen CA;

HUMA-) HUMAN GENOME SCI INC

97EP-0100117.

07-JAN-1997; 05-JAN-1996;

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37 AGNVSTHPSLSQRPGGSTKSHPEPQTPKDSPSKSSAEAQTPEDTPNKSGAEAKTQKDSSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 KADINQLADKGKLSPHAFKTESGEETDLISPPQEEVKSSEPTEDVE----PKEAEDDDT
                                                                                                                                                          Indels
11.4%; Score 281; DB 18; 22.9%; Pred. No. 1.9e-10; ive 73; Mismatches 170;
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                                                                     Local Similarity
nes 75; Conserv
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331 884

Computer readable medium; vaccine; S.aureus infection; immuno cellulitis; eyelid infection; food poisoning; osteomyelitis;

Staphylococcus aureus protein SEQ ID #5249.

(first entry)

16-MAR-1999

AAW89801

AAW89801 standard; Protein; 936 AA

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617 AA;
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB20884;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying ene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 TPN-----KSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSKSHSELQTP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 AKSPVKEEAKSPAEAKSPVKEEAKSPAEVKSPEKAKSPTKEEAKSPEKAKSPEKEEAKSP 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKAKSPVKAEAKSPEKAKSPVKAEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAK 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKAKTLDVKSPEAKTPAKEEARSPADKFPE 380
                                                                                                                                                                                                                                                       Human; foetal liver; gene expression; single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEPQTPKDSPS-----KSSAEAQTPED 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 617;
                                                                                                                                                                                                                Peptide #2951 encoded by human foetal liver single exon probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   larity 22.9%; Pred. No. 4.4e-10; Conservative 66; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank DR;
Db. 885 NASNKNEAKDSKEPLPDTGSEDEANTSL 912
                                                                                                 ABB35445 standard; Peptide; 617 AA
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2000US-0608408
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2000US-0234687
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                                                                                                                                                                                                                                                                                                                                  40200157277-A2.
                                                                                                                                                                                                                                                                                                 Homo sapiens.
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Best Local Simil
Matches 106; C
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30-JUN-2000;
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                                                                                                                                        ABB35445;
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                                                           RESULT 12
ABB35445
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA11355-BAB41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from Wipo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein #2883 encoded by probe for measuring heart cell gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                         381 KAKSPVKEEVKSPEKAKSPLKADAKAPEKEIPKKEEVKSPVKEEEKPQEVKVKEPPKKAE 440
                                                                                                                                                                  -SDNKELPKADTNQ----LADKGKLSPHAFKTESGEETDLI 305
--EQPSRKD 261
                                                                                                                                                                                                                                                 EEKAPATPKTEEKKDSKKEEAPKKEAPKPKVEEKKEPAVEKPKESKVEAKKEEAEDKKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene expression; heart: microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
                                                                                                                                                                                                                                                                                                                                     SPPOEEVKSS-EPTEDVEPKE-----AEDDDTGPEEGSPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 --- EKMSGSASSENREGTLSDSTGSEKDDLYPNGSGNGSAES 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      561 KPEEKPKTEAKAKEDDKTLSKEPSKPKAEKAEKSSSTDOKDS 602
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30-JAN-2001; 2001WO-US00670
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               Single
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                               brains
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                                                                                                                                                                                                                                                                                                                                                                                                                  임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             luman brain expressed single exon probe encoded protein SEQ ID NO: 28374.
                                                                                                                                                                                                                               : : | | | : | | | : | | EKAKSPVKAEAKSPKAEAKSPKEEAKSPEKAKSPVKEEAKSPEKAK 320
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                                                                                                                                                                                                                                                                                           SPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKAKTLDVKSPEAKTPAKEEARSPADKFPE 380
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                                              Gaps
                                                                            VKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEPQTPKDSPS-----KSSAEAQTPED 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uman; brain expressed exon; gene expression analysis; probe;
lcroarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                            80 TPN-----KSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSKSHSELQTP
                                                                                                                                                                AKSPVKEEAKSPAEAKSPVKEEAKSPEKAKSPEKAKSPEKAKSPEKEEAKSP
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                                              Indels 105;
               DB 22; Length 617;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPEEKPKTEAKAKEDDKTLSKEPSKPKAEKAEKSSSTDQKDS 602
                                              66; Mismatches 185;
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                              No. 4.4e-10;
               Score 272.5;
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0-JUN-2000; 20000S-0608408
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                                             Conservative
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                          Local Similarity
es 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pilepsy; cancer
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               Query Match
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13;
                                                                                                                                                                                                                                                                                                                                                   epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                         The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples,
                                                                                                                                                                                                                                                                                    which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis; schizophrenia,
nucleic acid probes for analyzing gene expression in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SDNKELPKADINQ----LADKGKLSPHAFKTESGEETDLI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEKAPATPKTEEKKDSKKEEAPKKEAPKPEEKKEPAVEKPKESKVEAKKEEAEDKKKV 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 VKSPEKAKSPAKEEAKSPPEAKSPEKEEAKSPAEVKSPEKAKSPAKEEAKSPAEAKSPEK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPN-----KSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSKSHSELQTP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKAKSPVKAEAKSPEKAKSPVKAEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAK 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 AKSPVKEEAKSPAEAKSPVKEEAKSPAEVKSPEKAKSPTKEEAKSPEKAKSPEKEEAKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A---DGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQ--GPID----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 105;
                                                                                                   Example 4; SEQ ID NO: 28374; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 272.5; DB 22;
Pred. No. 4.4e-10;
5; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKOEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEPQTPKDSPS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 --- EKMSGSASSENREGTLSDSTGSEKDDLYPNGSGNGSAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             561 KPEEKPKTEAKAKEDDKTLSKEPSKPKAEKAEKSSSTDQKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPPQEEVKSS-EPTEDVEPKE-----AEDDDTGPEEGSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GPSKSGAEEQTSKDSPNKVVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.1%;
ilarity 22.9%;
Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity Matches 106, Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     617 AA;
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13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e present invention relates to human single exon nucleic acid probes ENP: see AAI10068-AAI28459). The present sequence is a peptide encoded one such probe. The SENPs are derived from human HeLa cells. The SENPs and be used to produce a single exon microarray, which can be used for asuring human gene expression in a sample derived from human cervical ithelial cells. By measuring gene expression, the probes are therefore eful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lote: The sequence data for this patent did not form part of the printed pecification, but was obtained in electronic format directly from WIPO It ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 AKSPVKEEAKSPAEAKSPVKEEAKSPAEVKSPEKAKSPTKEEAKSPEKAKSPEKEEAKSP 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 EKAKSPVKAEAKSPEKAKSPVKAEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 A----DGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQ--GPID---- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 SPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKAKTLDVKSPEAKTPAKEEARSPADKFPE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381 KAKSPVKEEVKSPEKAKSPLKADAKAPEKEIPKKEEVKSPVKEEEKPOEVKVKEPPKKAE 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          501 PTPEKEAPAKVEVKEDAKPKEKTEVAKKEPDDAKAKEPSKPAEKKEAAPEKKDTKEEKAK 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 TPN-----KSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSKSHSELQTP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- DSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --EQPSRKD 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441 EEKAPATPKTEEKKDSKKEEAPKKEAPKPKVEEKKEPAVEKPKESKVEAKKEEAEDKKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.1%; Score 272.5; DB 22; Length 617; Best Local Similarity 22.9%; Pred. No. 4.4e-10; Matches 106; Conservative 66; Mismatches 185; Indels 105;
                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful f
analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 ---EKMSGSASSENREGTLSDSTGSEKDDLYPNGSGNGSAES 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KPEEKPKTEAKAKEDDKTLSKEPSKPKAEKAEKSSSTDQKDS 602
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                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27; SEQ ID No 21284; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------GPSKSGAEEQTSKDSPNKVVP--
                                                                                                                                                   Rank DR;
                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                   Chen W,
2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 KDSTGKSGAEAQTPE-
                                                                                                                                                   Penn SG, Hanzel DK,
                                                                                                                                                                                                                             4PI; 2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               617 AA;
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04-OCT-2000;
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```

4, 2003, 14:58:31

Search completed: March Job time : 46.1499 secs

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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: March 4, 2003, 14:53:52 ; Search time 21.5931 Seconds

(**Althout alignments)

2137.006 Million cell updates/sec
```

(without alignments)
2137.006 Million cell updates,
Perfect score: 2459
Sequence: 1 MREVVALVLINVAAAGAVPL......YIPLEKDERHQWIVLLSFQL 480
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

283224

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 MaxImum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARI

					SUMM	SUMMARIES	-
Result No.	Score	% Query .Match	Length	DB	ID		Description
1	677.5	27.6	380	7	S22415		
	673	27.4	361	7	B56940		
ı en	668	27.2	363	~	A56940		membi
4	306	12.4	1087	H	OFMSH		neurofilament trip
· LO	286.5	11.7	686	~	D89852		fibrinogen-binding
	284	11.5	854	7	S02003		neurofilament trip
7	284	11.5	933	7	S41539		fibrinogen-binding
· 00	283	11.5	.1072	-	A37221		ment tr
0	274.5	11.2	877	7	F90070		o
10	273	11.1	909	7	A43427	•	
11	272.5	11.1	1020	-	OFHUH		
12	259	10.5	1664	7	T18262		S-layer protein -
13	256.5	10.4	332	7	B43427		Lament
14	251.5	10.2	406	~	S38170	-	
15	251	10.2	066	~	151618		nucleolar phosphop
16	242.5	6.	1092	~	T30214		fibrinogen-binding
17	N	6	734	7	B42680		nucleolus-cytoplas
18	238.5	.0	813	?	S70795		
6	238.5	6	. 971	7	T19431		
20	236.5	9	916	~	A27864		neurofilament trip
21	233.5	9	635	~	T09648		
22	232	7.6	669	~	I38073		Ų
23	228	6	3507	~	T34513		tical
24	226.5	6	488	7	146014		
25	226.5	6	489	7	. A45988		dentin matrix acid
. 26	226.5		2 . 1337	~	T30291		
27	226.5	6	1385	٦.	D89824		hypothetical prote
28	225.5	6	2 6642	~	T29757		protein UNC-89 - C
00	224	Ó	1. 5327	'n	T13564		microtubule-associ

hypothetical prote hypothetical prote FmtB protein [impo hypothetical prote hypothetical prote neurofilament medi hypothetical prote glucan 1.4-alpha-9 NF-180 - sea lampr hypothetical prote rCOF1 protein - mo junctional sarcopl stable tubule only flbrinogen-binding surface antigen TC neurofilament prot	
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T34036 D90011 T102345 T102345 T102345 T29919 S48919 T51116 C89824 AC5930 JC5963 T28680	
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1359 2271 22481 1791 532 798 1367 1110 953 1320 906 3911 3911	
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219 218.5 218.5 217 215.5 215.5 214.5 214.5 213.5 213.5 213.5 213.5 211.5 211.5 210.5	
01088888888888888888888888888888888888	

## ALIGNMENTS

	RESULT 1
	52481. - membrane protein TGN38 long form precursor - rat N;Alternate names: membrane protein TGN41; trans Golgi network-specific 38K protein;
	C;Species: Rattus norvegicus (Norway rat) C;Date: 03.Feb-1994 #sequence_ravision 03-Feb-1994 #text_change 08-Oct-1999 C;bace: 03.7415, 03.6285; 03.1468
	C) ACCESSION: 523-15, 505-15,
	A: Accession: S22415 A: Accession: S22415
	A, CCOSS-references: EMBL: X64600; NID: 957350; PIDN: CAA45884.1; PID: 957351 P: Reaves: R: Wilde: A.: Banting, G.
	316, 1992 lon, molecula
	A; Reference number: S36285; MUID:92246851; PMID:1575675 A:Accession: S36285
	A; Molecule type: mRNA
	A; Kesidues: 321-300 XREAZ/ A; Cross-references: EMBL:X64600
	R;Luzio, J.P.; Brake, B.; Banting, G.; HOWELL, N.E.; Biagnetta, F.; Stunitz; Riochem J. 270, 97-102, 1990
	Arities: Identification, sequencing and expression of an integral membrane protein of
	A, Accession: S11468
	A) Meletence immuse: may red, most an all and a second a second and a second a second and a second a second and a second a
1	File 380/Product: membrane protein TGN38 long form #status predicted <mat></mat>
٠	
	F;325-380/Domain: intracellular #status predicted <cyt></cyt>
	F;348-353/Region: trans-Golgi network localization Signal F;25,26,140,147,297/Binding site: carbohydrate (Asn) (covalent) #status predicted
•	Query Match 27.6%; Score 677.5; DB 2; Length 380;
	×
	QY 1 MREVVALVLLNVAAAGAVPLLATESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHP 58
	Db 1 MQFLVALLLSVAVARAL

A)  1-1995  Qy  TGN41 in mouse. Qy  Qy  aps 9; Db  Qy  aps 9; Db  Qy  114  Qy  31  Db	449  380  Query Bast L  Matche  Qy  Db  340  Cy  Db  351;  Cy  Db  361;  Cy  Db  361;  Cy  Db  Cy  Cy  Cy  Cy  Cy  Cy  Cy  Cy  Cy  C
Db 85 GPRTAATDHSLGDSRRQPEKTDAELNETARPLSPVNPKLEKSDQSS Qy 175 TKDVPNKSGADGQTPKDGSSKSGAEDQTPKDGYPNKSGAEKQTPKDGSNKSGAEEQGPIDG	DD 131 TEDSGRETGGNSGRPTGGDSGRETGGDSDR QY 235 PSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGLSPHAF DD 161 PTEAGSNKATEDDSGKSTKVNIJNKPFKTSDNFF

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Takahashi, S.; Murakami, K.; Nakayama, K.
1. 270, 14471-14476, 1995
1. specific presence of two TGN38 isoforms and absence of TGN41 in mouse
number: A56940; MUID:95301533; PMID:7540170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurofilament triplet H protein - mouse
C; Species: Mus musculus (house mouse)
C; Accession: J1903 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
C; Accession: J70368; A43778; S42616
R; Julien, J.P.; Cote, F; Beaudet, L.; Sidky, M.; Flavell, D.; Grosveld, F.; Mushynsk
Gene 68, 307-314, 1988
A; Title: Sequence and structure of the mouse gene coding for the largest neurofilamen
A; Reference number: J70368; MUID:89121513; PMID:3220257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                         rrane protein TGN38B - mouse
is musculus (house mouse)
ct-1995 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
SNREGILSDSTGSEKDDLYPNGSGNGSAESSHFFAYLVTAAILVAVLYIAHHNKRKII 410
                   DSPSKSSAEAQTPEDTPNKSGAEAKT-----QKDSSNKSGAEAKTQKGSTSKSGS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKDSTSKSHSELOTPKDSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATDHSLGDSRRQPEK------TDAELKETARPLSPVNPKLEK-----SDQSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNKSGADGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SGKPTGGDSDK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GE----ETDLISPPQEEVKSSEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VALVLINVAAAGAVPLLATESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGILSDSTGSEKDDLYPNGSGNGSAESSHFFAYLVTAAILVAVLYIAHHNKRKII 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                  liminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.2%; Score 668; DB 2; Length 36; Similarity 39.7%; Pred. No. 1.9e-24; 7; Conservative 49; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKPTGGNSGKPTGGD------
                                                                             TEGKRSKVTRRPKASDYQRLDOK 436
                                                                                                     SGKRSKVTRRPKASDYQRLDQK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -363 <KAS>
ences: GB:D50031
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us-09-763-902b-1.rpr

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, I.; Cu1, L.; C.; Sekimizu,

GSPDB:GN00149

185

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Indels

Length

744

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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Seki C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Jancet 357, 1225-1240, 2001.
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                    001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 AEEAASPEKETKSPVKEEAKSPAEAKSPAEAKSPAEVKSPAVKSPAVAKSP-AEVKSPA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPSKSSAEAQTPEDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFKTESGEETDLI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPPQEEVKSSEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMS--GSASSENREGTLSDST 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDSESD---SDSDSDSDSDSDSDSDSDSDSDSDSDSTGSDNDSDSDSNSDSES 921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDSDSASDSDSASDSDSASDSDSASDSDSASDSDSASDSDSASDSDSDSDSDSDSDSDSD 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHSELQTPKDSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGAD
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A:Residues: 1-989 -KUN>
A:Cross-references: GB:BA000018; PID:g13700678; PIDN:BAB41975.1;
A:Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: EMBL:X13804; NID:957828; PIDN:CAA32038.1; Superfamily: neurofilament triplet H protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S02003
R;Breen, K.C.; Robinson, P.A.; Wion, D.; Anderton, B.H.
FEBS Lett. 241, 213-218, 1988
A;Title: Partial sequence of the rat heavy neurofilament
A;Reference number: S02003; WUID:89065087; PMID:3143606
A;Accession: S02003
                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.7%; Score 286.5; DB 2; 22.2%; Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137;
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    rat (fragment)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           922 GSNNNVVPPNSPKNGTNASN 941
                                  aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 22.2%
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                                  Staphylococcus
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                                                                                                                                                                                                                                              A; Accession: Dayoba
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: mRNA
                                                                               C; Accession: D89852
                                                                                                                                                                                                                                                                                        A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: clfA
                                                                                                                                                                                                                                                                                                                                                                                         :Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: neurofilament triplet H protein
| Reywords: colled coll; cytoskeleton; heterotrimer; intermediate filament; nerve; phosp; 1-97/Domain: amino-terminal cVTE>
| 19.7/Domain: amino-terminal cVTE>
| 19.408/Domain: carboxyl-terminal cCTE>
| 19.10-886/Region: 6-residue repeats | 19.20-886,592,598,604,610,616,622,628,634,640,64 |
| 19.20-26,532,538,544,550,556,562,568,574,580,586,592,598,604,610,616,622,628,634,640,64 |
| 19.8781nding site: phosphate (Ser) (covalent) #status predicted |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibrinogen-binding protein A, clumping factor [imported] - Staphylococcus aureus (strain
                                                                                                                                                  by
                                                                                                                                                                                                                                              dolecule type: mRNA
Residues: 'M',1-132,'QA',134-199,'R',200-280,'T',282-491,'G',493-533,'GEAKSP',534-545,
Pross-references: GB:M35131; NID:g200021; PIDN:AAA39809.1; PID:g200022
                                                                                                                                                                                                                                                                                                                                                                                                                                                          sidues: 1-132,'QA',134-199,'R',200-280,'T',282-491,'G',493-533,'GEAKSP',534-545,'R'
oss-references: EMBL:231012; NID:9463249; PIDN:CAA83229.1; PID:9463250
                                                                                                                                                  as revealed
'Residues: 1-1087 <JUL>
'Cross references: GB:M23349; GB:M24496; NID:9200034; PIDN:AAA39813.1; PID:9387493
'Shneidman, P.S.; Carden, M.J.; Lees, J.F.; Lazzarini, R.A.
'Bain Res. Mol. Brain Res. 4, 217-231, 1988

Title: The structure of the largest murine neurofilament protein (NF-H) as reveale
Reference number: A43778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 QKDSSN----KSGAEAKTQKGSTSKSGSEAQTTKDSTSKSHSELQTPKDSTGKSGAEAQT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAEAKSPAEAKSPAEAKSP--ATVKSPGEAKS--PSEAKSPAEAK--KSPAEAKS 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGADGQTPKDGSS----KSGAEDQT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : : | :: : | | :: | | : | PAEVKSPGEAKSPAEVKSPGEAKSPAEAKSPAEAKS 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKDVPNKSGAEKQTPKDGSN----KSGAEEQGPID------GPSKSGAEEQTSKDSPN 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.4%; Score 306; DB 1; Length 1087; 26.9%; Pred. No. 2.8e-07; ive 75; Mismatches 138; Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAGAVPLLATESVKQEEA - - - GVRPSAGNVSTHPSLSQRPG - - -
                                                                                                                                                                                                                                                                                                                 Jarden, M.J.
Smitted to the EMBL Data Library, March 1994
Reference number: S42616
Rocession: S42616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 KVVPEQPSRKDHSKPISNPSDNK--
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Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPOTPKD----
                                                                                                                                                                                                                atus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                atus: preliminary
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polypeptide (NF-H). Identifi

PID:957829

22;

Length 854;

Oy 382 SS 383    :   Db 884 SN 885	•	0/621 purofilament triplet H protein - rat Species: Rattus norvegicus (Norway rat) Date: 10-Sep-1999 #sequence_revision 10-Sep-1999	C;Accession: A37221; A25649; A30796; A32757; B25649 R;Chin, S.S.M.; Liem, R.K.H. J. Neurosci. 10; 3714-3726, 1990 A;Title: Transfected rat high-molecular-weight neurofillament (NF-H) coassembles with		A; Residues: 1-1072 <chi> A; Residues: 1-1072 <chi> A; Cross-references: GB; AF031879; NID: 92642597; PIDN: AAB87068.1; PID: 92642598 R; Robinson, P.A.; Wildn, D; Anderton, B.H. FEBS Lett. 209, 203-205, 1986</chi></chi>	A, Residues: 230-318;472-542 <rob> A, Cross-references: GB.M3727 R; Dautigny, A.; Pham-Dinh, D.; Roussel, C.; Felix, J.M.; Nussbaum, J.L.; Jolles, P. Blochem. Blophys. Res. Commun. 154, 1099-1106, 1988 A; Title: The large neurofilament subunit (NP-H) of the rat: cDNA cloning and in situ</rob>	A, Accession: A30796 A, Accession: A30796 A, Molecule type: mRNA A, Roll type: mRNA A, Cross-references: GB: M21964: NID: 9205685; PIDN: AAAA1695.1; PID: 9205686 A, Lieberburg, I.; Spinner, N.; Snyder, S.; Anderson, J.; Goldgaber, D.; Smulowitz, M.	Proc. Natl. Acad. Sci. U.S.A. 86, 2463-2467, 1989 A.Title: Cloning of a cDNA encoding the rat high molecular weight neurofilament pepti 22. A.Reference number: A32757; MUID:89184647; PMID:2928342 A.Accession: A32757 A.Status: preliminary	A; Molecule type: mRNA A; Rosadues: 559-566, E',568-967, 'V',969-997, 'GST',1001-1022,'E',1024-1072 <lle> A; Residues: 559-566, E',568-967, 'V',969-997, 'GST',1001-1022, 'E',1024-1072 <lle> A; Cross-references: GB: J04517; NID: 9205679; PIDN: AAA41692.1; PID: 9205680 C; Superfamily: neurofilament triplet H protein C; Keywords: coiled coil; heterotrimer; intermediate filament; nerve; phosphoprotein</lle></lle>	.072;	QY 13 AAAGAVPLLATESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEPQTPKDSPS 68	QY 69 KSSAEAQTPEDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTS 124 	QY 125 KSHSELQTPRDSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEA 172	QY 173 QTTKDVPNKSGADGQTPKDGSS	Qy 205 DVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDS 248       :  :       :  : 
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::  : :	105OKGSTSKGGSEAQTTKDSTSKSHSELQTPKDSTGKSGAEAQTPEDSPN 152 384 PASVKSPGEAKSPAEAKSPAEVKSPATVKSPVEAKSPAEVKSPVTKSPAEAKSPVEVKS 413	153 RSGAEAKTOKDSPSKSGSEAQTIKDVPNKSCADGOTPKDGSSKSGAEDQIPKDVPNKSGA 212 :::::	213 EKOTPKDGSNKSGAEEQGPID GPSKSGAEEGTSKDSPNKV 252 	253VPEQPSRKDHSKPISNPSDNKELPRADTNQLADKGKLSPHAFKTESG 299		RESULT 7 S41539 fibrinogen-binding protein - Staphylococcus aureus	sion 13-Jan-1995 #text_ch aux, P.; Foster, T.J.	A) Reference number: \$41539; MUID:94224142; PMID:8170386 A) Accession: \$41539; MUID:94224142; PMID:8170386 A) Status: preliminary A) Molecule type: DNA A) Residues: 1-933 - 400D>	Closs Tetclences: Embl: 1103; NID: 939/325; FIDN: CAA/9304.1; FID: 939/326  Query Match Best Local Similarity	37 AGNVSTHPSLSQRPGGSTKSHPEPOTPKDSPSKSSAEAQTPEDTPNKSGAEAK 89 :	90 TOKDSSNKSGAEAKTORGSTSKSGSEAQTTKDSTSKSHSELQTPRDSTGKSGAEAQTPED 149 :     : :           : :	150 SPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGADGQTPKDGSSKSGAEDQTPKDVPNK 209   :   :             :	210 SGAEKQTPKDGSNKSGAEEQGEPIDGPSKSGAEEQISKDSPNKVVPEQPSRKDHSKPISNP 269     :	270 SDNKELPRADTNOLADKGKLSPHAFKTESGEETDLISPPQEEVKSSEPTEDVE 322   1   1   1   1   1   1   1   1   1	323 PKEAEDDDTGPEEGSPPKEEKEKMSGSASSENREGTLSDS-TGSEKDDLYPUGSGNGSAE 381 

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neurofilament subunit (NF
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Superfamily: neurofilament triplet H protein
Keywords: colled coil; heterotrimer; intermediate filament; nerve; phosphoprotein
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                                                                                                                                                                                                       neurofilament
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Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jun-2000
                                    Species: Oryctolagus cuniculus (domestic rabbit)
Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 10-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275
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                                                                                          C; Accession: A43427
R; Soppet, D.R.; Beasley, L.L.; Willard, M.B.
J. Biol. Chem. 267, 17354-17361, 1992
A; Title: Evidence for unequal crossing over in the evolution of A; Reference number: A43427; MUID: 92381055; PMID:1512270
A; Accession: A43427
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C;Superfamily: neurofilament triplet H protein
C;Keywords: coiled coil; heterotrimer; intermediate filament;
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'Title: The structure and organization of the human heavy; Reference number: S00979; MUID:88328981; PMID:3138108
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Best Local Similarity 26,4%; Pred. No. 5.5e-06;
Matches 101; Conservative 71; Mismatches 151;
al protein - rabbit (fragment)
cuniculus (domestic rabbit)
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EKAKSPVKEEAKSPEKAKSPVKE 398
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       triplet Hl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: GB:BA000018; PID:g13702588; PIDN:BAB43728.1; GSPDB:GN00149 Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
Accession: F90070
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                                                                            783 PEKA--KSPVKEEIKPPAEVKSPEKAKSPMKEEAKSPEKAKTLDVKSPEAKTPAKEEAKR
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llarity 24.6%; Pred. No. 6.6e-06;
Conservative 64; Mismatches 150
          PNKVVPEOPSRKDHSKPISNPSDNK-ELPKADTNOLADKGKL
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ses 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA
Residues: 1-877 <KUR>
Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  950 KAAAPEEET
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A43427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics
       249
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;1-100/Domain: amino-terminal <ntd></ntd>	O. 140 DCDNDCGAFAFFOKDGKGGGFAOMMFD-VD
F;411-1020/Domain: Garboxyl-terminal <ctd> F;502-826/Region: 14-residue repeats F;503-511,518,526,532,546,552,560,566,574,580,586,594;600,606,614,620,628,634,640,64</ctd>	1154
F:732,768/Binding site: phosphate (Thr) (covalent) #status predicted  Query Match  Best Local Similarity 22,9%; Pred. No. 9.4e-06;  Matches 106; Conservative 66; Mismatches 185; Indels 105; Gaps 13;	SDEPTPSETPEE
NVSTHPSLSORPGGSTKSHPEPQTPKDSPSKSSAEAQTPED 79 :	1270
QY 80 TPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSKSHSELQTP 133	1329 -TPSDEPTPSDEPTPSDEE 365 SEKDDLYPNGSGNGSAES : :
QY 134 KDSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSG 183 :	Db 1386 TPTPSTTPTSGSGGSGGS 1403 REŞULT 13
OY 184 ADGGTPKDGSSKSGAEDGTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPID 233	B43427 neurofilament protein H form H2 (repetitiv C.Species: Oryctolagus cuniculus (domestic . C;Date: 04-Mar-1993 #sequence_revision 18-
Oy         234	C. Accession: B43427 R. Soppet, D.R.: Beasley, L.L.; Willard, M. J. Biol. Chem. 267, 17354-17361, 1992 A; Title: Evidence for unequal crossing ove
QY 262 HSKPISNPSDNKELPKADĪNQLADKGKLSPHAFKTESGEĒTDLI 305	A; Reference number: A43427; MUID: 92381035; A; Accession: B43427 A; Status: preliminary; not compared with c A; Molecule type: nucleic acid
OY 306 SPPQEEVKSS-EPTEDVEPKEAEDDDTGPEEGSPP	A. Exsidues: 1-33 <sop> A. Experimental source: brain A. Note: sequence extracted from NCBI backb C. Superfamily: neurofilament triplet H pro</sop>
QY 344EKMSGSASSENREGTLSDSTGSEKDDLYPNGSGNGSAES 382 	Query Match 10.4%; Score 25 Best Local Similarity 27.2%; Pred. No Matches 88; Conservative 63; Misma
RESULT 12 T18262	OY 51 GGSTKSHPEPQTPKDSPSKSSAEAQTPEDTPN
S-tayer protects: Clostridium thermocellum C:Species: Clostridium thermocellum C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C:Accession: T18262	QY 111 KSGSEAQTTKDSTSKSHSELQTPKDSTGKSGA 
Fulino, T.; Beguin, P.; Aubert, J.P. Bacteriol. 175, 1891-1899, 1993 Title: Organization of a Clostridium thermocellum gene cluster encoding the cellulosom	OY 169 GSEAQTTKDVPNKSGADGQTPKDGSSKSGAED
A; Keterence number: Z1884/; MUID: 95209931; PMID: 8458832 A; Accession: T18262 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA	Oy 229 QGPIDGPSKSGAEEQTSKDSPNKVVPEQ 1
Restudes: 1-1004 <2007 Cross-references: BMBL:X67506; NID:9296879; PID:9296881; PIDN:CAA47841.1  Ouery Match (10.5%; Score 259; DB 2; Length 1664;	OY 285 DKGKLSPHAFKTESGEETDLISPPQEEVKSSE         : :     :             Db 214 EKAK-SPVKEBAKSPEKAKSPVKEEAKSPE
	342
Qy       41 STHPSLSQRPGGS-TKSHPEP-QTPKDSPSKSSAEAQTPEDTPNKSGAEAKTQKDSSNKS 98         1	
99 GAE-AKTOKGSTSKSGSEAQTTKDSTSKSHSELQTPKDSTGKSGAEAQTPE 148 1094 PEEPIPTDTPSDEPTPSDEPTPSDEPTPSDEPTPSDEPTPSSTPEEPIPTDTPSDEPTPS 1153	KESULT 14 838170 SRP40 protein - yeast (Saccharomyces cerev N,Alternate names: protein YKR092c; protei

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ver in the evolution of the neurofilament pol 5; PMID:1512270
                                                                                                                                                                                                                                                                                                                                           ive region) - rabbit (fragment)
ic rabbit)
3-Nov-1994 #text_change 10-Jul-1998
VPNKSGADGOTPKDGSSKSG----AEDOTP 203
                                                         KSGAEEQCPIDGPSKSGAEEQTSKDSPNKV 252
                                                                                                                                      :| :|: | :|: || SDEPTPSDEPTPSTPEPTD- 1328
                                                                                                                                                                                                : | : | : | 1385
SEPTPSDEPTPSETPEEPTPTTP 1385
                                                                                                                   NDTNOLADKGKLSPHAFKTESGEE---TDL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKSGAEAKTOKDSSNKSGAEAKTOKGSTS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAEAQTPE--DSPNRSGAEAKTQKDSPSKS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDOTPKDVPNKSGAEKOTPKDGSNKSGAEE 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256.5; DB 2; Length 332;
No. 1.8e-05;
natches .134; Indels 39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conceptual translation
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Search completed: March
Job time : 25.5931 secs
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                                                                                                                                                                                                                     perimental source: strain 5388C

bu, G.; Esteban, P.F.; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.; Remacha, M.; Ji

st 9, 1349-1354, 1993

Itle: The complete sequence of a 15 820 bp segment of Saccharomyces cerevisiae chromo ference number: $40644; MUID:94205265; PMID:8154186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tion: Interactions between three common subunits of yeast RNA polymerases I and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title: Identification and cDNA cloning of a Xenopus nucleolar phosphoprotein, xNopp180
Reference number: I51618; MUID:96019267; PMID:7593294
                                                Esteban, P.F.; Garcia-Cantalejo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
#sequence_revision 03-May-1994 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pus laevis (African clawed frog)
1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 EQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFKTESGEETDLISPPQEEVKS 314
                                                                                                                                                                                                                                                                                                                                                                                                                                        11; NID:9450550; PIDN:CAA51946.1; PID:9450552
S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 KSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNKVVP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSKSHSELQTPKDST 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SSSDSESSSESDSSSS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKSGAEAQTPEDSPNRSGAEAKTQK---DSPSKSGSEAQTTKDVPNKSGADGQTPKDGSS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SSSSSSSSSSS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 VPLLATESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEPQTPKDSPSKSSAEAQTP 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ::| ||| |:: || |: || SGSSSELETKEATADESKAETPASSNESTPSASSSSSANKLNIPAGTDEIKEGQRK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSASSENR----EGTLSDSTGSEK 367
                                                                                                                                                                                                        oss-references: EMBL: 228317; NID: 9486580; PID: 9486581; MIPS: YKR092c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ues: 1-399,'N',401-406 <LAL>
-references: EMBL:L11275; NID:9295670; PID:9295671
                        Accession: $38170; $40645; $37702
Baladron, V.; Ballesta, J.P.G.; Bou, G.; del Rey, F.;
bmitted to the Protein Sequence Database, March 1994
Reference number: $38158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.2%; Score 251.5; DB 2; 23.0%; Pred. No. 3.7e-05; ive 67; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sentenac, A.; Thuriaux, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 VPKL---SVKEKEIEEKSSSSSSSSSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: SGD:S0001800; MIPS:YKR092c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                  res: 1-406 <BOU>
references: EMBL:X73541;
mental source: strain S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 23.09
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: I51618; S57757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ucleolar phosphoprotein
                                                                                                                                                                             1-406 <BAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGD:SRP40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315
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4, 2003, 15:04:25

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A; Cross-references: EMBL: X88927; NID: 9895920; PIDN: CAA61368.1; PID: 9895921
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                  SSDSSSDEETTTKPAAKTTPAKSAATPTSKTPTNSKATPTSKKTPAKPGTPKTSAAKKDS 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSKSSAEAQTPE-DTPNKSGAEAKTQKDSSNKSGAE--AKT---QKGSTSKSGSEAQTTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSSDSSDSSDEKKTPAKRAAKTTPAKPAAKTTPAKPAAKTTPAKPAAKSTPGKQVPTKK 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     573 ESSSSDSSDSSEDEKKSSAKPAVKT-TPGKATSKPVVASKPVPAKKASSSSDSDSSEEE 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAQTTKDVPNKSGA------DGQTPKDGSSKSGAEDQT-PKDVPNKSGAEKQTPKDGSN 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 632 TTKTTKPLTKLSPAVKTLPPKKAESSSDSSSDSDSEKKTKPAKPPAKSATPVNTKAPAQN 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 752 EKOKPKOAAAKDVKOGAKAAKPTPKKAASSSSED----SSSDEDVSKAKKTNTAVSKSP 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         808 VTTPKAVPAAKKESSSESSDSEDEKQGGKNTSTTKIANSTPKAAAAECSEESSSSEDEGK 867
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                             --KDS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGAEEQGPIDGPS-KSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ADTNQLADKGKLSPHAFKTESGEETDLISPPQEEVKSSEPTEDV---
                                                                                                                                                                                                                                                                                                                         92;
                                                                                                                                                                                                                                                                                                                                                                                ---VSTHPSLSQRPGGSTKSHPEPQTP---
                                                                                                                                                                                                                                                               Length 990
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                              A;Gene: xNopp180
C;Superfamily: nucleolus-cytoplasm shuttle.phosphoprotein
C;Reywords: phosphoprotein
                                                                                                                                                                                                                                                                                                                      63; Mismatches 181;
                                                                                                                                                                                                                                                         Score 251; DB 2;
Pred. No. 9e-05;
           translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSTS--KSHSELQTPKDSTGKSGAEAQTPEDSPNR-
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                                                                                                                                                                                                                                                               10.2%;
24.3%;
                                                                                                                                                                                                                                                                                                                                                                             22 ATESVKQEEAGVRPSAGN---
                                                                                                                                                                                                                                                                                                                      Matches 108; Conservative
                                                                                                                                                                                                                                                                                            Best Local Similarity
           preliminary;
type: mRNA
A; Status: pres.mRh
A; Molecule type: mRh
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210 SGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNP 269
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APPLICANT: McDevitt, Damien L.
TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene FILE REPERENCE: 0344.105011
CURRENT APPLICATION NUMBER: US/08/293,728D
CURRENT FILING DATE: 1994-08-22
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 2
LENGTH: 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08293728D Patent No. 6008341
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; ORGANISM: Staphylococcus aureus
US-08-293-728-2
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                                                                                                                                                                                                March 4, 2003, 14:55:07; Search time 16.6405 Seconds (without alignments) 848.711 Million cell updates/sec
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/cgn2_6/ptodata/1/laa/PcTUS_COMB.pep:*
. GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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1 MRFVVALVILINVAAAGAVPL.
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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83; Mismatches 173; Indels

Score 284; DB 3; Pred. No. 1.4e-13;

Length 933;

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	Appli	App11	Appl	Appl	Appli	App11	Appli	Appli	Appli	App11	Appl	, Appl	, Appl	, Appl	4, App	, Appl	, Appl	2, App	
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	US-09-203-453-5	US-07-667-276A-4	US-09-183-861-62	US-09-022-765-62	US-08-769-309A-5	US-08-994-570-5	US-09-086-912-2	US-09-203-453-2	US-08-790-912-3	US-08-790-912-2	US-07-757-022B-14	US-07-757-022B-84	US-07-757-022B-74	US-07-757-022B-58	US-07-757-022B-104	US-07-757-022B-44	US-07-757-022B-42	US-07-757-022B-142	
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## ALIGNMENTS

1997-07-03

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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional TITLE OF INVENTION: Elongation By HIV-1 TAT FILE REFERENCE: M0656/7042 CURRENT APPLICATION NUMBER: US/09/214,564A CURRENT FILING DATE: 1999-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 SGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNP 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 AGNVSTHPSLSQRPG--GSTKSHPE----PQTPKDSPSKSSAEAQTPEDTPNKSGAEAK 89
                                     Footer, Timothy J.
McDevitt, Damien L.
WENTION: The S. aureus Fibrinogen Binding Protein Gene
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                                                                                                                                                                                                                                                                                                                                83; Mismatches 173; Indels
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                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                    Score 284; DB 4;
Pred. No. 1.4e-13
                                                                                                       CURRENT APPLICATION NUMBER: US/09/421,868 CURRENT FILING DATE: 1999-10-19 PRIOR APPLICATION NUMBER: 08/293,728 PRIOR FILING DATE: 1994-08-22
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HER: US 60/021,218
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WBER: US 60/033,152
1996-12-13
upplication US/09421868
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                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-421-868-2
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22.1%;
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PRIOR APPLICATION NUMBER:
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                                                                                                                                                                  NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 80; Conserve
                                                       APPLICANT: McDevitt
FITLE OF INVENTION:
FILE REFERENCE: 053
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APPLICANT: Sharp, I
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884 SN 885
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
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                                                                                                                                                                                                                                                                                                                                                                          83 KSGAEAKTQKDSSN---KSGAEAKTQKGSTSKSGSEAQTTKDSTSKSHSELQTPKDSTGK 139
                                                                                                                                                                                                                                                                                                                               395 PSRARHFSEHPSTSKMNAQETATGMAFEEPIDEKKFEKTEDGGEFEEGASENNAKESSPE 454
                                                                                                                                                                                                                                                                                                                                                                                                          SGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGADG---QTPKDGSSKS 196
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                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEVKSSEPTEDVEPKEAEDDDTG----PEEGSPPK----EEKEKMSGSASSENREGTL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       680 DEDADGKEVEDADEKLFEDDSKLFPDESERKLFDDSDERGTLGGFGSVE--EGPL 737
                                                                                                                                                                                                                                                                                                        -- SKSSAEAQTPEDTPN 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 571;
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; Pred. No. 4e-08;
64; Mismatches 186;
                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                        35 PS-AGNVSTHPSLSQRPGGSTKSHPEPQTPKDSP----
                                                  FastSEQ for Windows Version 3.0
                                                                                                                                                                                                         8.9%; Score 219;
24.1%; Pred. No. 9
tive. 66; Mismatch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            llarity 20.4%;
Conservative 6
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3865
LENGTH: 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDST----GSEKDD 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              738 STGSSFILSSDDDD 751
                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 90; Conserv
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS
SOFTWARE: FastSEQ f
SEQ ID NO 2
LENGTH: 754
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Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -09-134-001C-3865
                                                                                                                                                         US-09-214-564A-2
                                                                                                                  TYPE: PRT
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66 SPSKSSAEAQTPEDTPNKSGAEAKTOK----DSSNKSGAEAKTOKGSTSKSGSEAQTTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 PLTAIHTPSTAEPSKFPFFPTKDSQHVSSVTQNQKQYDTSSKTHSNSQQGTSSMLEDDLQL 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            407 SDSEDSDSEQTPEKPPSSSAPPSAPOSLPEPVASAHSSSAESESTSDSDSSSDSESESS
                                                                                                                                                                                                                                                                                                                                                                                                                                               B: Woodcock Washburn Kurtz Macklewicz & No. 5633135ris
One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                 Detection and Treatment of Acute Leukemias
Resulting from Chromosome Abnormalities in
All-1 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1187;
                                                   1216 STSTSESDSTSESTSLSESTSTSVSDSTSASTSSVSDSBSA 1263
                   337 SPPKEEKEKMSGSAS-SENREGTLSDSTGSEKDDLYPNGSGNGSAESS 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --SQRPGGSTKSHPEPQTPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                             Therapeutics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7e-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 205.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MBER: US/07/888,830
27-MAY-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US/07/805,093
11-DEC-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/062,443
FILING DATE: 14 MAY 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JMBER: US/07/971,094
30-OCT-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/320,559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 PLLATESVKQEEAGVRPSAGNVSTHPSL--
                                                                                                                                                                                                                                                     APPLICANT: Croce, Carlo
APPLICANT: Canaan1, E11
TITLE OF INVENTION: Diagnostics,
                                                                                                                                      RESULT 6
US-08-320-559-28
'Sequence 28, Application US/08320559
'Patent No. 5633135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52;
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WORDPERFECT 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PS/2
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                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDRESSEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION:
TITLE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKSGSEAQTIKDVPNK--SGADGQIPKDGSSKSGAEDQIPKDVPNKSGAEKQIPKDGSNK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGAEEQGPIDGPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 AD--KGKLSPHAFKTESGEETDLISPPQEEVKSSEPTEDVEPKEAE--DDDTG---PEEG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 KGSTSKSGSEAQTTKDSTSKSHSELQTPKDSTGKSGAEAQTPEDSPNRSGAEAKTQKDSP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       923 TSISDSTSTSDSASIKASESASTSKLLSESVSTSTSDSASTSTSVSDSN-SASTSLSK 981
                                                                    145 ----QTPEDSPNRSGAEAKTOKDSPSKSGSEAQTTKDVPNK--SGADG---QTPKDGSSK 195
                                                                                                                                                                                                                387
                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                             GTTAPGNTNQDTQVKPNTDQTATGTPAGTDNQNTQQGNTEQNNQNAQPSAPGTTDQAGAT 447
                                                                                                                                                                                                                                                                                                                                                            360
                                                                                                                                                                                                                                                                                                                                                                                                      448 VRPGSAPNQDAEATPNPDQNNTPTNGQDGDQTNQSTQDDNDNQNTQQGNTKQNNQNAEQG 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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|SESASTSTSDSASESARKSESTSKSTSLSESTSTSVSDSASVSTSESASTSTSVSGSTS 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PKDSPS-KSSAEAQTPE-----DTPNKSGAEAKTQKDSSNKSGAEAKTQ 105
                                                                                                                272 PSGDSTPTGEPNKAD-DQDTQIKPTSNQGTTA-TINEIGNQKPSGQTGNTENTPNDGTQV 329
219.VT-----TGEQTGGKPAATKPEGASAETAPAPNNADENHAQPSPQTGGTTATQAGQVK 271
                                                                                                                                                                                            250 NKVVPEQPSRKDHSKPISNP-----SDNKELPKADTNQLADKGKLSPHAFKTESGEE
                                                                                                                                                                                                                                                                                                                                                            302 TDLISPPQEEVKSS-EPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSASSENREGTLS
                                                                                                                                                                 -- AEEQTSKDSP
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                                                                                                                                                                    196 SGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

8.5%; Score 208.5; DB 4;
Best Local Similarity 22.8%; Pred. No. 2.2e-07;
Matches 93; Conservative 77; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pplication US/09134001C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674
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508 NTGGTDKD 515
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LENGTH: 2137
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121 DSTSKSHSELQTPKDS-

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for Detection and Treatment of Acute Leukemias Resulting from Chromosome Abnormalities in the All-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 PLTAIHTPSTAEPSKFPFPTKDSQHVSSVTQNQKQYDTSSKTHSNSQQGTSSMLEDDLQL 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDSEDSDSEQTPEKPPSSSAPPSAPQSLPEPVASAHSSSAESESTSDSDSSSDSESSSS 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           526 D--SATSQEHSESKDPPPKSSSKAPRAPPEAPHPGKRSCQKSPAQQEPPQRQTVGTKQPK 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          584 K -- PVKASARAGSRISLQGEREP -- GLLPYGSRDQTSKDKPKVKTKGRPRAAASNEPKPA 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 VPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFK----TE-----SGE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         640 VPPSSEKKKHKSSLPAPSKALSGPEPAKDNVEDR---TPEHFALVPLTESQGPPHSGSGS 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPSKSSAEAQTPEDTPNKSGAEAKTOK----DSSNKSGAEAKTOKGSTSKSGSEAQTTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TGKSGAEAQTPE----DSPNRSGAEAKTOK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 DSPSKSGSEAQTTKDVPNKSG----ADGQTPKDGS---SKSGAEDQTPK-----DVPN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 --KEAEDDDTGPEEGSPPKEEKEKMSGSASS---ENREGTLSDSTGSEKDDLYPN-GSGN 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1187;
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VENTION: Diagnostics, Therapeutics and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 PLLATESVKQEEAGVRPSAGNVSTHPSL----SQRPGGSTKSHPEPQTPKD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
8.4%; Score 205.5; LGC, Score 205.5; LGC, Sect Local Similarity 23.4%; Pred. No. 1.7e-07; Concervative 52; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 KSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---DLISPPOEEVKSSEPTEDVEP--
                                                                                                 FILING DATE: 27-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/805,093
FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                           UMBER: US 07/888,839
27-MAY-1992
          ER: US 07/971,094
-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 28, Application PC/TUS940496
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Canaeni, Eli
                                                                                                                                                                                                               NAME: DeLUCA ESQ., MAFK
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPAN: (215) 568-3100
TELEPAN: (215) 568-3439
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                  1187 amino acids
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                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
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          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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for Detection and Treatment of Acute Leukemias
Resulting from Chromosome Abnormalities in the All-1 Region
                                   466 SSDSEENEPLETPAPEPEPPTTNKWQLDNWLTKVSQPAAPPEGPRSTEPPRRHPESKGSS 525
                                                                                                                                                                                                                            584 K--PVKASARAGSRTSLQGEREP--GLLPYGSRDQTSKDKPKVKTKGRPRAAASNEPKPA 639
                                                                                                                                                                                                                                                                           253 VPEQPSRKDHSKPISNPSDNKELPKADINQLADKGKLSPHAFK----TE-----SGE 300
                                                                                                                                                                                                                                                                                                                                                                                                                          697 RISGCRQAVVVQEDSRKDRLPLPLRDTKLLSPLRDTPPPQSLMVKITLDLLSRIPQPPGK 756
-TGKSGAEAQTPE----DSPNRSGAEAKTQK 162
                                                                                                                          526 D--SATSQEHSESKDPPPKSSSKAPRAPPEAPHPGKRSCQKSPAQQEPPQRQTVGTKQPK 583
                                                                                                                                                                                           ---SPNKV 252
                                                                                                                                                                                                                                                                                                                        640 VPPSSEKKKHKSSLPAPSKALSGPEPAKDNVEDR---TPEHFALVPLTESGGPPHSGSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 -- KEAEDDDIGPEEGSPPKEEKEKMSGSASS---ENREGTLSDSIGSEKDDLYPN-GSGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Woodcock, Washburn, Kurtz, Mackiewitz
                                                                                                                                                                               209 KSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKD----
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                                                                                                                                                                                                                                                                                                                                                                                  ---DLISPPQEEVKSSEPTEDVEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDRESSEE: No. 6040140ris
REET: One Liberty Place, 46th floor
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FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: PCT/US94/04496
.22-APR-1994
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DATE: 19-OCT-1994
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FILING DATE: 11-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 08/062,443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28, Application US/08545860D Patent No. 6040140
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SURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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APPLICATION NUMBER:
FILING DATE: '22-APR-1
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Canaan, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           378 GSAESSH 384
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US-08-545-860D-28
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US-08-320-559-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              466 SSDSEENEPLETPAPEPEPPTINKWQLDNWLTKVSQPAAPPEGPRSTEPPRRHPESKGSS 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     757 GSRQRKAEDKQPPAGK - KHSSEKRSSDSSSKLAKKRKGEAERDCDNKKIRLEKEIKSQS 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 PLTAIHTPSTAEPSKFPFPTKDSQHVSSVTQNQKQYDTSSKTHSNSQQGTSSMLEDDLQL 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDSEDSDSEQTPEKPPSSSAPPSAPOSLPEPVASAHSSSAESESTSDSDSSSDSESESS 465
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                                           ADDRESSEE: Woodcock, Washburn, Kurtz, Macklewitz
                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.25
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                                                                                        One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                     URRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Defuca Esg., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJ
BLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ITORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1187 amino acids
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Best Local Similarity 23.49
Matches 114; Conservative
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MOLECULE TYPE: protein
PCT-US94-04496-28
                    CORRESPONDENCE ADDRESS:
                                                                                                                                                Pennsylvania
                                                                                                                  Philadelphia
SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: '
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489 SSDSEENEPLETPAPEPEPPTTNKWQLDNWLTKVSQPAAPPEGPRSTEPPRRHPESKGSS 548
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                                                                                                                                                                                                                                                      E: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
One Liberty Place - 46th Floor
                                                                                                                                         Detection and Treatment of Acute Leukemias
Resulting from Chromosome Abnormalities in
All-1 Region
                                                             NEXAL A.T. Croce, Carlo
APPLICANT: Croce, Eli
APPLICANT: Canaani, Eli
APPLICANT: Canaani, Eli
APPLICANT: Canaani, Eli
ATTIF OF INVENTION: Diagnostics, Therapeutics and Methods for
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                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
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Pred. No. 1.0
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FILING DATE: 14 MAY 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/971,094
FILING DATE: 30-OCT-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,830
FILING DATE: 27-MAY-92
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11-DEC-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/320,559
Sequence 26, Application US/08320559
Patent No. 5633135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33,22
REFERENCE/DOCKET NUMBER: T
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TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSTEM: PC-DOS
WORDPERFECT 5.1
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                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock
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                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PS/2
                                                                                                                                                                                                                                                                                                   Philadelphia
                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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Matches 114; Conserv
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                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                        19103
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for Detection and Treatment of Acute Leukemias
Resulting from Chromosome Abnormalities in the All-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 SPSKSSAEAQTPEDTPNKSGAEAKTQK-----DSSNKSGAEAKTQKGSTSKSGSEAQTTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SPNKV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              720 RISGCRQAVVVQEDSRKDRLPLPLRDTKLLSPLRDTPPPQSLMVKITLDLLSRIPQPPGK 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 PLTAIHTPSTAEPSKFPFPTKDSQHVSSVTQNQKQYDTSSKTHSNSQQGTSSMLEDDLQL 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               607 K--PVKASARAGSRTSLOGEREP--GLLPYGSRDQTSKDKPKVKTKGRPRAAASNEPKPA 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 DSTSKSHSELQTPKDS-----TGKSGAEAQTPE----DSPNRSGAEAKTQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            549 D--SATSOEHSESKDPPPKSSSKAPRAPPEAPHPGKRSCOKSPAOOEPPORQTVGTKOPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --KEAEDDDTGPEEGSPPKEEKEKMSGSASS---ENREGTLSDSTGSEKDDLYPN-GSGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDSEDSDSEQTPEKPPSSSAPPSAPQSLPEPVASAHSSSAESESTSDSDSSSDSESESS-
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 133;
                                                                                                                                                                                                                                                                                                                                                                                                 Length 1210;
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Canaani, Eli
VENTION: Diagnostics, Therapeutics and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ADGQTPKDGS---SKSGAEDQTPK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 PLLATESVKQEEAGVRPSAGNVSTHPSL----SQRPGGSTKSHPEPQTPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz
ADDRESSEE: Norris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 VPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFK--
                                                                                                                                                                                                                                                                                                                                                                                                 8.4%; Score 205.5; DB 3;
(3.4%; Pred. No. 1.8e-07;
ve 52; Mismatches 188;
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PCT-US94-1496-26
Sequence 26, Application PC/TUS9404496
GENERAL INFORMATION:
                                             FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INRORMATION:
NAME: DeLuca Esq., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/POCKET NUMBER: TUU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
INFORMATION FOR SEQ. ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSPSKSGSEAQTIKDVPNKSG--
                                                                                                                                                                                                                                                                                                                                                                                                                     23.48;
                                                                                                                                                                                                                                                                    1210 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 23.44
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-860D-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: RENUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                             amino acid
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APPLICANT:
                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          489
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Resulting from Chromosome Abnormalities in the All-1 Region
720 RISGCRQAVVVQEDSRKDRLPLPLRDTKLLSPLRDTPPPQSLMVKITLDLLSRIPQPPGK 779
                                                                                                            607 K--PVKASARAGSRISLQGEREP--GLLPYGSRDQISKDKPKVKIKGRPRAAASNEPKPA 662
                                                                                                                                                                                                                                                                                                                                 324 -- KEAEDDDIGPEEGSPPKEEKEKMSGSASS---ENRECTLSDSTGSEKDDLYPN-GSGN 377
                                                                                                                                                                                                                                                                                                                                                             Therapeutics and Methods
                                                                                                                                                       253 VPEQPSRKDHSKPISNPSDNKELPKADINQLADKGKLSPHAFK----TE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz
ADDRESSEE: No. 6040140ris
STREET: One Liberty Place, 46th floor
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                                                                 209 KSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKD-
                                                                                                                                                                                                                                              -DLISPPQEEVKSSEPTEDVEP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/545,860D
FILING DATE: 07-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JMBER: PCI/US94/04496
22-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JHBER: US 08/320,559
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27-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26, Application US/08545860D Patent No. 6040140 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pennsylvania
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TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
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TITLE OF INVENTION: D
TITLE OF INVENTION: D
TITLE OF INVENTION: R
TITLE OF SEQUENCES:
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US-09-110-517-2
                                                           : Yuan, Chao X
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Patent No. 5633
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      607 K--PVKASARAGSRISLQGEREP--GLLPYGSRDQISKDKPKVKIKGRPRAAASNEPKPA 662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --DVPN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370 PLTAIHTPSTAEPSKFPFPTKDSQHVSSVTQNQKQYDTSSKTHSNSQQGTSSMLEDDLQL 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.4%; Score 205.5; DB 5; Length 1
23.4%; Pred. No. 1.8e-07;
tive 52; Mismatches 188; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 DSPSKSGSEAQTTKDVPNKSG----ADGQTPKDGS---SKSGAEDQTPK--
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                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
URRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 VPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFK-
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                                                                             OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                             NAME: DeLuca Esq., Mark
REGISTRATION NUMBER: 33,22;
REFERENCE/DOCKET NUMBER: 7
FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (215) 568-3100
TELERAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1210 amino acids
                                                                                                                                                                                                                                                                       TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 23.48
Matches 114; Conservative
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MOLECULE TYPE: protein
                      Pennsylvania
USA
Philadelphia
                                                                                                                                         OPERATING SYSTEM:
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838 SSSSSH 844
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Sequence 2, Application US/09110517A Patent No. 6248520

RESULT 12 US-09-110-517-2

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-----SGTSSSSGMKSSSGLGSSGSLSQKT----PPSSNSCTASSSSFSSSGSSM 1280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1124 SSKLSSSMYSSQGSSGSSQSKNSSQSGGK-----PGSSPITKHGLSSGSSSTKMKPQG 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 KPSSLMNPSLSKPNISPSHSRPPGGSDKLA--SPMKPVPGTPPSSKAKSPISSGSGGSHM 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KKADTEGKSPSHSSSNRPFTPPTSTGGSKSPGSAGRSQTPPGVATPPIPKIT 1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 PLLATESVKQEEAGVRPSAGNVSTH-----PSLSQRPGGSTKSHPEPQTPKDSPSKSSAE 73
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Resulting from Chromosome Abnormalities in the
All-1 Region
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: One Liberty Place - 46th Floor
Philadelphia
APPLICANT: Ito, Mitsuhiro
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING NUCLEAR HORMONE
TITLE OF INVENTION: RECEPTOR COACTIVATORS AND USES THEREOF
FILE REFERENCE: 600-1-22 CURRENT APPLICATION NUMBER: US/09/110,517A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 -----TTKDSTSKSHSELQTPKDSTGKSGAEAQTPEDSPNRSGAEAK-TQKDSPSKSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 AQIPEDIPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.3%; Score 204; DB 4; I
20.8%; Pred. No. 3.2e-07;
tive 56; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 FFAYLVTAAILVAVLYIAHHNKRKIIAFVLEGKRSK 420
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                                                                                                                                                            CURRENT FILING DATE: 1998-07-06
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity 20.8% 95; Conservative
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TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 IPLSAFSDPKK----TKPSHGSKDANKESSKTSKPHKVTKEHRE-RPRKDSESKSSSKEL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59; Mismatches 147; Indels
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz &
ADDRESSEE: No. 6040140ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                       One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/971,094
FILING DATE: 30-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,839
FILING DATE: 27-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/805,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US/08/545,860D
07-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US94/04496
FILING DATE: 22-APR-1994
RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US92/10930
FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELLING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 11-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,443
FILING DATE: 14-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/320,559
FILING DATE: 11-0CT-1994
Application US/08545860D
                                                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33,229
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ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: DeLuca Esq., Mark
REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                                                                                                                           OMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-545-860D-31
                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 GPPPPPPPPRASSKRPATADSPKPS------AKKQKKSSSK-GSRS------ 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 DGQTPKDGSSKSGAEDQTPKDVPNKSGAE---KQTPKDGSNKSGAEEQGPID----- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 ---GPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SELOTPKD---STGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 IPLSAFSDPKK----TKPSHGSKDANKESSKTSKPHKVTKEHRE-RPRKDSESKSSSKEL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 PHAFKTESGEETDLI---SPPQEEVKSSEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- POKPPPP---NSKVS 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 TPEDTPNKSGAEAKTQKDSSNK--SGAEAKTQKGSTSKSGSE-----AQTTKDSTSKSH 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 VPLLATESVKQEEAGVRPSAG--NVSTHPSLSQRPGGSTKSHPEPQTPKDSPSKSSAEAQ 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 8.1%; Score 199; DB 1; Length 559; Best Local Similarity 24.5%; Pred. No. 2.1e-07; Matches 96; Conservative 59; Mismatches 147; Indels
                                             DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424 EAAGKTNPGRDSRLSFSDSESDNSADSSLPSREPPP
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                                                                                                                                                                                                                                                                                                                        UMBER: US/07/971,094
30-OCT-92
                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE: 27-MAY-92
PRING APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0855
FELECOMMUNICATION INFORMATION:
                                                                                                                                     URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,559
                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/062,443
FILING DATE: 14 MAY 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/805,093 FILING DATE: 11-DEC-91
                                                                                     SYSTEM: PC-DOS
WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                       FILING DATE: 14 MAY 1 RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER: I
                                                                                                                                                                                                                CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-320-559-31
                    OMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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US-08-545-860D-31
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us-09-763-902b-1.rai

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for Detection and Treatment of Acute Leukemias
Resulting from Chromosome Abnormalities in the All-1
                                   219 ERE------QAKSSKDTSRKLGEGRLPKEEKAPPPRAAFKEPKMALKETKLESTSPNP 270
                                                                                                                                                                                                                          DGQTPKDGSSKSGAEDQTPKDVPNKSGAE---KQTPKDGSNKSGAEEQGPID----- 233
76 TPEDTPNKSGAEAKTQKDSSNK--SGAEAKTQKGSTSKSGSE-----AQTTKDSTSKSH 127
                                                                                                                                                                                                                                                                             312 PGTSPRTSSSSSFSDKKPAKDKSSTRGEKVKAESEPREAKKALEVEESNSEDEASFKSES 371
                                                                                                                                                                                                                                                                                                                                                                              ---GPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --POKPPPP---NSKVS 471
                                                                                                             128 SELQTPKD---STGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHAFKTESGEETDLI --- SPPQEEVKSSEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMS 347
                                                                                                                                                                  271 GPPPPPPPPRASSKRPATADSPKPS-----AKKOKKSSSK-GSRS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Woodcock, Washburn, Kurtz, Macklewitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                424 EAAGKTNPGRDSRLSFSDSESDNSADSSLPSREPPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----REGTLSDSTGSEKDDLY 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           472 GRRSPESCSKPEKILKKGTYDKAYTDELVELH 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ICATION NUMBER: PCT/US94/04496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application PC/TUS9404496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTORNEY/AGENT INFORMATION:
NAME: DeLuca Esq., Mark
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  559 amino acids
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 GSASSEN--
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18;

Gaps

Indels 90; Length 559;

Query Match
8.1%; Score 199; DB 5; L
Best Local Similarity 24.5%; Pred. No. 2.1e-07;
Matches 96; Conservative 59; Mismatches 147;

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234 ---GPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLS 290
                                                                       164 IPLSAFSDPKK----TKPSHGSKDANKESSKTSKPHKVTKEHRE-RPRKDSESKSSSKEL 218
                                                                                                                                                                                                                                          219 ERE-----OAKSSKDTSRKLGEGRLPKEEKAPPPKAAFKEPKMALKETKLESTSPNP 270
                                                                                                                                                                                                                                                                                                                                                                       -POKPPPP---NSKVS 471
                                                                                                                                                          76 TPEDTPNKSGAEAKTOKDSSNK--SGAEAKTOKGSTSKSGSE-----AQTTKDSTSKSH 127
                                                                                                                                                                                                                                                                                                                         128 SELQTPKD---STGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGA 184
18 VPLLATESVKQEEAGVRPSAG--NVSTHPSLSQRPGGSTKSHPEPQTPKDSPSKSSAEAQ 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :|: || |: : || | :| | 312 PGTSPRISSSSSSSSSKRPAKKALEVEESNSEDEASFKSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 PHAFKTESGEETDLI---SPPQEEVKSSEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472 GRRSPESCSKPEKILKKGTYDKAYTDELVELH 503
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4, 2003, 15:05:59 Search completed: March Job time: 23.6405 secs Sequence Sequence Sequence

Sednence Sed

OM protein

Run on:

Searched:

Database

Result

Sequence:

Title:

us-09-763-902b-1.rapb

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APPLICANT: Haselbeck, Kobert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yau, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prockaryotes
TITLE OF INVENTION: Prockaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 06/29/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/253,308
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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Pred. No. 1.7e-09;
US-10-174-590-310
US-10-176-58-310
US-10-063-56-100
US-10-063-502-100
US-10-063-502-100
US-10-175-738-310
US-10-175-752-310
US-10-176-482-310
US-10-176-482-310
US-10-176-913-310
US-10-176-913-310
US-10-176-913-310
US-10-176-913-310
US-10-176-913-310
US-10-176-913-310
US-10-176-913-310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5471, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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US-09-815-242-5471
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22.3%;
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Best Local Similarity
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LENGTH: 1021
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                                                                                                                                                                                          pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                   US-09-763-902B-1
2459.
1 MREVVALVLINVAAAGAVPL......XIPLEKDERHQWIVLLSFOL 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US10_PUBCONB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*/
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               GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd
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0.8-09-815-242-12544
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0.8-09-815-242-1313
0.8-09-815-242-13137
0.8-09-815-242-12967
0.8-09-815-242-5816
0.8-09-912-25578-3
0.8-09-815-242-5578
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US-09-815-242-12389
US-09-815-242-12769
US-09-815-242-5836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188354 seqs, 42170167 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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1770
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                                                                                                                                                                                                                                                                                                                                                            Perfect score:
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Length 1021;

81; Mismatches

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Conservative
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JRRENT APPLIC
                 84;
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               Matches
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                                                        QTPEDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSKSHSELQTPK.134
                                                                                                                                        135 DSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGADGQTPKDGSS 194
                                                                                                                                                           195 KSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNKVVP 254
                                                                                                                                                                                                                        EQPSRKDHSKPISNPSDNKELPKADINQLADKGKLSPHAFKTESGEETDLISPPQEEVĶS 314
                                                                                                                                                                                                                                                                                                           SEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSAS---SENREGTLSDS----TGSE 366
                                                                                                                                                                                                                                                                                                                                       SDSDSGSDSDSASDSDSGSDSDSSDSDSASDSTSDTESDNDSDSESDSNSDSDSGSN 956
                                  --TKSHPEPQTPKDSPSKSSAEA 74
           24;
                                                                                                                                                                                                                                                                               Indels
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        Mismatches 188;
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Pred. No. 1.7e-09;
                              22 ATESVKQEEAGVRPSAGNVSTHPSLSQRPGGS--
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FastSEQ for Windows Version 4.0
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US20020061569A1
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APPLICATION NUMBER: 60/191,078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/207,727
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       81;
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ILE REFERENCE: ELITRA.011A
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Judith W.
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22.3%;
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    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-05-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER:
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Best Local Similarity
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  84;
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Matches
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Length 1021;

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TILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
                                                                        Gaps
                                                                                                                                                   195 KSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNKVVP 254
                                                                                                                                                                                                                                                                                                                                                               EQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFKTESGEETDLISPPQEEVKS 314
                                                                                                                                                                                                                                                                                                                                                                                               75 QTPEDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSKSHSELQTPK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       897 SDSDSGSDSDSASDSGSDSDSDSDSDSDSASDSTSDTESDNDSDSESDSNSDSDSGSN 956
                                    ATESVKQEEAGVRPSAGNVSTHPSLSQRPGGS-----TKSHPEPQTPKDSPSKSSAEA 74
                                                                                                                                                                                                DSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGADGQTPKDGSS
        24;
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188; Indels
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APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIOR APPLICATION NUMBER: US 60/180,312
RIOR FILING DATE: 2000-02-04
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APPLICATION NUMBER: GB 24263.6
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2002-02-13
80
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US-10-073-256-78
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24.7%;
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Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 24.7'
Matches 66; Conservative
    CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin ve
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LENGTH: 2344
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TITLE OF INVENTION: System and Method for Tracking and Controlling Infections
FILE REFERENCE: 19124.0002
CURRENT APPLICATION NUMBER: US/10/073,256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 VKSPEKAKSPAKEEAKSPPEAKSPEKEEAKSPAEVKSPEKAKSPAKEEAKSPAEAKSPEK 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 AKSPVKEEAKSPAEAKSPVKEEAKSPAEVKSPEKAKSPTKEEAKSPEKAKSPEKEEAKSP 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A----DGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQ--GPID---- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --EOPSRKD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL - 5.6
OTHER INFORMATION: SWISSPROT HIT: P12036, EVALUE 2.00e-33
OTHER INFORMATION: EST_HOMAN HIT: BF445754.1, EVALUE 3.00e-22
                                                                                                                                                                                                                                                                                                                                                                                      IN HELA, SIGNAL = 1.3
IN HEL100, SIGNAL = 0.94
IN HEART, SIGNAL = 1.3
IN ADULT LIVER, SIGNAL = 1.1.
IN PETAL LIVER, SIGNAL = 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 ---EKMSGSASSENREGTLSDSTGSEKDDLYPNGSGNGSAES 382
                                                     PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SED ID NO 36182
LENGTH: 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 11.1%; Score 272.5; DB 10; Best Local Similarity 22.9%; Pred. No. 4.2e-08; Matches 106; Conservative 66; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 VKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEPQTPKDSPS
         APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 ------GPSKSGAEEQTSKDSPNKVVP-
                   2001-01-30
MITWRER: US 60/234,687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kreiswirth, Barry N
                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 HSKPISNP-
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109 TSKSGSEAQTTKDSTSKSHSELQTPKDSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKS 168
                                                                                                                                                                                                                                                                                                                              229 QGPIDGPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQLADKGK 288
                                                                                                                                                                                                                                                                                                                                                                                                                   50 PGGSTKSHPEPQTPKDSPSKSSAEAQTPEDTPNK-SGAEAKTQKDSSNKSGAEAKTQKGS 108
                                                                                                                                                                                                                                                                                  169 GSEAQTIKDVPNKSGADGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEE 228
                                                     Gaps
                                                                                                                           Score 260.5; DB 12; Length 265; Pred. No. 8e-08;
                                                  133; Indels
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                                                  61; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 DSDSDSDSDSDSRVTPPNNEQKA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 LSPHAFKTESGEETD-LISPPQEEVKS 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LING DATE: 2000-05-26
PLICATION NUMBER: 60/242,578
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PLICATION NUMBER: 60/253,625
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TPVISSTIESSSAPVPTPSSSITESSS---APVPTPSSSTIESSSAPAPTPSSSTIESSS 623
                                                                                                                                                                                                                                                                        -EEQGPIDGPSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDN-KELP 276
                                                                                                                                                                                                                                                                                                                                                                     KADINQLADKGKLSPHAFKTESGEETDLISPPQEEVKSSE---PTEDVEPKEAEDDDTGP 333
                                                                                                                                                                                                                                                                                                                                                                                                                      SAPVTSSTTESSSAPVTSSTTESSSAPVPTPSSSTTESSSAPVPT----PSSSTTESSSA 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSPSKSSAEAQTPEDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTS 124
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                                                                                                                                                                       ---TKDVPNKSGADGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQ-----TPKDGSNKSGA
                                                                                                                                                                                                                                                                                                                 624 APVISSITESSSAPVPIPS-SSITESSSAPVP---TPSSSITESSSAPVPIPSSSITESS
                                                                       KSHSELQTPKDSTGK-SGAEAQTPEDSPNRSGAEAKTQK------DSPSKSGSEAQT
                                                                                                                        SSSAPVPTPSSSTTESSSAPAPTPSSSTTESSSAPVTSSTTESSSAPVPTPSSSSTTESSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLE OF INVENTION: Identification of Essential Genes in TLE OF INVENTION: Prokaryotes
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Pred. No. 0.0002;
); · Mismatches 93;
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRACEEQ for Windows Version
SEQ ID NO 5898
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Patent No. US20020061569A1
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APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
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LING DATE: 2000-05-26
PELICATION NUMBER: 60/242,578
LING DATE: 2000-10-23
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APPLICATION NUMBER: 60/191,078
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; ORGANISM: Staphylococcus aureus
US-09-815-242-5898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rawick, John D.
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                                                                                                                                                                                                                                                    1008 SEMISDSMSTSGSLAASDSKSMSVSSSMSTSQSGSTSESLSDSISTSDSDSKSLSLSTSQ 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                  948 STSKLESQSTSISLSTSDSKSMSTSESLSDSTSTSDSVSGSLSVAGSQSVSTSTSDSMST 1007
                                                                                                                                                                                                                                                                                                                                           74 AQTPEDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSK--SHSELQ 131
                                                                                                                                                                                                                                                                                                                                                                                                           192 GSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNK 251
                                                                                                                                                                                                                                                                                                               132 TPKDSTGKSGAEAQTPEDSPNRSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGADGQTPKD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 VVPEQPSRKDHSKPISNPSDNKELPKADINQLADKGKLSPHAFKTESGEETDLISPPQEE 311
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                                                                       Gaps
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                                                                                                                 22 ATESVKQEEAGVRPSAG----NVSTHPSLSQRPGGS----TKSHPEPQTPKDSPSKSSAE 73
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                                                                       46;
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                                              ; Pred. No. 0.00021;
59; Mismatches 162; Indels
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8.7%; Score 214.5; DB 10;
Best Local Similarity 23.1%; Pred. No. 0.00015;
Matches 96; Conservative 52; Mismatches 209;
                       DB 10;
0.00021;
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                       Score 216;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JRRENT APPLICATION NUMBER: US/09/801,368
JRRENT FILING DATE: 2001-03-07
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US20020128250A1
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                 Query Match
Best Local Similarity 25.2%;
Matches 90; Conservative 5
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SOFTWARE: Patentin version 3.0
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SEQ ID NO 108
LENGTH: 1367
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2087 NANATPENTGQPNVSETTANGKADASPTTPNNS-----DAATGETTATSATDDANDKPQ 2140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 SSNKSGAEAKTOKGSTSKSGSEAQTTKDSTSKSHSELQTPKDSTGKSGAEAQ--TP-EDS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 PNRSGAEAKTOKDSPSKSGSEAQTTKDVPNKSGADGQTPKDGSSKSGAEDQTPKDVPNKS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 GAEKOTPKD-----GSNKSGAEEQGPIDGPSKSGAEEQT----SKDSPNKVVPEQPSRK 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 NVSTHPSLSQRPGGST----KSHPEPQTPKDSPSKSSAEAQTPEDTPNKSGAEAKTQKD 93
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; Pred. No. 0.00039;
58; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                               ITLE OF INVENTION: Identification of Essential Genes in ITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2010 2.1 17 PRIOR FILING DATE: 2000-03-21 PRIOR FILING DATE: 2000-03-21 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206, 848 PRIOR APPLICATION NUMBER: 60/207, 727 PRIOR APPLICATION NUMBER: 60/242, 578 PRIOR FILING DATE: 2000-10-23 PRIOR FILING DATE: 2000-10-23 PRIOR FILING DATE: 2000-11-27 PRIOR FILING DATE: 2000-11-27 PRIOR PLILING DATE: 2000-11-27 PRIOR APPLICATION NUMBER: 60/253, 625 PRIOR APPLICATION NUMBER: 60/257, 931
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Patent No. US20020061569A1
                                                    ce 5816, Application US/09815242
No. US20020061569A1
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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US-09-815-242-5816
                                                                                                                                                                                                                                                                                                amamoto, Robert T
                                                                                                                                                            Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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Best Local Similarity 25.6%;
Matches 90; Conservative 5
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Trawick,
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US-09-815-242-12967
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ORGANISM:
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65 DSPSKSSAEAQTPEDTPNKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTS 124
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                                                                             185 DGQTPKDGSSKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQT 244
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                                                                                                                              1249 DSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDAGKRTPVKPMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT: Xu, H. Howard
TLE OF INVENTION: Identification of Essential Genes in
TLE OF INVENTION: Prokarvotes
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Best Local Similarity 25.4%; Pred. No. 0.0002;
Matches 54; Conservative 50; Mismatches 93;
                                                                                                                                                                                                                                       --- NNGSNNATL 1327
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SEGTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13137
LENGTH: 1349
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 13137, Application US/09815242 Patent No. US20020061569A1
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IOR APPLICATION NUMBER: 60/242,578
IOR FILING DATE: 2000-10-23
IOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IOR FILING DATE: 2000-03-21
IOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IOR APPLICATION NUMBER: 60/191,078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
TLING DATE: 2000-12-22
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Staphylococcus aureus
-09-815-242-13137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amamoto, Robert T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                    1302 TKDHHNKAKALPETGSE-
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16;

Gaps

49;

Length 2478;

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REFERENCE: 600-1-269N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2191 TNNNSTTTATNENAPIGSTATAPTTASTEAASSADS---KDNASVNDSKQNA--EVNN-- 2243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2087 NANATPENTGOPNVSETTANGKADASPTTPNNS-----DAATGETTATSATDDANDKPQ 2140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2244 SAESQSTNDKVAQPKSENKAKAEKDGS-DSTNQSMVESTTETLPSADITEPNVPSNTS-K 2301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2141 ANNNSSVDASTNSPIMD-----NDVTSKPEVE-SINNGTIDKPVIETDNATPAEST 2190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2302 DKEESTINGIDAGQL-KSEINVASNEADKSPSKADTEVSNKPSISASSEAKEKMISINVS 2360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 PNRSGAEAKTOKDSPSKSGSEAQTTKDVPNKSGADGQTPKDGSSKSGAEDQTPKDVPNKS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAEKQIPKD-----GSNKSGAEEQGPIDGPSKSGAEEQI----SKDSPNKVVPEQPSRK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHSKPISNPSDNKELPKADTNQLADKGKLSPHAFKTESGEE--TDLISPPQEEVKSSEPT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 SSNKSGAEAKTOKGSTSKSGSEAQTTKDSTSKSHSELQTPKDSTGKSGAEAQ--TP-EDS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Estable, Mario
APPLICANT: Roeder, Robert
TITLE OF INVENTION: MCEF, A No. US20030039658Alel Transcription Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 NVSTHPSLSQRPGGST-----KSHPEPQTPKDSPSKSSAEAQTPEDTPNKSGAEAKTQKD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 2478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

8.6%; Score 211.5; DB 10; Length
Best Local Similarity 25.6%; Pred. No. 0.00039;
Matches 90; Conservative 58; Mismatches 155; Indels
                                                                                                                                                                                                                                                                 ITLE OF INVENTION: Identification of Essential Genes in ITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                        ILE REFERENCE: ELITRA.011A
URRENT APPLICATION NUMBER: US/09/815,242
URRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
RIOR PROFIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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3 DATE: 2000-05-23
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RIOR APPLICATION NUMBER: 60/253,625
RIOR FILING DATE: 2000-11-27
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US-09-932-257A-3
Sequence 3, Application US/09932257A
Publication No. US20030039658A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IOR APPLICATION NUMBER: 60/207,727
IOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12967
                                                                                                                                                                           Carr, Grant J.
Kamamoto, Robert T
                                                                                                                                                rawick, John D.
                                                                                                                    all, Daniel
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LENGTH: 2478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 NOLADKGK---LSPHAFKTESGEETDLISPPQEEVKSSEPTED------VEPKEA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           622 RPTAEKKKYKSTSKSSOKSREIIETDTSSSDSDESESLPPSSOTPKYPESNRTPVKPSSV 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 PRSTPGSNSEPSHHNSEGAD-NSRDDSSSHSGSESSS--GSDSESGS-----SSSD 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: || | : || |: || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- ||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- NKSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSKSH 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SELQIPKDSIGKSGAEAQIPEDSP---NRSGAEAKTQKDSPSKSGSEAQIIKDVPNKSGA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TESVKQEEAGV-----RPSAGNVSTHPSLSORPGGSTKSHPEPOTPKDSPSKSSAEAQT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEANEPSOSA ----- SPEPEPPPTNKWQLDNWLNKVNPHKVSPASSVDSNIPSSQGY
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ITLE OF INVENTION: Prokaryotes
ILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.6%; Score 210.5; DB 23.8%; Pred. No. 0.0002
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/226,339
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 1163
                                                                                                                         PRIOR APPLICATION NUMBER: 60/226,340 PRIOR FILING DATE: 2000-08-18
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Carr, Grant J.
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Best Local Similarity 23.8<sup>3</sup>
Matches 97; Conservative
LICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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RESULT 14
US-10-108-605-307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.5%; Score 210; DB 10; Best Local Similarity 21.9%; Pred. No. 0.00017; Matches 59; Conservative 53; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 QRPGGSTKSHPEPQTPKDSPSKSSAEAQTPEDTPNKSGAE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5578
LENGTH: 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSTVKDHHNKAKALPETGSENNNSNNGTL 910
                                                                                                                         PRIOR FILING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
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No. US20020061569A1
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; ORGANISM: Staphylococcus aureus
US-09-815-242-5578
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LE REFERENCE: ELITRA.011A
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u, H. Howard
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Zyskind, Judith W.
Wall, Daniel
2000-02-23
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APPLICATION NUMBER: 60/
FILING DATE: 2000-05-23
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APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Rachmann, Jane
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCOD
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 31133B
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663 EKPAGLTQT-------GTNTTEDDKDADGGEVDVTITDHDDFTLDNGYYEE 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 NKSGAEAKTOKDSSNKSGAEAKTOKGS--TSKSGSEAQTTKDSTSKSHSELQTPKDSTGK 139
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 SVKQEEAGVRPSAGNVSTHPSLSQRPGGS-TKSHPEPQTPKD--SPSKSSAEAQTPEDTP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- AKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTTKDSTSKSHSELQTPKDSTGKSGAEAQ
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                                                                                                                                                                                                                                                                                  Length.932;
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; Pred. No. 0.00034;
68; Mismatches 124;
                                                                                                                                                                                                                                                                                    , DB 10;
0.00017;
                                                                                                                                                                                                                                                                                                                                      Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                       48 ORPGGSTKSHPEPQTPKDSPSKSSAEAQTPEDTPNKSGAE-
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12438
LENGTH: 932
                                                                                                                                                                                                                                                                                    Score 210;
Pred. No. (
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CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
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Patent No. US20020160934A1
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 21.9%; -Pred.
Matches 59; Conservative 53; Mi
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                                                                                                                                                                                                            Staphylococcus aureus
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Best Local Similarity 21.7%;
Matches 76; Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver. 2.
SEQ ID NO 307
LENGTH: 724
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                                                                                                                                                                                                         ; ORGANISM: Staph
US-09-815-242-12438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 SSAEAQTPEDTPN--KSGAEAKTQKDSSNKSGAEAKTQKGSTSKSGSEAQTT-----KD 121
                                                                                                                         --SGSDQEKKKSGSDSDI 270
                      SKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDGPSKSGAEEQTSKDSPNKVV 253
                                                                                                                                                                   254 PEQPSRKDHSKPISNPSDNKELPKADTNQLADKGKLSPHAFKT--ESGEETDLISPPQEE 311
140 SGAEAQTPEDSPN-----RSGAEAKTQKDSPSKSGSEAQTTKDVPNKSGADGQTPKDGS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 VAAAGAVPLLATESVKQEEAGVRPSAGNVSTHPSLSQRPGGSTKSHPEPQT--PKDSPSK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50;
                                                                                                                                                                                             Length 2368;
                                                                                                                                                                                                                                                         312 VKSSEPTEDVEPKEAEDDDTGPEEGSPPKEEKEKMSGSASSENREGTLSDS 362
                                                                                                                                                                                                                                                                                   -- DEDEAGPAARKSPVRSKSRSQSKSHSHSRSMSHSRS 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LICATION NUMBER: US/09/815,242
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                                                                                                              SRSGS------ASGSGSDVGVPKKKARRA--
                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09815242
0020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NT FILING DATE: 2001-03-21
APPLICATION NUMBER: 60/191,078
FILING DATE: 2000-03-21
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G DATE: 2000-05-23
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Best Local Similarity 24.2
Matches 95; Conservative
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235 PSKSGAEEQTSKDSPNKVVPEQPSRKDHSKPISNPSDNKELPKADTNQL-----ADKGK 288
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179 PNKSGADGQTPKDGS----SKSGAEDQTPKDVPNKSGAEKQTPKDGSNKSGAEEQGPIDG 234
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.	OM protein - protein search, using sw model	<pre>Run on: March 4, 2003, 14:50:41; Search time 11.9604 Seconds (without alignments) 1559.740 Million cell updates/sec</pre>	Title: Derfect score: 732 Sequence: 1 MASVDFKTYVDQACRAAEEFPSNTVWKIASDCFRFQDWAS 140	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 908470 seqs, 133250620 residues	Total number of hits satisfying chosen parameters: 908470	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Detabase: A_Geneseq_101002:*    STDS2/gcddata/geneseq/geneseqp-embl/AA1980 DAT:*   STDS2/gcddata/geneseq/geneseqp-embl/AA1980 DAT:*   STDS2/gcddata/geneseq/geneseqp-embl/AA1981 DAT:*   STDS2/gcddata/geneseq/geneseqp-embl/AA1991 DAT:*   SCORE Walter than or equal to the score of the result being printed   SCORE Walter than or equal to the score of the result bei

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11	13	112	16	17	18	19	20	21	22		24		26	27	28	29	30	31	32	33	34	35			38	39	40	41	42	.43	44	45

## ALIGNMENTS

protein transport regulator; cancer; ferative disorder; Human; protein transport molecule; PTAM; diagnosis; cytostatic; antiinflammatory; antiHIV; protein transport regulator; climune disorder; cell proliferative disorder; secretory durticaria; allergy; abnormal vesicle trafficking; asthmas; autoimmune haemolytic anaemia. Human protein transport molecule (PTAM) SEQ ID NO:2. AAY82318 standard; Protein; 140 AA. 99WO-US19616. 98US-0098206. 19-JUN-2000 (first entry) (INCY-) INCYTE PHARM INC. antlarthritic; an antiallergic; and dermatological; WO200012703-A2. Homo sapiens. 26-AUG-1999; 27-AUG-1998; 09-MAR-2000 AAY82318; ESULT 1 AY82318

Corley NC, Guegler KJ;

Tang YT, Lal P, Bandman O, Yue H, Gorgone GA, Baughn MR, Patterson C;

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cytostatic, antiarthritic, antialergic, antidiabetic, antilipaemic, antiarthritic, antialergic, antidiabetic, antilipaemic, antiarthritic, antiallergic, antidiabetic, antilipaemic, antiarthritic, dermatological, antianaemic, antipsoriatic, antiantenmatic, antianaemic, antipsoriatic, antiantenmatic, antianaemic, antipsoriatic, cateopathic, dermatological, and antianic, antipsoriatic, equilate protein transport. PAMP proteins and antignous are useful for preventing or treating a disorder associated with decreased or increased expression or activity of PTAM. PTAM polynucleotides are useful for diagnosing conditions associated with PTAM, comprising detecting PTAM by forming a hybridisation complex, preferably after PCR amplifying the biological sample. Diseases prevented, treated or diagnosed include cell proliferative disorders such as cancers, immune disorders, secretory disorders and other conditions associated with abnormal vesicle trafficking, such as allergies, asthma, urticaria and autoimmune trafficking, such as allergies, asthma, urticaria and autoimmune a targeting or delivery mechanism for bringing pharmaceutical agents into cells or tissues expressing PTAM and for diagnosis of PTAMF. Telated disorders. PTAMF, its catalytic or immunogenic fragments are useful for drug screening using libraries of compounds. PTAM polynucleotides are useful for generating phybridisation probes useful in mapping the naturally occurring genomic sequences.
                                                                                                          New human protein transport-associated polypeptide and polynucleotide useful for diagnosis, prevention and treatment of cell proliferative and secretory disorders such as leukemia, cystic fibrosis
                                                                                                                                                                                                                                                                                         AAA08035 to AAA08042 encode the human protein transport-associated molecules (PTAMs) given in AAY82317 to AAY82324. The PTAMs have
                                                                                                                                                                                                                                     Claim 1; Page 61-62; 75pp; English.
                        WPI; 2000-256642/22.
N-PSDB; AAA08036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 140 AA;
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100.0%; illarity 100.0%; Conservative 0 Query Match Best Local Similarity Matches 140; Conserv

1 MASVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSE ; 0 ; Score 732; DB 21; Length 140; ; Pred. No. 2.16-80; 0; Mismatches 0; Indels 0;

Human novel secreted protein, Seq ID 1181;

Human; immunösuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective, nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebrovascular anglogenesis; 

nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.

17-JAN-2001; 2001WO-USÖ1341

17-MAR-2000

38-JUN-2000

38-SEP-2 18-SEP-2

29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 02-OCT-2000; 02-OCT-2000;

-OCT-2000

-0CT-20 -0CT-20

-0CT-20 -0CT-20 -0CT-20

10-OCT-2000; 10-OCT-2000; 10-OCT-2000; 11-NOV-2000;

OCT-1

38-NOV-200 08-NOV-200

-202-

-NOV-

- NON - 8

-NOV-20

NOV-2 NOV-2 NOV-2

-NOV-2

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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebral adsorders e.g. cardiac arrest, cerebral disorders e.g. cardiac arrest, cerebral disorders e.g. cardiac arrest, cerebral disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and funging occular disorders e.g. corneal infection, and many other called and wound healing and epithelial cell proliferation, to be used to ald wound healing and epithelial cell proliferation, to be used to ald wound healing and epithelial cell proliferation, to be used to all and process the analyse of all and the specification. The polypeptides can also be used to all and process the all proliferation, to be used to all and process the analyse of all and all and the specification of an analyse of all and all a
                                                                                                                                                                                                                                                    New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MASVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSE
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100.0%; Score 732; DB 22;
Best Local Similarity 100.0%; Pred. No. 2.7e-80;
Matches 140; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; SEQ ID No 1181; 980pp; English.
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Ruben SM;
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Rosen CA, Barash SC,
                                                                                                    WPI; 2001-488783/53.
N-PSDB; AAS26215.
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(HUMA-) HUMAN GENOME SCI

-DEC-2000;

-NOV-2000; DEC-2000; -DEC-2000;

NOV-2000

NOV-2

NOV-2

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The present invention provides the protein and coding sequences of human NTF2 associated protein 16. The sequences can be used in the treatment of cancer and HIV infection, as well as other diseases. The present sequence is the protein of the invention.
                                          Human; NTF2 associated protein 16; cancer; HIV infection; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 EMLPSSEFQISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 DILPSSEFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      duman; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 SLDFKTYVDQACRAAEEFVNIYYETWDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide-human NTF2 associated protein 16 and polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.8%; Score 584; DB 23;
75.4%; Pred. No. 1.8e-62;
ive 22; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 26(Disclosure); 32pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein sequence SEQ ID NO:17707.
                                                                                                                                                                                                                                                                                                                         (BODE-) BODE GENE DEV CO LTD SHANGHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB95379 standard; Protein; 197 AA
Human NTF2 associated protein 16.
                                                                                                                                                                                                                                                                          5-MAR-2000; 2000CN-0114918
                                                                                                                                                                                                                             15-MAR-2000; 2000CN-0114918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 NTVWKIASDCFRFQDWAS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 NTVWKIASDCFRFQDWSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000JP-0118776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-042199/06.
N-PSDB; ABA05754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 AA;
                                                                                                                                                                                                                                                                                                                                                                   Mao Y, Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-AUG-1999;
11-JAN-2000;
                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1074617-A2
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                                                                                                                                   CN1313332-A
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                                                                                                                                                                                19-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB95379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
molecules (PTAMS) given in AAY82317 to AAY82324. The PTAMS have cytostatic, antiathic, antiathmatic, immunosuppressant, antiatharthicits, antiathmatic, immunosuppressant, antiathericis, antiatharthicis, antiathmatic, immunosuppressant, antitherentic setepathic, dermatological, antianaemic, antipaemic, antistoper, antistoper, antistoper, antistoper, and antially antistoristic, preparation transport. PTAM proteins and antagonists are useful for preventing or treating a disorder associated with decreased or increased dispression or activity of PTAM protynucleotides are useful for dispression or activity of PTAM. Protonicis and set useful for forming a hybridisation complex, preferably after PCR amplifying the forming a hybridisation complex, preferably after PCR amplifying the ploingies and samples biseases prevented, treated or disprosed include cell protiferative disorders such as cancers, immune disorders, secretory disorders and other conditions associated with abnormal vesicle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nemolytic anaemia. Anti-PTAM antibodies may be used as antagonists, as targeting or delivery mechanism for bringing pharmaceutical agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         into cells or tissues expressing PTAM and for diagnosis of PTAM related disorders. PTAM, its catalytic or immunogenic fragments are useful for drug screening using libraries of compounds. PTAM polynuclectides are useful for generating hybridisation probes useful in mapping the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMLPSSEFQISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPS 122 : ||||||||::::||||||::||| ||:||:|| DTLPSSEFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFPNQNFLLTAQSTPN 123
                                                                                                                                                                                                                                                                                                                                                                                 New human protein transport-associated polypeptide and polynucleotide useful for diagnosis, prevention and treatment of cell proliferative and secretory disorders such as leukemia, cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA08035 to AAA08042 encode the human protein transport-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rafficking, such as allergies, asthma, urticaria and autoimmune
                                                                                                                                                                                                                                                  Guegler KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 142;
                                                                                                                                                                                                                                                Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.8%; Score 584; DB 21; 75.4%; Pred. No. 1.8e-62; 1ve 22; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       naturally occurring genomic sequences
                                                                                                                                                                                                                                             Lal P, Bandman O, Yue H;
A, Baughn MR, Patterson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB04459 standard; Protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 68; 75pp; English
                                                                                                         99WO-US19616.
                                                                                                                                                      98US-0098206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                 (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                     Gorgone GA, Baughn MR,
                                                                                                                                                                                                                                                                                                                  WPI; 2000-256642/22.
N-PSDB; AAA08041:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 104; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 AA;
                WO200012703-A2
                                                                                                         26-AUG-1999;
                                                                                                                                                      27-AUG-1998;
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                                                             09-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                ang YT,
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ID ABB0
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AC ABB0
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DT 04-1*
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Gaps

Length 142; Indels

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The present invention describes primer sets for synthesising 5602 (2011-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide comprises a 3'-end sequence complementary to a complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to a complementary strand of a sequence of sequence of the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in comprise therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the protein send of the full-length cDNAs. The primers also useful for the connext of the full-length cDNAs and AHUS1363 and AHUS1363 to AAHUS1363 to AAHUS1363 to AAHUS1632 and AAHUS1633 to AAHUS1632 and AAHUS1633 to AAHUS1632 and AAHUS1633 to A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis;
                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 SVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFF 62
                                                                                                                                         Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                      Saito.K, Y
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID 17707; 2537pp + CD ROM; English.
                                                                                                                              Ota T, Isogal T, Nishikawa T, Hayashi K, S
Ishii S, Sugiyama T, Wakamatsu A, Nagal K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human novel secreted protein, Seg ID 1180.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTVWKIASDCFRFQDWAS 140
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09-JUN-2000; 2000JP-0241899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 75.4
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the present invention
                                                                                 (HELI-) HELIX RES INST.
                                                                                                                                                                                                                     WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 AA;
                                                                                                                                                                                                                                                                                                                                                      full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2001
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AAU16227.
XX
AC AAU1.
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XX
DT 07-in
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XX
CHUMA
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KW HUMA
KW CYLC
KW CHUMA
KW CYLC
KW CHUM
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cérebrovascular disorder; cerebral ischaemia; anglogenesis; nervous system disorder; Alzhelmer; a disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
cardiovascular disorder;
hyperproliferative disorder;
cerebrovascular disorder; cer
                                                                                                                                                                                                        17-JAN-2001; 2001WO-US01341
                                                                                                                                     WO200155322-A2.
                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4-SEP-2000
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30-AUG-2000
31-SEP-2000
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                                                                                                                                                                       02-AUG-2001
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                                                                                                                                                                                                                                                                                                                                 -MAR-2000
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Ruben SM;

Barash SC,

Rosen CA,

WPI; 2001-488783/53. N-PSDB; AAS26214.

(HUMA-) HUMAN GENOME SCI INC 11-DEC-2000; 2000US-0254097 05-JAN-2001; 2001US-0259678

2000US-0251989. 2000US-0251990. 2000US-0254097.

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26-SEP-2000
          -SEP-200(
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rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosting a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also to a pathological condition. Antibodies to the proteins can also to a pathological condition. Antibodies to the proteins can also to a pathological condition. Antibodies to the proteins can also the used in alleviating symptoms associated with the disorders and in diagnostic immunosospae (g. rabbit). Disorders which are diagnosed or treated immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autofinamen disorders e.g. rhoumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, nervous system disorders e.g. cremental isohaemia, and/openesis, nervous system disorders e.g. alzheimer's disease, infections caused by bacteria, viruses and fungi and coular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also the contractive disorders listed in the specification. The polypeptides can also the contractive disorders listed in the specification. The polypeptides can also the contractive disorders listed in the specification. The polypeptides can also the contractive disorders listed in the specification. The polypeptides can also the contractive disorders listed in the specification. The polypeptides can also the contractive disorders listed in the specification. The polypeptides can also the contractive disorders listed in the specification. The polypeptides can also the contractive disorders listed in the specification. The polypeptides can also the contractive disorders listed in the specification.
                                                                                                                                                                                                                                                                                                                       New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEM 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ransplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be as a food additive or preservative to increase or decrease storage capabilities, fat content lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prevent skin aging due to sunburn, to maintain organs before
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.1%; Score 579; DB 22; 75.7%; Pred. No. 8.9e-62; 11ve 21; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; SEQ ID No 1180; 980pp; English.
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Best Local Simi
Matches 103;
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Drosophila melanogaster

WO200171042-A2.

27-SEP-2001

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 DCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIASDCFRF 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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; Pred. No. 3.7e-05;
19; Mismatches 54;
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11-JUL-2000; 2000US-0614150
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                                             23-MAR-2000; .2000US-191637P
11-JUL-2000; 2000US-0614150
23-MAR-2001; 2001WO-USO9231
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ABB66052
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Length 133, Indels

Score 308; DB 22; Pred. No. 4.4e-29; 27; Mismatches

42.18;

133 AA

Sequence.

Query Match Best Local Similarity 41.4%;

47;

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

Drosophila melanogaster

WO200171042-A2

27-SEP-2001

Orosophila melanogaster polypeptide SEQ ID NO 29004

26-MAR-2002\* (first entry)

ABB67404;

ABB67404 ID ABB67404 standard; Protein; 688 AA.

||: |||:|| KWKVVSDCYRMQE 132 125 VWKIASDCFRFQD 137

120

invention relates to an isolated nucleic acid detection reagent ble of detecting 1000 or more genes from Drosophila. The invention

Disclosure; SEQ ID NO 21843; 21pp + Sequence Listing; English.

nteractions

iseful in developmental biology and in elucidating cell signalling and

interactions in higher eukaryotes for the development of

insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL36511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB22072).

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell

Myers EW;

L1 PWD,

Adams M,

enter JC,

PEKE ) PE CORP NY.

WPI; 2001-656860/75. N-PSDB; ABL09120:

33-MAR-2001; 2001WO-US09231 23-MAR-2000; 2000US-191637P 11-JUL-2000; 2000US-0614150 ŝ

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99US-0130077.
99US-0130449.
99US-0130510.
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                       08-APR-1999;
16-APR-1999;
19-APR-1999;
21-APR-1999;
23-APR-1999;
28-APR-1999;
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30-APR-1999
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  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 DCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIASDCFRF 135
                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 30.3%; Pred. No. 3.7e-05;
Matches 37; Conservative 19; Mismatches 54; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           19 EFVRQYYTLLNKAPNHLHRFYNHNSSYIHGESKLVVGQREIHNRIQQLNFNDCHAKISGV 78
                                                                                                                                                                                                                                                                                                                                                                                                            19 EFVNVYYTTMDKRRRLLSRLYMGTATLV-WNGNAVSGQESLSEFFEMLPSSE--FQISVV 75
                                                                                                                                                      Disclosure; SEQ ID NO 24948; 21pp + Sequence Listing; English.
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                                     L1 PWD, Myers EW;
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990S-0123180.
990S-0123548.
990S-0126264.
990S-0126264.
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                                     Adams M,
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                                                           WPI; 2001-656860/75.
N-PSDB; ABL10155.
           (PEKE ) PE CORP NY
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29-MAR-1999;
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                                     Venter JC,
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ID AAG1
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RR 13-7UL-1999; 9918-0144331.

PR 13-7UL-1999; 9918-0144332.

PR 13-7UL-1999; 9918-0144332.

PR 20-7UL-1999; 9918-0144332.

PR 20-7UL-1999; 9918-0144814.

PR 21-7UL-1999; 9918-014684.

PR 21-7UL-1999; 9918-014684.

PR 22-7UL-1999; 9918-014614.

PR 22-7UL-1999; 9918-014634.

PR 22-7UL-1999; 9918-014634.

PR 22-7UL-1999; 9918-014634.

PR 22-7UL-1999; 9918-014322.

PR 22-7UL-1999; 9918-014432.

PR 22-7UL-1999; 9918-01499.

PR 23-7UL-1999; 9918-01
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                   75 VDCQPVHDEATPSQTTVLVVICGSVKFEG-NKQRDFNQNFILTAQASPSNTVWKIASDCF 133
                                                                                                                                                                                                                                                                                      ----SICN 114
                                        Query Match 16.2%; Score 118.5; DB 21; Length 125; Best Local Similarity 30.1%; Pred. No. 3.6e-06; Matches 37; Conservative 17; Mismatches 50; Indels 19; Gaps
                                                                                                                                                                            11 ASAFVNHYYHLFDNDRSSLSSLYNPTSLLTFEGQTIYGVDNISNKLKQLPFDQCHHLIST 70
                                                                                                                                        17 AEEFVNVYYTIMDKRRKLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLPSSEFQ--ISV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 1441.
                                                                                                                                                                                                                                                                    AAG05145 standard; Protein; 153 AA.
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90S-0162142
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990S-0121825. 990S-0123180. 990S-0123548. 990S-0125788.

25-FEB-1999; 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 25-MAR-1999;

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hybridisation assay; genetic mapping; gene expression control; promotex
termination sequence.
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                                                                                                                                                                                                                                                                                                                                                              14 ASLSLKMSQMDPDAVSKAFVEHYYSTFDTNRVGLAGLYQEASMLTFEGQKIQGVQSIVAK 73
                                                                                                                                                                                                                                                                                                                                           2 ASVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEF 61
                                                                                                                                                                                                                                                                                                    Ouery Match
16.2%; Score 118.5; DB 21; Length 153;
Best Local Similarity 28.6%; Pred. No. 4.8e-06;
Matches 40; Conservative 24; Mismatches 61; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 6317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG08682 standard; Protein; 123 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                           129 PQGS----FYVFNDIFSWR 143
                                                                                                                                                                                                                                                                                                                                                                                                                             117 AQASPSNTVWKIASDCFRFQ 136
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99US-0123180.
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99US-0125788.
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05-MAR-1999;
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ID AACO
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RR 16-JUL_19999 990S-0144086.

RR 19-JUL_19999 990S-01444325.

RR 19-JUL_19999 990S-01444332.

RR 19-JUL_19999 990S-01444332.

RR 19-JUL_19999 990S-01444332.

RR 19-JUL_19999 990S-01444332.

RR 22-JUL_19999 990S-0144433.

RR 11-JUL_19999 990S-014443.

RR 11-JUL_19
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75 VDCQPVHDEATPSQTTVLVVICGSVKFEGNKQR-DFNQNFIL--TAQASPSNTVWKIASD 131
                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                        DB 21; Length 123;
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30.1%; Pred. No. 4.7e
ive 22; Mismatches
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tes 37; Conserv
132 CFR 134
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Matches
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

Arabidopsis thallana

EP1033405-A2.

06-SEP-2000

99US-0121825. 99US-0123180. 99US-0123548.

25-FEB-1999; 05-MAR-1999; 09-MAR-1999;

25-FEB-2000; 2000EP-0301439.

Arabidopsis thaliana protein fragment SEQ ID NO: 6316.

17-OCT-2000 (first entry)

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99US-0131449
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
16-APR-1999;
                                                                                                                                   8-APR-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 VDCQP-----SGPASGMLVFVSGNLQLAGEEHALKFSQMFHLMPTPQGS-----FYVFND 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 VDCQPVHDEATPSQTTVLVVICGSVKFEGNKQR-DFNQNFIL--TAQASPSNTVWKIASD 131
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 30.1%; Pred. No. 4.8e-06;
Matches 37; Conservative 22; Mismatches 49; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 AEEFVNVYYTTMDKRRILLSRLYMGTATLVWNGNAVSGQESLSEFFEMLP--SSEFQISV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thallana protein fragment SEQ ID NO: 1443.
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ID AAG05147 standard; Protein; 131 AA.
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99US-0123180
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05-MAR-1999;
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RR 15-VIL. 1999

RR 16-VIL. 1999

RR 16-VIL. 1999

RR 11-VIL. 1999

RR 21-VIL. 1999

RR 21-
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                               75 VDCQPVHDEATPSQTTVLVVICGSVKFEGNKQR-DFNQNFIL--TAQASPSNTVWKIASD 131
                                                                                                                                                                                                              VDCQP-----SGPASGMLVFVSGNLQLAGEKHALKFSQMFHLMPTPQGS-----FYVFND 116
                                                                                                                      17 AEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLP--SSEFQISV 74
  DB 21; Length 131;
                                               50; Indels
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16.1%; Score 117.5; DB 2
29.6%; Pred. No. 5.1e-06;
tive 23; Mismatches 50
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ID AAG05146 standard; Protein; 134 AA.
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  Query Match
Best Local Similarity 29.6%
Matches 37; Conservative
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25-FEB-2000; 2000EP-0301439.

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DB\_21; Length 134; Query Match
16.1%; Score 117.5; DB 21;
Best Local Similarity 29.6%; Pred. No. 5.3e-06;
Matches 37; Conservative 23; Mismatches 50;

132 CFRFQ 136

120 IFSWR 124

Search completed: March 4, 2003, 14:58:32 Job time : 13:1032 secs

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

protein search, using sw model OM protein March 4, 2003, 14:53:52; Search time 6.29798 Seconds (without alignments) 2137.006 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-763-902B-2.
732
1 MASVDFKTYVDQACRAAEEF......PSNTVWKIASDCFRFQDWAS 140

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched: 283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% ... Maximum Match 100% Listing first 45 su

Database :

PIR\_73:\* 1: pir1:\* 2: pir2:\* pir3:\* pir4:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

	Description	placental protein	probable nuclear t	nuclear transport	protein T23J18.22	probable nuclear t	hypothetical prote	protein F17L21.10		٠.	٠.		hypothetical prote	endopeptidase La h	gene 284 protein -	embryonal lethal (	syndecan-4 precurs		heterocyst differe	Ig light chain C r			hypothetical prote	-	hypothetical prote	hypothetical prote	gene 34 protein -	probable obtusifol	deoxyribonuclease	penicillin-binding
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hypothetical prote hypothetical prote	hypothetical prote hypothetical prote	probable formate C hypothetical prote	hypothetical prote	metnyi-accepting c exopolysaccharide	hypothetical prote	hypothetical prote	fibronectin precur	<ul> <li>hypothetical prote</li> </ul>	hypothetical prote	hypothetical prote
AG1085 AE1332	T22932 T47163	E69144 T48028	T47693	89/U12 A98290	AB2994	T28651 H64861	S14428	H64172	AH2214	T31705
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70	69.5	69	68.5	68.5 68.5	68.5	68.5	67.5	67	67	67
30	3 8	3.4	36	37	39	40	4 4	. 43	44	45

## ALIGNMENTS

	RESULT 1.
	S00751
	placental protein 15 - human
_	NyAlternate names: PPL5
	C):Species: Homo Sables (mail)
_	C. Accession: S00751
	R; Grundmann, U.; Nerlich, C.; Rein, T.; Lottspeich, F.; Kuepper, H.A.
_	. Nucleic Acids Res. 16, 4721, 1988
	A; Title: Isolation of CDNA coding for the placental protein 15 (PP15).
×	A; Reference number: 'S00751; MUID:88247772; PMID:3380696
	A; Accession: S00751
_	A; Molecule type: mRNA
	A; Residues: 1-127 <gru></gru>
_	A;Cross-references: EMBL:X07315; NID:935578; PIDN:CAA30278.1; PID:935579
	C; Superfamily: yeast nuclear transport factor NTF2
	Ouerv Match 16.9%; Score 124; DB 2; Length 127;
	Best Local Similarity 26.5%; Pred. No. 1.9e-05;
_	MATCHES 31; CONSELVALIVE 20; MISSHACCHES 31; LINGELS 12; CAPU
_	Qy 20 FVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLPSSEFQISVVDC 77
-	٠
	Db 14 FIGHYYQLFDNDRTQLGAIYIDASCLTWEGOQFQGKAAIVEKLSSLFFQKIQHSLTAUDH /3.
	AQASPSNTVWK
	,
	Db 74 QPTPDSCIISMVVGQLKADEDFINGFHQMFDLNNINDAWVCINDMFK 120

c.species: Arabidopsis thaliana (mouse-ear cress) c.bate: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001 - Arabidopsis thaliana nuclear probable

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

4; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo (er, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. a; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719; PMID:11130712

A;Cross-references: GB:AE005172; NID:g11024877; PIDN:AAG26961.1; GSPDB:GN00141

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A, Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo Ref. M.; Ru, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                   Alathors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
                                                                                                                                                                                                                                                                  R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alc
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 409, 816-820, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: EMBL:Z68197; PIDN:CAA92380.1; GSPDB:GN00066; SPDB:SPAC15F9.03c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, C.M. nitted to the EMBL Data Library, August 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable nuclear transport factor 2 - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GB:AE005172; NID:96554189; PIDN:AAF16635.1; GSPDB:GN00141
                                                                                                                                                                                 C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Schizosaccharomyces pombe
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 ASAFVNHYYHLEDNDRSSLSSLYNPTSLLTFEGQTIYGVDNISNKLKQLPFDQCHHLIST 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
Library, December 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 AEEFVNVYYTTMDKRRKLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLPSSEFQ--ISV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDCQPVHDEATPSQTTVLVVICGSVKFEG-NKQRDFNQNFIL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 VDSQP--SSMAGGCGGILVFVSGSIQLHGEDHPLRFSQTFHL 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 116.5; DB 2;
Pred. No. 0.00057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 107; DB 2;
Pred. No. 0.00099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Introns: 3/1; 30/3; 54/3; 88/3
C; Superfamily: yeast nuclear transport factor NTF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (perimental source: strain 972h-; cosmid c1B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McDougall, R.C.; Rajandream, M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 33.3%;
Matches 34; Conservative 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.6%;
28.9%;
                      -- PDGNSYYVFNDIFR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: T38039; T37728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reference number: Z21764
Accession: T38039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reference number: 221740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene: SPDB:SPAC1B9.01c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-123 <MCD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: DNA
Residues: 1-522 <S'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: DNA
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                      107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: EMBL:U18778; NID:g603592; PIDN:AAB64542.1; PID:g603601; MIPS:YER0094; Haarer, B.K.; Petzold, A.S.; Brown, S.S.
Ubmitted to the EMBL Data Library, July 1993; Description: Identification of mutations that are synthetically lethal with altered ye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: EMBL:L22204; NID:g347714; PIDN:AAB49379.1; PID:g347715
Haarer, B.K.; Corbett, A.; Kweon, Y.; Petzold, A.S.; Silver, P.; Brown, S.S.
netics 144, 495-510, 1996
Title: SEC3 mutations are synthetically lethal with profillin mutations and cause defected mumber: S72237; MUID:9704444; PMID:8889515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9867, and lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pecies: Saccharomyces cerevisiae
ate: 28-Jan-1995 #sequence_revision 12-May-1995 #text_change 24-Sep-1999
ccession: S50467; S41793; S72237
                                                                                                                                                                                                                                                                                                                                                                   VDCQPVHDEATPSQTTVLVVICGSVKFEGNKQR-DFNQNFIL--TAQASPSNTVWKIASD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ross-references: EMBL:L22204; NID:g347714; PIDN:AAB49379.1; PID:g347715
                                                                                                                                                                                                                   17 AEBEVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLP--SSEFQISV 74
                                                                                                                                                                                                                                                       63 EMLPSSEFQ--ISVVDCQPVHDEATPSQTTVLVVICGS--VKFEGNKQRDFNQNFILTAQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 SLDFNT-----LAQNFTQFYYNQFDTDRSQLGNLYRNESMLTFETSQLQGAKDIVEKL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      itted to the EMBL Data Library, December 1994
scription: The sequence of S. cerevisiae cosmids 9537, 9581, 9495,
ference number: S50459
cession: S50467
                                                                                                                                                                            15;
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                                                                                                                          Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.9%; Score 116.5; DB 2; Length 125; Itarity 30.9%; Pred. No. 0.00011; Conservative 19; Mismatches 54; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lear transport factor NTF2 - yeast (Saccharomyces cerevisiae)
lternate names: protein YER009w
                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                               ; Score 117.5; DB 2; Pred. No. 8.5e-05; 22; Mismatches 49
C;Genetics:
A;Map position: 1
C;Superfamily: yeast nuclear transport factor NTF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Map position: 5R
C;Superfamily: yeast nuclear transport factor NTF2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross·references: SGD:S0000811; MIPS:YER009w
                                                                                                               16.1%;
30.1%;
                                                                                                         Ouery Match
Best Local Similarity 30.1
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASPSNTVWKIASDCFR 134
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Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lecule type: DNA
sidues: 1-125 <DIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: DNA
Residues: 1-84 <HAA>
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Gaps

48;

Length

Length 123;

4

Matches

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Species:

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Cross-references: EMBL:275546; PIDN:CAA99890.1; GSPDB:GN00019; CESP:R05D11.3
Experimental source: clone R05D11
A; Cross-references: GB: AE005172; NID: 99802547; PIDN: AAF99749.1; GSPDB: GN00141
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable RNA-binding protein - fission yeast (Schizosaccharomyces pombe)
C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 Q--ISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNT-VWK 127
                                                                                                                                                                                                                                                                                                                                                                                                75 VDCQPVHDEATPSQTTVLVVICGSVKFEGNKQR-DFNQNFILTAQASPSNTVWKIASDCF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                     67 VDCQP-----SGPAGGMLVFVSGNLQLAGEQHALKFSQMFHLISNQGN-----YYVFNDIF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEEFVNVYYTTMD ----KRRKLLSRLY-MGTATLVWNGNAVSGQESLSEFFEMLPSSEF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 AKAFIQHYYSKFDVGDGMSRAQGLSDLYDPENSYMTFEGQQAKGRDGILQKFTTLGFTKI 70
                                                                                                                                                                                                                                                                                                                        17 AEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLP--SSEFQISV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: T40805
R;Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z21949
                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 133;
                                                                                                                                                                         Length 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R05D11.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;;
                                                                                                                                                                      14.3%; Score 105; DB 2; ilarity 27.3%; Pred. No. 0.0016; Conservative 22; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.7%; Score 100.5; DB ilarity 26.8%; Pred. No. 0.005; Conservative 29; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary; translated from GB/EMBL/DDBJ
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 1
A;Introns: 33/1; 63/3; 96/3
C;Superfamily: yeast nuclear transport factor NTF2
                                                               A;Gene: F17L21.10
A;Map position: 1
C;Superfamily: yeast nuclear transport factor NTF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                libmitted to the EMBL Data Library, June 1996 Reference number: 219818
                                                                                                                                                                                             Local Similarity
les 33; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Residues: 1-133 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: CESP:R05D11.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :: | |
121 IGNEIFR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 IASDCFR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 R 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 R 118
                                                                                                                                                                                 Query Match
                                                                                                                                                                                                        Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-620, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: EMBL: 268879; PIDN: CAA93082.1; GSPDB: GN00022; CESP: K08F4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Arabidopsis thaliana (mouse-ear cress)
Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 QISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIAS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 KIQSIKGYP----TPHKQGVIINVIGTVNL-----RPFLQSFLLGQGGKK---YYVES 202
                                                                                                                                                                                                              75 VDCQPVHDEATPSQTTVLVVICGSVKF-EGNKQRDFNQNFILTAQASPSNTVWKIASDCF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 AAEE----FVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLP-SSEF 70
                                                                                                               8 ATQFTQFYYQTFDSDRSQLSSLYREESMLSFEGAQLQGTKAIVEKLVSLPFQRVQHRIST 67
                 12; Gaps
                                                                    17 AEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGOESLSEFFEMLPSSEFO--ISV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               r, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 537
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                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48;
                 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
14.5%; Score 106; DB 2;
Best Local Similarity 23.6%; Pred. No. 0.007;
Matches 30; Conservative 31; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rotein F17L21.10 [imported] - Arabidopsis thaliana
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A;Introns: 66/3; 99/1; 140/3; 161/3; 338/1; 419/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, January 1996
A; Reference number: 219746
A; Accession: T23479
                 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Experimental source: clone KO8F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein K08F4.2
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Residues: 1-537 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA
Residues: 1-122 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: T23479
                 35;
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                                                                                                                                                                                                                                                                                     134 R 134
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203

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108 DFNQNFILTAQASPSNTVWKIASDCFRF 135
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                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: DNA
Residues: 1-316,'T' <CUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: S27440
Molecule type: DNA
Residues: 350-441 <CUW>
816-820, 2000
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Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-428 <S'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: DNA
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                                                                                                                                                                                                                                                                                                             A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                31;
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Best Local S
Matches 31
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunder, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A; Li, T.; Lin, X.; Liu, X.; Liu, Z.S.; Maiti, E.; Kim, C. C.A.; Li, T.; Lin, X.; Liu, Z.X.; Liu, Z.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: E96716
A;Accession: E96716
                A;Cross-references: EMBL:AL032684; PIDN:CAA21796.1; GSPDB:CN00067; SPDB:SPBP8B7.11
A;Experimental source; strain 972h-; clone pl p8B7
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R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H ansen, N.F.; Hughes, B.; Hulzar, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable RNA-binding protein F23010.17 [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) C.Species: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEFFEMLPSSEFQISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 VPSAQDIAAEFVRQYYHVLGQLPHEARRLYVDASVVSRPDVTGTMMSFTSVEAIN-KHIL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDQACRAAEEFVNVYYTTMDKRRLLSRLYM------GTATLVWNGNAVSGQESL 58
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                 20 FVNVYYTTMDKRRRLLSRLYMGTATLVW--NGNAVSGOESLSEFFEMLPSSEFQISVVDC 77
                                                                                                                                                                                                                                                                                                           22 FVQEYYTYLNKEPNRLHCFYTKKSTLIHGDEGESISLCHGQQEIHNKILDLDFQNCKVLI 81
                                                                                                                                                                                                                                                                                                                                                       78 QPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIASDCFRF 135
                                                                                                                                                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                        7;
                                                                                                                                                                            Length 434;
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Pred. No. 1.2;
                                                                                                                                                                        ; DB 0.17;
                                                                                                                                                                          ; Score 91.5; DI
; Pred. No. 0.17,
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27; Mismatches
                                                                                                                                                                            12.5%;
27.1%;
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25.2%;
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                                                                                                                                                                                               Best Local Similarity 27.1%
Matches 32, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA
Residues: 1-427 <STO>
A; Residues: 1-434 <BEC>
                                                                  C; Genetics:
A; Gene: SPDB:SPBP8B7.11
                                                                                                         A;Map position: 2
A;Introns: 38/3; 63/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary
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                                                                                                                                                                            Query Match
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F86270
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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo-ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MuID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: EMBL:271666; NID:g1302565; PID:e239594; PID:g1302566; MIPS:YNR051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE005172; NID:g8920577; PIDN:AAF81299.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: hypothetical protein N3465
C;Species: Saccharonyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
C;Accession: S63382; S27439; S27440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QPVHDEATPSQTTVLVVICG -- SVKFEGNKQRDFNQNFILTAQASPSNTVWKIASDCFRF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 QESLSEFFE----MLPSSEFQISVVDCQ---PVHDEATPSQTTVLVVICGSVKFEGNKQR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---KSILIMATGEMFWTGTPVY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 FVEKYYNLLYKSPSQVHQFYLDDSVLGRPGSDGEMVSVKSLKAINEQIMSFDYEISKIQI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 FVNVYYTTMDKRRRLLSRLYMGTATLVWNGN--AVSGQESLSEFFEMLPSSEFQISVVDC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 VQDICFA---FLQNYYERMRTDPSKLAYFYASTAELTHTNYQSKSTNEKDDVLPTVKVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
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    yeast (Saccharomyces cerevisiae)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID: 9172081
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A; Accession: S63382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52;
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                                                                                                                                                                                                                                                                                                                                                                                                                   5;
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                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 80:5; DB
Pred. No. 2.2;
86; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cusick, M.E. abmitted to the EMBL Data Library, March 1992 Reference number: $27437 Accession: $27439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:M88607; NID:g172079;
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                                                                                                                                                                                                                                                                                                                                                                                               11.0%; Scc.
25.8%; Pred
26;
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A; Kurzik-Dumke, U.; Lohmann, E.
submitted to the EMBL Data Library, February 1994
A; Description: Sequence of a new Drosophila small heat shock gene embryonal lethal (2), Reference number: S42032
                                                                                                                                                                                                                                                                                                                                       06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- ASRDQQGCSRASGSPSAVQEDGRGQRELDRRVSEVLEQLPQQT 317
                                                                                                                                                                                                                                                                          embryonal lethal (2)13-1 (el(2)13-1) - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 EATPSQTTV----LVVICGSVKFE-----GNKQRDFNQNFILTAQASPSNTVWKIASD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 KRRRLLSRLYMGTATLV-----WNGNAVSGQESLSEFFEMLPSSEFQISVVDCQPVHD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 KRDDLMSSVWNSRPTVLRSGYLRPWHTNSLQKQESGSTL--NIDSEKFEV-ILDVQ---- 86
                                                         70 F-----QISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILT 116
                                                                                                               318 FPGDRGTMYSMIQCKP-SDSTSQEKCTVYSVVQPSRK-SGSKKR--NQNYSLS 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26; Mismatches
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -references: EMBL:X77635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: alpha-crystallin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
   261 KEPLTIYEYVKDSR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: March
Job time : 8.29798 secs
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-187 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene: FlyBase:1(2)ef]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                          Accession: S42032
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                                                                                                                                                                                                                                                                                                                                   Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; on, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Authors, 1996
Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.; Fraser, C.M.; Smith, H.O.; Woese, G.T. Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschil Reference number: A64300; MUID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mathew, P.A.; Garni-Wagner, B.A.; Land, K.; Takashima, A.; Stoneman, E.; Bennett, M.; Immunol. 151, 5328-5337, 1993
Title: Cloning and characterization of the 284 gene encoding a molecule associated wit Reference number: I49443; MUID:94044757; PMID:8228228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Map position: FOR1378485-1380434
Superfamily: Methanococcus endopeptidase La homolog; Methanococcus endopeptidase La Superfamily: Methanococcus endopeptidase La Homolog; serine proteinase Keywords: ATP; hydrolase; nucleotide binding; P-loop; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:U67582; GB:L77117; NID:g1592064; PIDN:AAB99427.1; PID:g1592066;
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.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                          .0-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 19-Jan-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- PVHDEATPSOT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MASVDFKT------YVDQACRAAEEFVNVYYTTMDKRRR--LLSRLYMGTATLVWN 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SEFFEMLPSSE 69
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                                                                                                                                                                              idopeptidase La homolog (EC 3.4.21.-) - Methanococcus jannaschii Alternate names: ATP-dependent proteinase lon homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6-89/Domain: Methanococcus endopeptidase La homol.
47-54/Region: nucleotide-binding motif A (P-loop)
238-243/Region: nucleotide-binding motif B
550/Active site: Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match
Local Similarity 25.0%; Pred. No. 5.8;
les 37; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 4.1;
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   115 KFCQTFILL--PSNGSTFDITNDIRF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 TVLVVICGSVKFEGNKQRDFNQNFILTA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 TLLLIMIGAILLSEYLLKYLPQNYLLAA 142
                                                                                                                                                                                                                                                 Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 GNAVSGQESLSEFFEMLPSSEFQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.6%;
30.1%;
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Best Local Similarity
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27; Gaps

Length 187; Indels

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

US-09-763-902B-2
732
1 MASVDFKTYVDQACRAAEEF.....PSNTVWKIASDCFREQDWAS 140 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	homo				7 caenc	homo sap	xenobns			sacc	ω.		_	schiz	Q13283 homo sapien		-	-	_			drosop)	6 gall		sacchai	-	•	trit			0782	ທ	P75990 escherichia	
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FINC_MOUSE FINC_RAT WGIE_HABEIN WUGIE_HABEIN WUGIE_ASEEL ERF1_SCHPO TYMO3_CABEL ILIR HUMAN DAPB_BRUME TICSG_TETPY CPS1_SORBI WYH3_HUMAN
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## ALIGNMENTS

LITI  WAYL HUMAN  NATILHUMAN  NATILHUMAN  NATILHUMAN  STANDARD; PRT; 140 AA.  16-OCT-2001 (Rel. 40, Created)  16-OCT-2001 (Rel. 40, Last annotation update)  16-OCT-2001 (Rel. 41, Last annotation update)  16-OCT-2002 (Rel. 41, Last annotation update)  NTF2-related export protein 1 (pl5 protein).  NATIL  NATIL  NATIL  NATIL  NATIL  NATIL  NOBLES (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enkamamalia; Eutheria; Primates; Catarrhini; Hominidae; BNCBLINCE-20036817; PubMed-10567585;  Black B.E., Levesque L., Holaska J.M., Wood T.C., Pass Black B.E., Levesque L., Holaska J.M., Wood T.C., Pass Black B.E., Levesque L., Holaska J.M., Wood T.C., Pass Black B.E., Stavildes G., Anhaneida J.P., Babbage A.K., Beare B.I.B. Stavildes G., Anhaneida J.P., Babbage A.K., Balack B.C., Carter C. Clamp M., Clark G., Clark L.N., Stavildes G., Anhaneida J.P., Babbage A.K., Balakey S.P., Butler A.P., Carder C., Barlow K.F., Bates K.N., Bearley O.P., Bird C.P., Butler A.P., Carder C., Carter Chapman J.C., Clamp M., Clark G., Clark L.N., Clark G., Burrill W.D., Butler A.P., Carder C., Burler A.P., Carder C., Burler A.P., Carder C., Burler A.P., Fraser A., French L., Elington A., Cobley V.E., Collier R.E., Connor R.E., Collier R.E., Connor R.E., Hunt A.R., Hunt A.K., Hoth P.D., Ho S., Holden J. Huckle E., Hunt A.K., Hunt A.K., Hoth P.D., Ho S., Holden J. Huckle E., Hunt A.K., Hunt A.K., Knights A., Erakard C.A., Skrand C.M., Sycamore N., Tromans A.C., Vaudin M., Wall M., Sycamore N., Taylor R., Penner D., Tracey P., Whittehead S.L., Whittaker P., Whittehead S.L., Whittaker P., Whitthehead S.L., Whitthehead S.L., Whitthehead S.L., Whitthehead S.L., Whitthehead S.L., Whitthehead	SEQUENCE FI	Strausberg R.;	StrausDerg R.; c.bmittod (EBB-2001) to	Submittod.	Surguend A.,	Strausberg R.;	Strangherd R.	'AIDPERING'	RC TISSUE-Lung, Placenta, and Uterus;	Troche Ting		RP SEQUENCE FROM N.A.						דוור חוווי מלוניו	"The DNA sequence	I ode	NO SET S	Roders		Wilming	501 101 00	wurrened	whiteher	T T T T T	Tracev A	N atomost C a decided a second	Swann R.M., Sycamore N., Taylor K., Itee L., Inclinas D.M.,	A TOUR N TOURS N TOURS	Skuce C.D., Smitch M.D., Souchtain C., Schart	Skince C.D. Smith M.L., Soderlund C., Steward C.A., Suist	CT CONTROL OF THE PARTY OF THE	Kice C.M., Ross M.I., Scott C.E., Seinta	Ding of M Boss M T Scott C E. Sehra H.K.,	PALLILIMOIG B.O.C.T., FIGURALINGUM COMMING	Phillimore B.J.C.T., Prathalingam S.R., Plumb K.W.,	111111111111111111111111111111111111111	OTIVEL N., Parker N., Facer N., Feares 1111111	Oliver K Darker A Patel R. Pearce T.A.V.,	MALLING CONTRACT TO THE PROPERTY OF THE PROPER	Milne S.A., Mistry D., Moore M.J.F., Mullinin J.C.,	Milno C D Mistry	Control of the contro	Marsh V.L., Martin S.L., McConnachite L.J., McLay M.	T. Manager of I. Manager to I. Manager to I. T. T. Manager to I. T. Manag	TOTAL	Tehvaslatho M.H., Leversha M.A., Lloyd C., Lloyd D.M.,		Kay M.P., Almoetter A.M., Almy A., Mitgines		MICHAEL DISCOURT OF THE PROPERTY OF THE PROPER		Tohnson	namination of the parties of the par	usemond a Harley I I. Heath P.D. Ho	(0) 6 6 14444	Grainam D.V., Gillithis C., Gillithis in	Constrain D to Contestable Contestable M.N.D.	ETITING CON U.G. 1 TRUNKERING CO	Filington A G . Frankland J.A., Fraser A., French	COCOLD & P. STATE OF THE STATE	Courson A., Covitte 4.0., Deadman N., Diramt 1.5.	Company Contille C. T. Deadman R. Dhami P.D.	C C C C C C C C C C C C C C C C C C C	Cledd S., Cobley V.E., Collict N.E., Common N.E.,	Collier R.E., Collier R.E., Connor R.E.,	Citabilitation of Committee of the Commi	Charman I.C., Clamb M., Clark G., Clark L.N., Clark S.I.,		BUCK D., BUILILL W.D., BUCKET A.F., Cuider C., Curter	40.00	beastey O.F., bita C.E., beand o.E.	Doselow	Dairey O., Darron	Ha Lec	٠									**************************************												_							ומפדמתו היים וומפדמתו	ובחתושובם וותרדבתי לייתו	regulaces increar process	redulates nuclear procesu																																				
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                                                                                                                                                                                                                                                                                                                                                                         A Read J. Shinagawa A. Shibata K. Yoshino M., Itoh M., Ishii Y., A Rakawa T., Shinagawa A., Shibata K. Yoshino M., Itoh M., Ishii Y., A Atawa T., Hara A., Fukunishi Y., Kiyosawa H., Radchi J., Eukua S., Asato K., Yoshino H., Kasukawa T., Saito R., Saito T., Cokazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Redota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ashburner M., Batalov S., Casavant T., Ashburner M., Batalov S., Cochwa H., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Rakai K., Tomita M., Wagner L., Washio T., Rashio T., Pomita M., Wagner L., Washio T., Rashio T., Pomita M., Garboldi M.F., Ashai K., Selelli D., Bolunga N., Carninci.P., de Bonaldo M.F., A Brownstein M.J., Bult C., Fletcher C., Fujita M., Garboldi M., Rakaining L., Machionni L., Mashima J., Marzarelli J., Mombaerts P., R. Nordone P., Ring B., Kingwald M., Rodriguez I., Sakamcko N., Sacaki H., Toyo-oka K., Wang K. H., Weitz C., Whittaker C., Wilming L., Burschianly N., Rakashia J., Kawaji H., Kohtsuki S., Kan Warshaw Boris A., Yashida K., Hasegawa Y., Kawaji H., Rohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- FUNCTION: Stimulator of protein export for NES-containing
-1- FUNCTION: Stimulator of protein export for NES-containing
-1- FUNCTION: Also plays a role in the nuclear export of UI snRNA,
-1- SUBUNIT: Preferentially binds Ran-GTP. Associates with NXF1, NXF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FFEMLPSSEFOISVVDCOPVHDEATPSOTTVLVVICGSVKFEGNKQRDFNQNFILTAQAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear. Shuttles between the nucleus and
                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MASVDEKTIYDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20036817; PubMed-10567585; Black B.E., Levesque L., Holaska J.M., Wood T.C., Paschal B.M.; "Identification of an NTF2-related factor that binds Ran-GTP and Mol. Cell. Biol. 19:8616-8624(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Functional annotation of a full-length mouse CDNA collection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ransport; Protein transport; mRNA transport; Nuclear protein; OMAIN 16 135 NTF2.
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98.6%; Pred. No. 2.2e-68;
Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 100 K -> N (IN REF. 2), 140 AA; 15847 MW; 358EAFDC19FE4594 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6J; TISSUE=Embryo;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02136; NTF2; 1.
PROSITE; PS50177; NTF2_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF156958; AAD54943.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:1929619; NXL1.
rPro; IPR002075; NTF2.
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                 musculus (Mouse)
                                                                                                                                        SEQUENCE FROM N.A.
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Matches 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                         Guzik B.W., Levesque L., Prasad S., Bor Y.C., Black B.E.,
Paschal B.M., Rekosh D., Hammarskjold M.L.;
"NXTI (p15) is a crucial cellular cofactor in TAP-dependent export of
intron-containing RNA in mammalian cells.",
Mol. Cell. Biol. 21:2549-254(2001)
-1-FUNCTION: Stimulator of protein export for NES-containing
proteins. Also plays a role in the nuclear export of ul snRNA,
tRNA, and mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Preferentially binds Ran-GTP. Associates with NXF1, NXF2 NXF3 and NXF5.
                                                                      "RanGTP-binding protein NXT1 facilitates nuclear export of different classes of RNA in vitro."; "Appl. Cell. Biol. 20:4562-4571(2000).
                         Ossareh-Nazari B., Maison C., Black B.E., Levesque L., Paschal B.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear. Shuttles between the nucleus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FFEMLPSSEFQISVVDCOPVHDEATPSQTTVLVVICGSVKFEGNKORDFNONFILTAQAS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358FA86AC3944594 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 732; DB 1; 100.0%; Pred. No. 5.3e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ransport; Protein transport; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the cytoplasm.
SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
MEDLINE-20307861; PubMed-10848583;
                                                                                                                                                                                          MEDLINE-21160285; PubMed=11259602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF156957; AAD54942.1; -.
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SEQUENCE 140 AA; 15847 MW;
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16-OCT-2001 (Rel. 40, Last sequ
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 PSNTVWKIASDCFRFQDWAS 140
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BC003029; AAH03029.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:15913; NXT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NXT1_MOUSE
Q9QZV9; Q9D1P7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
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EMBL:

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Gaps

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NXT1\_MOUSE ID NXT1\_MC AC 0902V9; DT 16-OCT-DT 15-JUN-DE NTF2-FG GN NXT1

RESULT 2

8 ò 요 õ Length 140;

us-09-763-902b-2.rsp

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Query Match
Best Local
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                                                                                                        EMBL;
                                                                                                                    EMBL;
                                                                                                                                  EMBL;
                                                                                                                                                            EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).

TISSUE—Ovarian carcinoma;

ISOGAT, Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

ISOGAT T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Yamamnoto J., Wakamateu A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayanagi T.;
61 FFEMLPSSEFQISVVDCQPVHDDATPSQTTVLVVICGTVKFEGNKQRDFNQNFILTAQAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Also plays a role in mRNA nuclear export.
SUBUNIT: Associates with NXF1, NXF2, NXF3 and NXF5.
SUBCELLULAR LOCATION: Nuclear. Shuttles between the nucleus and
                                                                                                                                                                                                                          Eukaryota; Mekazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                     Herold A., Suyama M., Rodrigues J.P., Braun I.C., Kutay U., Carmo-Fonseca C., Bork P., Izaurralde E., "TAP (WRI) Belongs to a multigene family of putative RNA export factors with a conserved modular architecture."; Mol. Cell. Biol. 23:8996-9008(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NXT2_HUMAN STANDARD; PRT; 142 AA.
O9NDAS; 09H8U0; 09NRL7; 09Y3M5; 09N064;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
NTF2-related export protein 2 (p15-2 protein) (DC9) (BM025).
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
Anny Y., Cullen B.;
"p15-2, a homologous protein of p15, interacts with Tap.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
Li Y., Peng Y., Li N., Gu W., Han Z., Fu G., Chen Z.,
"Novel genes expressed in human dentitic cell.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao M., Song H., Li N., Peng Y., Han Z., Chen Z., "A novel gene expressed in human bone marrow."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                TISSUE=Test1s;
MEDLINE=20528640; PubMed=11073998;
                                     PSNTVWKIASDCFRFQDWAS 140
                                                                                                                                                                                                                saplens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISSUE-Bone marrow;
                         121
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FLIPERTLSWEIARGGDVG (IN ISOFORM B).
009B4E8929A6BA6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMLPSSEFQISVVDCOPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SVDFKTYVDQACRAAEEFVNVYYTTMDKRRLLSRLYMGTATLVWNGNAVSGQESLSEFF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTRAIN-Berkeley;
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Annanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapo
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroldea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Black B.E., Levesque L., Holaska J.M., Wood T.C., Paschal B.M.; "Identification of an NTF2-related factor that binds Ran-GTP and reculates nuclear protein export.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; Iravers: 1.

Pfam; PF02136; NTF2; 1.

PROSITE; PS01077; NTF2_DOMAIN; 1.

Transport; Protein transport; mRNA transport; Nuclear protein;

Alternative splicing: NTF2.

DOMAIN 17 136 NTF2.

MATSL -> VINHVPALCTAGRGPFFAARPAGF FILPERTLSWEIAFGGDVG (IN ISOFORM FLIPERTLSWEIAFGGDVG (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.8%; Score 584; DB 1; Length 142; 75.4%; Pred. No. 1.2e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-CUN-2002 (Rel. 41, Last annotation update)
NTF2-related export protein (p15)
NXTI OR CG12752.
                                                                                                                                                      or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AK023289; BAB14511.1; ALT_INIT.
AF212223; AAR87325.1; ALT_INIT.
AL031387; CAB41301.1; -.
AL031387; CAB41302.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulates nuclear protein export.";
Mol. Cell. Biol. 19:8616-8624(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20036817; Pubmed-10567585;
                                                                                                                                                                                                                                                 EMBL; AJ277591; CAB96371.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF86878.1
                                                                                                                                                                                                                                                                                                                                            AAF78034.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR002075; NTF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 75.49
04; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                             AF201942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300320;
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Q9V3H8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 104;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.

(Rel. 40, Created) (Rel. 40, Last sequence update) (Rel. 41, Last annotation update)

NTF2-related export protein.

5-JUN-2002 6-0CT-2001 16-OCT-2001

Caenorhabditis elegans

CBI\_TaxID=6239

137 AA.

PRT;

STANDARD;

NXT1\_CAEEL Q9U757;

RESULT 5

Black B.E., Levesque L., Holaska J.M., Wood T.C., Paschal B.M.; "identification of an NFF2-related factor that binds Ran-GTP and property of the control of

SEQUENCE FROM N.A. MEDLINE-20036817; Pubmed-10567585;

regulates nuclear protein export."; Mol. Cell. Biol. 19:8616-8624(1999)

STRAIN-Bristol N2; SEQUENCE FROM N.A.

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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Encitier P., Bustler H., Cadleu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dunn D., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Doublin K.J., Evangelista C.C., Ferraz C., Ferraz C., Ferras S.M., Dunkov B.C., Dunn P., Bolthia N.J., Evangelista C.C., Ferraz C., Ferras G., Paritara S., Fleischmann W., Rolson C., Gabriellan A.B., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Garg N.S., Gelbart W.M., Glasser K., Houston K.A., Howland T.J., Weinmandez J.R., Harvey D., Heiman T.J., Weinmandez J.R., Rotins C.D., Karpen G.H., Re.Z., Kenison J.R., Ketchum K.A., Howland T.J., Weil M.H., Ibeywan C., Jalali M., Ralush F., Morfacton J., Wolbarty C., Morris J., Moshrefi A., Andlish N., Walson T.C., McDeargon D., Merkulov G., Milshima N.V., Mobarry C., Morris J., Moshrefi A., Murphy B., Murphy L., Musskern D.R., Pacleb J.M., Pallazolo M.N., Pitten G.S., Pan S., Pollard J., Puri V., Realen K., Nelson K., Sunger B., Spier E., Spradling A.C., Stapleton M., Strong R., Smith T., Shen H., Shue B.C., Siden-Kiamos I., Weinsten E., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinsten E., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinsten E., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinsten E., Shen G., Zhao Q., Zhao G., Zhu S., Zhu 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; ir.v.

)fan, PP0215; NTF2; 1.

PROSITE; PS0177; NTF2_DOMAIN; 1.

Pransport; Protein transport; mRNA transport; Nuclear protein.

Transport; Protein transport; mRNA transport; Nuclear protein.

Transport; Protein transport; mRNA transport; Nuclear protein.

Transport; Protein transport; mRNA transport; Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I- SUBCELLUIAR LOCATION: Nuclear (By similarity).
I- SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.1%; Score 308; DB 1; 41.4%; Pred. No. 4.7e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'lyBase; FBgn0028411; Nxt1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with NXF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 DIQSLDAQRLPEGVTGDMSGGMLLNVAGAVTVDGDSKRAFTQTLLLGVE----DGKYKVK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOACRAAEEFVNVYYTTMDKRRKLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLPSSEF 70
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--- FUNCTION: Stimulator of protein export for NES-containing proteins. Also plays a role in the nuclear export of. Ul snRNA, tRNA, and mRNA (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
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    I- SUBUNIT: Preferentially binds Ran-GTP (By similarity).
    I- SUBCELLULAR LOCATION: Nuclear (By similarity).
    I- SIMILARITY: CONTAINS 1 NTF2 DOMAIN.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC024852; AAK66028.1; -. P13662; 10UN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF156960; AAD54945.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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P13662;
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47; Indels

27; Mismatches

55; Conservative

Best Local Similarity

Matches

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EMBL;
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EMBL;
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Matches
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MEDLINE-980$5028; PubMed-9368653;
Clarkson W.D., Corbett A.H., Paschal B.M., Kent H.M., McCoy A.J.,
Clarkson L., Silver P.A., Stewart M.;
"Nuclear protein import is decreased by engineered mutants of nuclear transport factor 2 (NTF2) that do not bind GDP-Ran.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stewart M., Kent H.M., McCoy A.J.; structural basis for molecular recognition between nuclear transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-Human;
MEDLINE-96300214; PubMed-8757804;
MEDLINCK T.L., Clarkson W.D., Kent H.M., Stewart M.;
"The 1.6-A resolution crystal structure of nuclear transport factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES—MOUSE; STAIN—C57BL/6J; TISSUE—Kidney;
Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima J.
Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
Shibata K., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata M., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paschal B.M., Gerace L.;
Indentification of NTF2, a cytosolic factor for nuclear import that
Interacts with nuclear pore complex protein p62.";
J. Cell Biol. 129:925-937(1995).
       Created)
Last sequence update)
Last annotation update)
tor 2 (NTF-2) (Placental protein 15) (PP15).
                                                                                                                                                                                      Rattus norvegicus (Rat).
Sukaryota; Metazos, Chordata; Cranlata; Vertebrata; Euteleostomi;
Mamalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_raxID=9606, 10090, 10116;
                                                                                                                                                                                                                                                                                                                                                                                         Grundmann U., Nerlich C., Rein T., Lottspeich F., Kuepper H.A.; "Isolation of cDNA coding for the placental protein 15 (PP15)."; Nucleic Acids Res. 16:4721-4721(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH RAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES Rat; TISSUE-Kidney;
Kent H.M., Clarkson W.D., Bullock T.L., Stewart M.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ibmitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muramatsu M., Hayashizaki Y.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS)
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MEDLINE-98202576; Pubmed-9533885;
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-88247772; Pubmed-3380696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95263674; Pubmed-7744965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Biol. 260:422-431(1996).
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01-JAN-1990 (Rel. 13, Creat 01-JAN-1990 (Rel. 13, Last 15-JUN-2002 (Rel. 41, Last Nuclear transport factor 2 NTF2 OR PP15.
                                                                                                                                                                 (Mouse), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A. PECIES-Human, and Mouse;
                                                                                                                                    Homo sapiens (Human),
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                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                 Mus musculus
       RARRER REPRESENTAR REPRESENTAR
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                                                                   J. Mol. Biol. 277:635-646(1998).
-1- FUNCTION: FACILITATES PROTEIN TRANSPORT INTO THE NUCLEUS.
INTERACTS WITH THE NUCLEDRORIN P62 AND WITH RAN. ACTS AT A
INTERATIVELY LATE STAGE OF NUCLEAR PROTEIN IMPORT, SUBSEQUENT TO THE
INITIAL DOCKING OF NUCLEAR IMPORT LIGAND AT THE NUCLEAR ENVELOPE.
COULD BE PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS THAT
ASSEMBLE AT THE PORE COMPLEX DURING NUCLEAR IMPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 FVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLPSSEFQISVV--DC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 QPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIASDCFR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 QPTPD-----SCIISMVVGQLKADEDPIMGFHQMFLL----KNINDAWVCTNDMFR 120
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
factor 2 (NTF2) and the GDP-bound form of the Ras-family GTPase Ran."; J. Mol. Biol. 277:635-646(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 AA; 14478 MW; 817752F20E262FD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 16.9%; Score 124; DB 1; Similarity 26.5%; Pred. No. 5.4e-06; 31; Conservative 20; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nuclear transport factor 2 (NIF-2) (P10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4IM; 60361.3

MGD; MGI:895065; Ntf2.

DitemPro; IPR002075; NTF2.

PFam; PF03136; NTF2; 1.

PROSITE; PS50177; NTF2_DOMAIN; 1.

Transport; Protein transport; 3D-structure.
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                                                                                                                                                                                                                                                       -i - SUBUNIT: HOMODIMER.
-i - SUBCELLULAR LOCATION: Cytoplasmic.
-i - SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
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BC002348; AAH02348.1;
AK002461; BAB22117.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10UN; 01-APR-97.
1ARO; 24-DEC-97.
1ASK; 28-JAN-98.
1A2K; 29-APR-98.
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NCBI_TaxID=8355;
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Pu R.T., Shelsta H
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SEQUENCE
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                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration veen the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
"Identification of a p10(NTF2) homologue in Xenopus.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: FACILITATES PROTEIN TRANSPORT INTO THE NUCLEUS.
INTERACTS WITH THE NUCLEOPORIN P62 AND WITH RAN. ACTS AT A
RELATIVELY LATE STAGE OF NUCLEAR PROTEIN IMPORT, SUBSEQUENT TO THE
INITIAL DOCKING OF NUCLEAR PROTEIN IMPORT, SUBSEQUENT TO THE
COULD BE PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS
ASSEMBLE AT THE PORE COMPLEX DURING NUCLEAR IMPORT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 FVNVYYTTMDKRRILSRLYMGTATLVWNGNAVSGQESLSEFFEMLPSSEFQISVV--DC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIASDCFR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATCC 26555;
Blanchin-Roland S., Cordero-Otero R., Gaillardin C., Herrero A.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 QPTPD-----SCIISMVVGQLKADDDPIMGFHQVFLL----KNIQDAWVCINDMFR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharon
Saccharomycetales; mitosporic Saccharomycetales; Candida
NCBI_TaxID=5476;
                                                                                                              SIMILARITY).
SUBCELLULAR LOCATION: CYtoplasmic (By similarity).
SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                  127 AA; 14477 MW; 97110D6828268259 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 1; L4
6.8e-06;
ches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last sequence update)
16-00T-2001 (Rel. 40, Last annotation update)
Nuclear transport factor 2 (NTF-2).
                                                                                                                                                                                                                                                                                                                                                                                                          124 AA
                                                                                                                                                                                                                                                                                                HSSP; P13662; 1A2K.
InterPro; IPR002075; NTF2.
PR051TE; P550177; NTF2_DOMAIN; 1.
Transport; Protein transport.
                                                                                                                                                                                                                                                                                                                                                                           NTF2
                                                                                                                                                                                                                                                                                      EMBL; AF023911; AAB81276.1;
                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 26.59 les 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida albicans (Yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dominguez A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTF2_CANAL
Q9P926;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
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   removed. Usage by and for commercial nt (See http://www.isb-sib.ch/announce/
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Anticline-Zillian A., Plane C.J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
White O., Alonso J., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
A. Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fulit C.Y.,
A. Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hulzar L.,
A. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
A. Langin-Hooper S., Lee A., Lee J.M., Len Z., Khaykin E.,
A. Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
A. Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
A. Millischer J., Miranda M., Nguyen M., Niguyen M., Niconey T., Rowley D.,
Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sakano H., Tallon L.J., Tambunga G., Torluml M.J., Town C.D.,
W. Utterback T., Wan Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
A. Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
T. "Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 408:816-820(2000).

-I- FUNCTION: FACILITATES PROTEIN TRANSPORT INTO THE NUCLEUS. COULD BE PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS THAT ASSEMBLE AT THE PORE COMPLEX DURING NUCLEAR IMPORT (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: CYTOPLESMIC (BY SIMILARITY).

-I- SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 EMLPSSE--FQISVVDCQPVHDEATPSQTTVLVVICGS--VKFEGNKQRDFNQNFILTAQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 ASLPFOKVAHRISTLDAQP-----ASANGDILVMVTGELLIDEEQNAQR-YSQVFHLI-- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SVDFNA-----VATEFCNFYYNQFDSDRSQLGNLYRNESMLTFETSQLQGARDIVEKL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 124;
                                                                                                                                                                                                                                                                                                                                                                   8 121 NTF2.
124 AA; 14193 MW; B799D1ABA828A049 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last sequence update)
Nuclear transport factor 2 (NTF-2).
NTF2 OR AT1027970 OR F13K9.26.
Arabidopsis thallana (Mouse-ear crees)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA
modified and this statement is not remo
entities requires a license agreement (
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-cv. Columbia;
MEDLINE-21016719; PubMed-11130712;
                                                                                                                                                                                                              InterPro; IPR002075; NTF2.
Pfam; PF02136; NTF2; 1.
PROSITE; PS50177; NTF2_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                     Transport; Protein transport.
                                                                                                                                             EMBL; AF145758; AAF66701.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 29.4%
hes 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 -- PDNGSYYVENDIFR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 ASPSNTVWKIASDCFR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                       P13662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTF2_ARATH
Q9C7F5;
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THE KARYOPHERIN ALPHA-BETA COMPLEX,
                                                                                                                                                                                                                                     HSSP; P13662; 10UN.
SGD; S0000811; NTF2.
InterPro; IPR002075; NTF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 -- PDGNSYYVFNDIFR 120
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 ASPSNTVWKIASDCFR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Human).
                                                                                                                                                                                                                        S41793; S41793
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G3BP2 OR KIAA0660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rissue-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo saptens
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
G3B2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
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            between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- FUNCTION: FACILITATES PROTEIN TRANSPORT INTO THE NUCLEUS.
INTERACTS WITH VARIOUS NUCLEOPORINS AND WITH RAN-GDP. COULD BE
PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS THAT ASSEMBLE
AT THE PORE COMPLEX DURING NUCLEAR IMPORT. IN VITRO, THE NTF2-RAN-
GDP ASSOCIATION, IN THE PRESENCE OF GTP, TRIGGERS DISSOCIATION OF
                                                                                                                                                                                                                                                                                                                                                                     75 VDCQPVHDEATPSQTTVLVVICGSVKFEGNKQR-DFNQNFIL--TAQASPSNTVWKIASD 131
                                                                                                                                                                                                                                                                                                                                                                                                     70 VDCQP----SGPASGMLVFVSGNLQLAGEEHALKFSQMFHLMPTPQGS-----FYVFND 119
                                                                                                                                                                                                                                                                                                             17 AEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLP--SSEFQISV 74
                                                                                                                                                                                                                                                                                                                                          10 SKAFVEHYYSTFDTNRVGLAGLYQEASMLTFEGQKIQGVQSIVAKLTSLPFQQCKHHIST 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288c./ AB972;
Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Avlies E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M. Chung E., Duncan M., Braman E., Hartzell G., Hunlcke-Smith S., Hyman R., Kayser A., Komp C., Lashkarl D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Offner P., Oh C., Taylor P., Wel Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nuclear transport factor 2 (NTF-2) (Nuclear transport factor P10).
NTF2 OR YER009W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nehrbass U., Blobel G.; "Role of the nuclear import.";
                                                                                                                                                                                                                                                     Length 126;
                                                           Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-84 FROM N.A. Haarer B.K., Petzold A.S., Brown S.S., Submitted (JUL-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                        263E06A7A8903E3B CRC64;
                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                16.1%; Score 117.5; DB 1
30.1%; Pred. No. 2.5e-05;
tive 22; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 AA.
                                                          modified and this statement is not removed.
                                                                                                                                                                                                          NTF2.
                                                                                                                                            Interpro; IPR002075; NTF2.
Pfam; PF02136; NTF2; 1.
PROSITE; PS50177; NTF2_DOMAIN; 1.
Pransport; Proffin Transport.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION.
MEDLINE-96178681; PubMed-8600522;
                                                                                                                  EMBL; AC069471; AAG51491.1; -. HSSP; P13662; 10UN.
                                                                                                                                                                                                                    126 AA; 14002 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 272:120-122(1996).
                                                                                                                                                                                                                                                              Local Similarity 30.19
                                                                                                                                                                                                                                                                                                                                                                                                                                   132 CFR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
NTF2_YEAST
ID NTF2_YEAST
                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                   Query Match
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ALLOWING NUCLEAR TRANSLOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 EMLPSSEFQ--ISVVDCQPVHDEATPSQTTVLVVICGS--VKFEGNKQRDFNQNFILTAQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kennedy D., Mattick J.S.;
"Characterisation and chromosomal location of G3BP-1 and G3BP-2a/b,
members of a novel SH3 domain-binding and RNA-binding protein family
implicated in signal transduction.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SLDFNT-----LAQNFTQFYYNQFDTDRSQLGNLYRNESMLTFETSQLQGAKDIVEKL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G3B2_HUMAN STANDARD, PRT; 482 AA. 699URB1, 699URB6, 075149, 060666, 030HRB1; 16-OCT-2001 (Rel. 40, Created) 116-OCT-2001 (Rel. 40, Last sequence update) 115-UBY-2002 (Rel. 41, Last annoctation update) Ras-GTPase-activating protein binding protein 2) (G3BP-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.9%; Score 116.5; DB 1; Length 125; 30.9%; Pred. No. 3.2e-05; 1.1ve 19; Mismatches 54; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      shikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5660D8C00E634714 CRC64;
                                OF KARYOPHERIN ALPHA AND THE NLS SUBSTRATE.
                                                                         -!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS A AND B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98403880; PubMed-9734811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02136; NTF2; 1.
PROSITE; PS50177; NTF2_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 AA; 14453 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'ransport; Protein transport.
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71 QISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIAS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50177; NTF2_DOMAIN; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEC.
Transport; RNA-binding; Alternative splicing.
                                                                                                                                                                                                                                        482 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS A AND B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nterPro, IPR002075; NTF2.
nterPro, IPR000504; RNA_rec_mot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF145285; AAD51933.1;
                                                                                                                                                                                                                                                                                                                                                         binding protein 2) (G3BP-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U65313; AAC53553.1;
                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGD; MGI:1346339; G3bp2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00076; rrm; 1
PF02136; NTF2;
                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P09651; 1HA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                   131 DCFRFQD 137
                                                                                                                                       DMFRYED 135
                                                                                                                                                                                                  RESULT 12
G3B2_MOUSE
ID G3B2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tam;
                                                                                                                                                                                                                                                                                                                                                                              G3BP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fam;
                                                                                                                                         129
                                                            g
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                                                                                                                             . Q
                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                 [6]
INTERACTION WITH IKAPPABALPHA.
INTERACTION WITH IKAPPABALPHA.
PRIGENT M., Barlat I., Langen H., Dargemont C.;
RispapaBalpha and IKappaBalpha /NF Kappa B complexes are retained in the cytoplasm through interaction with a novel partner, RasGAP
SH3-binding protein 2.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 275:36441-36449(2000).
-1- FUNCTION: PROBABLE SCAFFOLD PROTEIN THAT MAY BE INVOLVED IN MRNA
TRANSPORT (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFVNVYYTTMDKRRRLLSRLYMGTATLVWNG------NAVSGQESLSEFEMLPSSEF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBUNIT: BINDS TO THE N-TERMINAL DOMAIN OF IKAPPABALPHA.
-i- SUBCELLUIAR LOCATION: CYtOPlasmic.
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
-i- SIMILARITY: CONTAINS 1 RNA RECCGNITION MOTIF (RRW).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 115.5; DB 1; Length 482;
Pred. No. 0.00021;
8; Mismatches 58; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                             Kennedy D., Ru K., Mattick J.S.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> V (IN REF. 3).
-> I (IN REF. 3).
2545C6A3FlAAE218 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISSING (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA-BINDING (RRM).
GLU-RICH.
GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA-binding; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00030; RRM_RNP_1; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>^</u>
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¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROSITE; PS50177; NTF2_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000504; RNA_rec_mot
                      [3]
SEQUENCE FROM N.A. (ISOFORM B)
                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54111 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.8%; 29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF145284; AAD51932.1;
EMBL; ABO14560; BAA31635.1;
EMBL; AF051311; AAC15705.1;
EMBL; AF051535; AAC95292.1;
EMBL; BC011731; AAH11731.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterPro; IPR002075; NTF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38; Conservative
5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE, PS50102; RRM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fam; PF00076; rrm; 1. fam; PF02136; NTF2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P09651; 1HA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                              rissue-B-cell;
                                                          rISSUE-Brain;
                                                                                                                                                             ISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ransport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
SEQUENCE
    Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
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13 Matches

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**NIWO** MAIN DOMAIN

HSSP;

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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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74 HTKI---RHVDAHATLSD-GVVVQVMGLLSNSGQPERKFWQTFVLAPEGSVPNKFY-VHN 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of a mouse orthologue of the human ras-GAP-SH3-domain binding protein and structural confirmation that these proteins contain an RNA recognition motif."; Blomed. Pept. Proteins Nucleic Acids 2:93-99(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          implicated in signal transduction.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLE SCAFFOLD PROTEIN THAT MAY BE INVOLVED IN MRNA
TRANSFORT (POTENTIAL).
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kennedy D., Mattick J.S.; "Characterisation of G3BP-1 and G3BP-2a/b, members of a novel SH3 domain-binding and RNA-binding protein family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                               P97379; Q9R1B8;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ras-GTPase-activating protein binding protein 2 (GAP SH3-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM B).
BEDLINE-98236259; PubMed-9575347;
Kennedy D., Wood S.A., Ramsdale T., Tam P.P., Steiner K.A.,
Mattick J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: CONTAINS 1 NTF2 DOMAIN, -:- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLY-RICH.
MISSING (IN ISOFORM B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA-BINDING (RRM)
GLU-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
VARSPLIC
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VDCQPVHDEATPSQTTVLVVICGSVKFEGNKQ-RDFNQNFILTAQASPSNTVWKIASDCF 133

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134 R 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: FACILITATES PROTEIN TRANSPORT INTO THE NUCLEUS. COULD BE PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS THAT ASSEMBLE THE THE NORE COMPLEX DURING NUCLEAR IMPORT (BY SIMILARITY). SUBCELLULAR LOCATION: CYTOPLSSMIC (BY SIMILARITY). SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
RETGORR -> TLHRTASLKSHCWOFWQWYLTHRVCILVKF
FWLWNVTQPF (IN REF. 1).
FB8BC2086123A5CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              71 QISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIAS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 HTKI---RHVDAHATLSD-GVVVQVMGLLSNSGQPERKFWQTFVLAPEGSVPNKFY-VHN 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Gaps
                                                                                                                                                                                                                                                                                                                    14 EFVRQYYTLLNKAPEYLHRFYGRNSSYVHGGVDASGKPQEAVYGQNDIHHKVLSLNFSEC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLPSSE--FQISV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 AKAFVEHYYRTFDTNRPALVSLYQDGSMLTFEGQQFLGAAAIAGKLGSLPFAQCHHDINT 66
                                                                                                                                                                                                                                                                         19 EFVNVYYTTMDKRRRLLSRLYMGTATLVWNG------NAVSGQESLSEFFEMLPSSEF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Lillopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsuki R., Iwasaki T., Jiang C., Yamamoto N.;
"Molecular cloning of a cDNA encoding nuclear transport factor
                                                                                                                                 15.8%; Score 115.5; DB 1; Length 482; 29.9%; Pred. No. 0.00021; Live 18; Mismatches 58; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ransport; Brotein transport.
OMAIN 6 119 NTF2.
SEQUENCE 122 AA; 13354 MW; 84100EBB62AB1BD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.6%; Score 107; DB 1;
11arity 28.9%; Pred. No. 0.0003;
Conservative 21; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Nuclear transport factor 2 (NTF-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROSITE; PS50177; NTF2_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                    482 AA; 54088 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB011262; BAA81910.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002075; NTF2.
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-cv. Nipponbare;
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Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P13662; 1A2K
                                                                                                                                                          Local Similarity
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DMFRYED 135
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Q9XJ54;
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collins M., Connor B., Cronin B., Causter C. C., Collins M., Connor R., Cronin B., Davis P., Cluster C. C., Collins M., Connor R., Cronin B., Davis P., Hidalgo J., Hodgson G., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., A Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., A Nother K., O'Nell S., Pearson D., Quall M.A., Rabbinowitsch E., Asther S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor R.G., Tivey A., Walsh S.V., Marren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Rainer M., Medler H., Reinhardt R., Pohl T. M., Eger P., Zimmermann W., Wedler H., Reinhardt R., Purnelle B., Coffeau A., Cadleu E., Dreano S., Gloux S., Lelaure V., Mottier S., A Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rocchet M., Gallbert M., Manbutt R., Purnelle B., Deninguez A., Revuelta J.L., Moreno S., Amstrong J., Forsburg S.L., Allang Z., Allang S.L., Moreno S., Amstrong J., Persburg S.L., Allang S.L., Moreno S., Amstrong J., Persburg S.L., Allang S.L., Moreno S., Amstrong J., Persburg S.L.,
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-1-SUBGELLULAR LOCATION: Cytoplasmic (By similarity).
-1-SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no restrictions on ng as its content is in no
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Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
                                                                                                                                                                                                                                                                                                                     Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable nuclear transport factor 2 (NTF-2).
123 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wood V., Gwilliam R., Rajandream M.A.,
                                                                                                                                                                                                                 OR SPAC15F9.03C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21848401; PubMed-11859360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL109951; CAB53052.1;
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Pfam; PF02136; NTF2; 1.
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STANDARD;
                                                                                                                                                                                                              OR SPAC1B9.01C
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                                                   01-FEB-1996 (Rel.
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   NTF2_SCHPO
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ise by non-profit institutions as rows ... ise by non-profit institutions as rows ... Usage by and for commercat modified and this statement is not removed. Usage by and for commercational income agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                              TRANSPORT (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                          VDCQPVHDEATPSQTTVLVVICGSVKF.EGNKQRDFNQNFILTAQASPSNTVWKIASDCF 133
                                                                                                                                                                                                                                                                                                                 8 ATQFTQFYYQTFDSDRSQLSSLYREESMLSFECAQLQGTKAIVEKLVSLPFQRVQHRIST 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             itted (APR-2001) to the EMBL/GenBank/DDBJ databases.
FUNCTION: PROBABLE SCAFFOLD PROTEIN THAT MAY BE INVOLVED IN MRNA
                                                                                                                                                                                                                                                              17 AEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLPSSEFQ--ISV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ras-GTPase-activating protein binding protein 1 (GAP SH3-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ebussche L., Dugue A., Schweighoffer F., Tocque B.;
A Ras-GTPase-activating protein SH3-domain-binding protein.";
ol. Cell. Biol. 16:2561-2569(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I., Duchesne M., Faucher D.,
                                                        76 TT -> SL (IN REF. 1; CAA92380).
14078 MW; F587303CAA3270E6 CRC64;
                                                                                                                                            14.6%; Score 107; DB 1; Length 123; llarity 28.9%; Pred. No. 0.0003; Conservative 21; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - TISSUE SPECIFICITY: UBIQUITOUS.
- SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
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                                NTF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDLINE-96220439; PubMed-8649363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40, Created)
Transport; Protein transport.
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                                                                                      123 AA;
                                                                                                                                                                       Local Similarity
nes 35; Conserv
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                                                        CONFLICT
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71 QISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIAS 130
                                                                                                                                                                                                                                                                                                14 EFVRQYYTLLNQAPDMLHRFYGKNSSYVHGGLDSNGKPADAVYGOK---EIHRKVMSONF 70
                                                                                                                                                                                                                       19 EFVNVYYTTMDKRRRLLSRLYMGTATLVWNG------NAVSGQESLSEFFEMLPSSEF 70
                                                                                                                                                           ; Score 105.5; DB 1; Length 466; Pred. No. 0.0022; 21; Mismatches 57; Indels 13
                                                                                                                GLY-RICH.
: 0F9429D78E0C7F59 CRC64;
                                                                                 RNA-BINDING (RRM).
GLU-RICH.
            PROSITE; PS50177; NTF2_DOMAIN; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
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Job time : 4.35122 secs
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1 Similarity 28.3%;
36; Conservative 2
                                                           ransport; RNA-binding
                                                                                                                   430 4
466 AA;
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Q8tfr7 saccharomyc Q9tgr8 saccharomyc Q9tgr8 saccharomyc Q9utgr schizosacch Q9sas9 arabidopsis Q9vgr4 drosophila Q9vgr3 drosophila Q95sb9 drosophila Q95sb9 drosophila Q95sv8 drosophila

08TFB8 09UTG3 09SAA9

Q8vyj4 arabidopsis Q8tns3 methanosarc Q91v37 human calic Q918b6 norwalk-lik

Q91sg2 arabidopsi

044024 Q9LSG2 Q8VYJ4

Q8TNS3

Q9VGR3 Q95SH9

Q8v778 norwalk vir Q8tfx3 aspergillus O52507 serratia 11

Q91V37 Q918B6 Q8V778 Q8TFX3

Length 167; Indels

091mx6 arabidopsis 007763 mus musculu 09477 linum usita 091s0 mus musculu 095t2 gallus gall 099f50 arabidopsis 064784 anabaena sp 087t88 saccharomyc

09LDI9 09LMX6 007763 09ATY7 09JIE0 099TY2

arabidopsis arabidopsis

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PSSEFQISVVDCQPV--HDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSN 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-AX4;
Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
Lehmann R., Baumgart C., Parra G., April J.F., Gulgo R., Kumpf K.
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel
"Sequence and Analysis of Chromosome 2 of Dictyostellum.";
Soumbitteed (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: AC115607; AAL92371.1;
Hypothetical protein.
SEQUENCE 167 AA; 19039 MW; E16E4A5F4DA00BAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 19.0 kDa protein.
Dictyostellum discoldeum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.7%; Score 151.5; DB 5;
llarity 29.0%; Pred. No. 1e.08;
Conservative 22; Mismatches 64;
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-LFYLSYDCIR 164
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es 38; Conserv
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091715 drosophila
09h72 drosophila
09vft4 drosophila
09lpy0 arabidopsis
09fvr3 emricella
021351 caenorhabdi
091985 drosophila
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Q9fnd0 arabidopsis
Q9vrd6 drosophila
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Ogru32 oryza sativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8t2d5 dictyosteli
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                                                                                               March 4, 2003, 14:53:32 ; Search time 9.59142 Seconds
    (without alignments)
    3007.543 Million cell updates/sec
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                                                                                                                                                                            732
1 MASVDEKTYVDQACRAAEEF......PSNTVWKIASDCFREQDWAS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                             671580
             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                             Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09VFT4
09LPY0
096VN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9FZK4
Q9FND0
Q9VRD6
Q9FME2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8T2G7
Q9HDY6
Q8RU32
Q8T2D5
Q9P8H0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0917J5
09NH72
                                                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organelle:*
                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_archea:*
sp_bacteria:'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_rvirus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_rodent:*
                                                                                                                                                             US-09-763-902B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_organerasp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fund1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3p_mhc: *
                                                                                                                                                                                                                        BLOSUM62
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Match
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125.5
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116.5
112.5
112.5
106.5
105.9
105.8
88.5
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                                                                                                                                                                               Perfect score:
                                                                          OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
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                                                                                                     Run on:
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ALIGNMENTS

9 X GH 60

ACCOCCOS DET SERVICE S

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Q--ISVVDCQPVHDEATPS-QTTVLVVICGSVKFEGNK-QRDFNQNFILTAQASPSNTVW 126
                                                                                                                                                                                                                                                                                                                                                             Putative nuclear transport factor similar to nuclear transport factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIVELPFQQTNRKINSIDCQQTY----QPGIMITVTGTLIIDGEAK---NQLKFVQVF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FFEMLP--SSEFQISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQ-NFILTA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MASVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                     83 RHAVCTVDCQP-----TPSFPGGILVFVSGNLQLAGEEHQLRFSQMFQLVPNEQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kump Tunggal B., Cox E., Quail M.A. Platzer M., Rosenthal A., Noe "Sequence and Analysis of Chromosome 2 of Dictyostellum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
Cordero Otero R.R., Lepingle A., Gaillardin C.;
"RPH1 gene from Yarrowia lipolytica.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence and Analysis of Chromosome 2 of Dictyostellum
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
EMBL, AC115613, AAM10776.1, -
SEQUENCE 127 AA, 14317 WW, 2D45B1B20021B298 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Rojas Quijano R., Lepingle A., Gaillardin C.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF260231; AAF70316.1; -.
                                                                                                                                                                                                                                                                                                                                                                                  2 (NTF2) from.
Dictyostellum discoideum (Slime mold).
Eukaryostellum discoideum (Slime mold).
NCBI_TaxID-44689;
                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 128.5; DB 5;
Pred. No. 2.5e-06;
9; Mismatches 56;
                                                                                                                                                                                                                                                    Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 AA
                                                                                                                                                                                                                                                    127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (arrowia lipolytica (Candida lipolytica).
                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.6%; Sco
25.5%; Pre
tive 29;
                                                                                                                                                                                                                                                                                            (TrEMBLrel. 21, (TrEMBLrel. 21, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 OASPSNTVWKIASDCFR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 NLASNNGSFLLINDFFR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                      127 KIASDCFR 134
                                                                                                                             135 FVQNDIFR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4952;
                                                                                                                                                                                                                                                                                            01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-AX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9P8H0
                                                                                                                                                                                                                                                Q8T2D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
  71
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Q9P8H0
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STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEFQISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVW 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 VDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEM---LP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DQACRAAEBEVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLPSSEF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                               STRAIN-972H.;
O'Neil S., Harris D., Wood V., Rajandream M.A., Barrell
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AL512562; CAC21476.1;
InterPro; IRR002075; NTF2.
Pfam; PF02136; NTF2;
SEQUENCE 200 AA; 23029 MW; B05E47D62B27B7FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone:P0415A04.";

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AP003345; BAB90110.1;

SEOURNCE 146 AA; 15796 MW; 496BE9A02E1E9670 CRC64;
                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                      16, Last sequence update)
21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
18.4%; Score 135; DB 10;
Best Local Similarity 32.8%; Pred. No. 5.7e-07;
Matches 42; Conservative 19; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.4e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                     200 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Mismatches
                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.4%; Score 142; 25.6%; Pred. No. 1
                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                 Created
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                  Putative nuclear export factor. SPAPBIA10.03.
                                                                          01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 25.6
Matches 31; Conservative
                                     PRELIMINARY;
                                                                                                 01-MAR-2001 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                       NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-JUN-2002
1-JUN-2002
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RESULT 3

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Query Match

P0415A04.24

Best Loca Matches

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Gaps

17;

Length 127; Indels

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SEQUENCE
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Matches
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Q9NH72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 EMLPSSE--FQISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                            3 SVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFF 62
                                                                                                                                                                                                                                                          2 SVDFNTLAKQFC----EF---YYQTFDTDRSQLGNLYRDHSMLTFTGTQHQGAQAIVEKL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        radling A.C., Stapleton M., Strong R., Sun E.,
Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Massarman D.A., Weinstock G.M., Weissenbach J.,
, Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
                                                                                                                                                                                                                                                                                                                                    Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta
HSSP; P13662; 10UN.
InterPro; IPR002075; NTF2.
Pfam: PF02136; NTF2; 1
SEQUENCE 123 AA; 13696 WW; 3E6CB9SCF0058251 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                             17.1%; Score 125.5; DB 3; 29.9%; Pred. No. 5e-06; ive 20; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saunders R.D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Palazzolo M., Pittman G.S
Reinert K., Remington K.,
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           | : : : | ||
107 PDGSSYYVFNDIFR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                   PSNTVWKIASDCFR 134
                                                                                                                Query Match
Best Local Similarity
Matches 40; Conserv
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0917J5;
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091735.
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Zheng L.,
Smith H.O.,
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIASDCFRF 135
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Pazman C., Mayes C.A., Fanto M., Haynes S.R., Mlodzik M.;
Raspptin, the Drosophila homolog of the RasGAP SH3 binding protein,
factors in Ras and Rho mediated signaling.";
Development 127:1715-1725(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 EFVNVYYTTMDKRRRLLSRLYMGTÅTLV-WNGNAVSGQESLSEFFEMLPSSE--FQISVV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 EFVRQYYTLLNKAPNHLHRFYNHNSSYIHGESKLVVGQREIHNRIQQLNFNDCHAKISQV
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3., Zhao Q.,
S., Zhu X.,
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                                                                                                                                                                                                                                                   Pfam: PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
SEQUENCE 688 AA; 74713 MW; 9E329949E7248C19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
Ye J., Yeh R.-F., Zaverl J.S., Zhan M., Zhang G., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Glibbs R.A., Myers B.W., Rubin G.M., Venter J.C.; Sthe genome sequence of Drosophila melanogaster."; Science 287.2185-2195(2000).
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30.3%; Pred. No. 0.00023;
tive 19; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                    16.3%; Score 119; DB 5;
30.3%; Pred. No. 0.00023;
Live 19; Mismatches 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interPro; IPR002075; NTF2.
interPro; IPR000504; RNA_rec_mot.
                                                                                                                                                              InterPro; IPR002075; NTF2.
InterPro; IPR000504; NNA_rec_mot
Pfam; PF02136; NTF2; 1.
Pfam; PF00076; rrm; 1.
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                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 30.3%
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SMART; SM00360; RRM; 1
PROSITE; PS50102; RRM;
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PF00076; rrm; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ephydroidea; Dr. NCBI_TaxID=7227
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EMBL; AY058617; AAL13846.1;
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AMEDLE-ZU19000; PUDDEG-10/31132;
AMEDLE-ZU19000; PUDDEG-10/31132;
AMEDLE-ZU19000; PUDDEG-10/31132;
AMEDLE-ZU1900; PUDDEG-1 SE. Richards S., Abbunner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Apbayani A., An H. J., Andrews Frannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Baytakeroglu L., Beasley E.M.,
Beson K.Y., Benos P.V., Bareman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Borkova D., Botchan M.R., Buller H., Cadleu E., Center A., Chandra I.,
RA Burtla K.G., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Bortson K., Downes M., Doyan Roche S., Pleischmann W.,
RA Bortsolian A.E., Garry N.S., Gelbart W.M., Glasser K.,
A. Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kenlson J.A.,
Rimmel B.E., Kodira C. D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Jalali M., Malush F., Karpen G.H., Ke Z., Kenlson D.A.,
Muttel B.E., McIntosh T.C., McLeod M.P., McIharson D.,
Muttel B.E., McIntosh T.C., McLeod M.P., Morphy B.,
Murny W. M., Nelson M.A., Now M. Murphy B., Murphy L., Murshy B.,
Murny S., Manger J., Balled J., Wang X.,
Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Sanith T.,
Syliskas R., Tector C., Turner R., Venter E., Wang X.,
Wang Z.-Y., Wassarman D.A., Weilscock G.M., Websenbach J.,
Shubs R.A., Monger T., Wong M., Wang S., Zhu X., Zhon G., Zhan M.,
Shubs R.A., Monger T., Zhan M., Zhon G., Zhon G., Zhon G.,
Shong F.W., Werse E.W., Rhong F.W., Zhan G., Zhan G., Zhan M.,
79 DAQATLGNG-----VVVQVTGELSNDGQPMRRFTQTFVLAAQ-SPKK--YYVHNDIFRY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
CG9412 protein (LD31194P).
RIN OR CG9412.
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DCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIASDCFRF 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Sperimatophyta, Magnollophyta, eudicotyledons, core eudicots, Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                  12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               19 EFVROYYTLLNKAPNHLHRFYNHNSSYIHGESKLVVGQREIHNRIQQLNFNDCHAKISQV 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khar Kim C., Altafi H., Bei Q., Chin C., Chioù J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri Forlumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
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                                                                                                                                                                                                                                         Length 690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO, IPRO02075; NTF2.
Pfam; PF02136; NTF2; 1.
SEQUENCE 522 AA; 58484 MW; 74FBB3FDFEE5BBE6 CRC64;
                                                                                                                                                                            74943 MW; 40C5AC6F9F4EB353 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                               54;
                                                                                                                                                                                                                                   / Match 16.3%; Score 119; DB 5; Local Similarity 30.3%; Pred. No. 0.00023; Nes 37; Conservative 19; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
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IPR002075; NTF2. IPR000504; RNA_rec_mot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, 01-0UN-2002 (TrEMBLrel. 21, T2318.22.
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Matches 34; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                SMART; SM00360; RRM; 1, PROSITE; PS50102; RRM;
                                                      Pfam; PF02136; NTF2;
Pfam; PF00076; rrm;
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nterPro; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 QD 137
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                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                   Query Match
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DAFQYID 209
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30;
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                                                                                                                                                                                                                                                                                                                                    203
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       9VJ8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 VDCQPVHDEATPSQTTVLVVICGSVKFEGNKQ-RDFNQNFILTAQASPSNTVWKIASDCF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 AQQEVIFYYQTFDGNRAGLAPLYRDHSMLTFETSAIQGVAGIIEKLTSLPFQKVQHQVST 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 AEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLP--SSEFQISV 74
                                                                                                                                                                                                              Eukaryota; Fung1; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NOBI_TaxID=5072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 112.5; DB 3; Length 125; Pred. No. 0.00014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53; Indels
                                                                                                                                                                                                                                                                                                                                                                     Espeso E.A., Penalva M.A.;
"Nuclear transport factor 2 from Aspergillus nidulans.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY038983; AAK71467.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hembry C.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 AA; 13871 MW; 8FC18BDFC597E2F2 CRC64;
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Last annotation update)
                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                            (Aspergillus nidulans)
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                                                        Created)
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MEDLINE-99069613; PubMed-9851916;
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                                                     (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.4%; 27.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                       Nuclear transport factor 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002075; NTF2.
Pfam; PF02136; NTF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33; Conservative
PRELIMINARY;
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Best Local Similarity
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Best Local Similarity
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                                                                               01-DEC-2001
01-MAR-2002
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Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
A manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A deorge R.A., Lewis S.E., Richards S., Abhurner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A Borkova D., Botchan M.R., Bouck J., Broxtein P., Brottler P.,
Burtis K.C., Busam D.A., Bulke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P.,
A Porler C., Gabriellan A.E., Garg N.S., Gelbert W., Classer K.,
                                                        71 QISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIAS 130
                                                                                                                                                                                                                                                                   156 KIQSIKGYP-----TPHKQGVIINVIGTVNL-----RPFLQSFLLGQQGQKK---YYVES 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   terygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
phydroidea; Drosophilidae; Drosophila.
16. AAEE----FVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLP-SSEF 70
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Zhan M., Zhang G., Zhao Q., Zheng
, Zhou X., Zhu S., Zhu X., Smith
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Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
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., Stapleton M., Strong R., S
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Last annotation update)
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1-MAY-2000 (TrEMBLrel. 13, 1-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                              --ISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 RVITTVDSQPTSDGG-----VLIIVLGRLKCDDDPPHAFSQIFLL----KPNGGSLFVA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic sequence for Arabidopsis thaliana BAC F17L21 from chromosome
                                                                                                                                                                                                                                                                                                          18 EEFVNVYYTTMD--KRRELLSRLYMGT-ATLVWNGNAVSGQESLSEFFEMLPSSEFQ--- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J. Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Ecker J.R.;
                                                                                                                                                                                                                21;
                                                                                                                                                  14.4%; Score 105.5; DB 5; Length 130; 28.0%; Pred. No. 0.00085; ive 19; Mismatches 50; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases
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                                                                                          39286FBC5BD7C34E CRC64;
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Last annotation update)
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   CG10174.
                                                                                          14582 MW;
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FlyBase; FBgn0032680; CG101
InterPro; IPR002075; NTF2.
Pfam; PF02136; NTF2; 1.
SEQUENCE 130 AA; 14582 N
                                                                                                                                                                                 Best Local Similarity 28.0 Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDCFR 134
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                                                                                                                                                     Query Match
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   SORDE
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VDCQPVHDEATPSQTTVLVVICGSVKFEGNKQR-DFNQNFILTAQASPSNTVWKIASDCF 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structural analysis of Arabidopsis thaliana chromosome 5. II. Sequence features of the regions of 1,044,062 bp covered by thirteen bhysically assigned Pl clones.";
DNA Res. 4:291-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.
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Goldsmith A.D., Lee J.M., Quach H.L., Toriuml M., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.
Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawi Kim C., Lin J., Liu S.Y., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                    Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M., Panalm C.J., Bowser L., Jones T., Banh J., Carninol P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J.; Theologis A., Davis R.W.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 AEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLP--SSEFQISV
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13527 MW; E7CDD9486631A1D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2001 (TrEMBLrel. 16, Created)
1-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 11, Last annotation update)
6b|AAD20086.1 (Hypothetical 50.1 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.3%; Score 105; DB 10;
ilarity 27.3%; Pred. No. 0.00089;
Conservative 22; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-COLUMBIA;
MEDLINE-98069011; Pubmed-9405937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AC004557; AAF99749.1; -. EMBL; AX042889; AAK68829.1; -. EMBL; AX072473; AAL66888.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02136; NTF2;
SEQUENCE 122 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
tes 33; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P13662; LOUN
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Search completed: March
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 ISVVDCQPVHDEATPSQTTVLVVICGSVKF-EGNKQRDFNQNFILTAQASPSNTVWKIAS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 -TAIEVKTI-NSVESWEGGVLVVVSGSVKTKEFSNRRSFVQTFFL----APQEKGYFVLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Miranda M., Narusaka M., Nguyen M.; Palm C.J., Sakurai T., Satou M.,
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 ACRAAEEFVNVYYTTMDKRRILLSRLYMGTATLV-WNGNAVSGQESLSEFFEMLPSSEFQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                              Theologis A.;
"Arabidopsis Full Length cDNA Clones.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases:
EMBL, AB006703; BAB309056.1;
EMBL, AY080755; AAL86001.1;
InterPro; IPR002075; NTF2.
                                                                                                                                                                                                                                                                                                                                                                                                                           DDACB46F7019F1FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CG1740 protein (GM08921p).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.5%; Score 91.5; DB 10; 26.0%; Pred. No. 0.14; 11ve 25; Mismatches 60;
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                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSS0102; RRM; 1.
Hypothetical protein.
SEQUENCE: 450 AA; 50122 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 26.0%
Matches 33; Conservative
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                                                                                                                                                                                                                                                                                Pfam; PF02136; NTF2; 1.
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09VRD6
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CO 09VRD6
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Lasko P., Lel Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Relazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang S., Yao Q.A.,
RA Syirskas R., Tector C., Turner R., Weissenbach J.,
RA Syirskas R., Tector C., Turner R., Wenter E., Wang S., Yao Q.A.,
RA Syirskas R., Tector C., Turner R., Weissenbach J.,
RA Syirskas R., Tector C., Turner R., Wenter E., Wang S., Yao Q.A.,
RA Syirskas R., Roodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA L., Kan, Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.",
Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 FVQQYYAIFDDPANRANVVNFYSATDSFMTFEGHQIQGAPKI---LEKVQSLSFQKITRV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 FVNVYYTTMD--KRRRLLSRLYMGT-ATLVWNGNAVSGQESLSEFFEMLPSSEFO---- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzallez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.1%; Score 88.5; DB 5; Length 130; 26.8%; Pred. No. 0.063; Live '18; Mismatches 51; Indels' 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases EMBL; AE003569; AAF50866.1; -. EMBL; AY094761; AAM11114.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D1EFF05367D6A565 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 AA; 14565 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0031145; Ntf-2.
InterPro; IPR002075; NTF2.
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Matches 33; Conserv
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COUNTRY: US
ZIP: 19426
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                                                                                                                                                                                                                                                                                                                                                           JS-08-836-791-9
                                                                                                                                                                                                                                                                                                                                             RESULT 1
                                                                                      March 4, 2003, 14:55:07; Search time 4.85349 Seconds (without alignments) 848.711 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                  1 MASVDFKTYVDQACRAAEEF........PSNTVWKIASDCFRFQDWAS 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                   rotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                 262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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732
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Sequence 10, Appl	Sequence 50, Appl	Sequence 120, App	Sequence 118, App	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 20, Appl	Sequence 20, Appl	Sequence 20, Appl	Sequence 10, Appl	Seguence 10, Appl	Sequence 1, Appli	Sequence 14, Appl	Sequence 3716, Ap	Sequence 12, App]	Sequence 2, Appl:	Sequence 2, Appl:
US-09-454-818-10	US-08-313-075A-50	US-08-961-083-120	US-08-961-083-118	US-08-095-737-4	US-08-480-145-4	US-08-477-389-4	US-08-449-645A-20	US-08-702-367A-20	PCT-US95-04681-20	US-08-570-311-10	US-08-353-485-10	US-08-943-600A-1	US-09-619-353-14	US-09-134-001C-3716	US-09-016-366A-12	US-08-655-352-2	US-09-258-016-2
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219	496	522	1040	897	897	897	866	866	866	1732	1732	310	863	1335.	2386	193	193
8.3	8.3	. 8	8.3	8.5	8.2	8.5	8.2	8	8	.8.2	8.2	8.1	8.1	8.1	8.1	8.1	8.1
61	60.5	60.5	60.5	09	09	9	09	9	09	9	9	59.5	59.5	59.5	59.5	65	59
28	29	30	100	32	ee.	34	35	9	37	38	36	40	41	. 42	43	44	45

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                                                                                                                                                                                                                                                       122 IDESEESAEESIAISIAQMEK--RLLHGLIHNVLPYVGTSVKTLVLAYSSAVSSKMVRQI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 EFVNVYYTTMDKRRRLLSRLYMGTATLVWNG------NAVSGQESLSEFFEMLPSSEF 70
                                                                                                                              14; Gaps
                                                                                                                                                                                     ---COPVHDEATPSQTTVLVVI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 VDQACRAAEEFVNVYYTIMDKRRRLLSRL----YMGTA--TLVWNGNAVSGQESLSEF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 519;
                                                                                          DB 2; Length 466; 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
9.4%; Score 68.5; DB 4; Length 5.
Best Local Similarity 19.7%; Pred. No. 5.9;
Matches 30; Conservative 27; Mismatches 48; Indels
                                                                                                                            57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Harper, Jeffrey W.
APPLICANT: Elledge, Stephen J.
TITLE OF INVENTION: F-BOX PROTEINS AND GENES
FILE REFERENCE: BCM-03510
CURRENT APPLICATION NUMBER: US/09/172,841
CURRENT FILING DATE: 1998-10-15
ERALIER APPLICATION NUMBER: 08/951,621
ERALIER FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 60
                                                                                      Match 12.3%; Score 90; DB Local Similarity 27.6%; Pred. No. 0.01 es 35; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGSVKFEGNKQRDFNQNFILTAQASPSNTVWK 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 55, Application US/09172841
Patent No. 6232081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pplication US/08570311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 FEMLPSSEF----QISVVD-----
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Lepine, Guylaine
Han, Naiming
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 55
LENGTH: 519
single
             TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-836-791-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-172-841-55
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Applicat
Patent No. 5824791
GENERAL INFORMATION:
STRANDEDNESS:
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129 D-IRYOD 134
                                                                                                                                                                                                                                                                                                        DCFRFQD 137
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ASVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTA-----TLVW---NG--NA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 VSGQESLSEFFEM-LPSSEFQISVVDCQPVHDEAT----PSQTTVL---VVICGS----V 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soluble Interleukin-1 Receptors
                                                                                                                                 SOFTWARE: Datentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/NR/FT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 KFEGNKQRDFNQNFILTAQASPSN----TVWKIASD 131
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3: Ted W. Whitlock
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.4%; Score 68.5;
27.6%; Pred. No. 61;
                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US '08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                        25-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/241,640 FILING DATE: 08-SEP-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    456 AGVSPKVCKDVTVEGSNEFAHVONLT --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/07821716
Patent No. 5319071
                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Whitlock, Ted W. REGISTRATION NUMBER: 36,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: UF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dower, Steven K
March, Carl J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                     ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-570-311-14
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Best Local Similarity
                                      Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES;
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                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5319071
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                     STATE: FI
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18 EEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLPSSEFQISVVDC 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 569;
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Connective Tissue of a Mammalian Host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.1%; Score 66.5; DB 2; 1
Best Local Similarity 22.5%; Pred. No. 12;
Matches 25; Conservative 20; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                 Patentin Release #1.0, Version #1.25
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STREET: 1700 Market Street Suite 3232
CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION, DATA:
APPLICATION NUMBER: US/08/027;750
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/924,376
                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,603
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glorioso, Joseph C.
Evans, Christopher H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08924376
Patent No. 6159464
                                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gould, Jr., Lewis F.
REGISTATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 1090
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                             (215) 575-600(
(215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                      : 569 amino acids
amino acid
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LENGTH: 569 amino acid
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                                                                                                                                                                                                                                                                                                                                       TELEX: 866172
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-381-603-2
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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APPLICANT:
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APPLICANT: Glorioso, Joseph C.
APPLICANT: Glorioso, Christopher H.
APPLICANT: Evans, Christopher H.
APPLICANT: K Robbins, Paul D.
TITLE OF INVENTION: Gene Transfer For Treating a Connective Tissue of a TITLE OF INVENTION: Mammalian Host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 EDIVEVINENVKKSRRLIIILVRETSGFSWLGG--SSEEQIA-MYNALVQDGIKVVLLEL 490
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CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/821,716
FILING DATE: 19920114
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1700 Market Street Suite 3232
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Best Local Similarity 22.5%; Pred. No. 12;
Matches 25; Conservative 20; Mismatches
                                                                                                                                                         COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                   US-08-381-603-2; Sequence 2, Application US/08381603; Patent No. 5858355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 691551
FILING DATE: 25-APR-1991
TYRNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                       CLASSLICATION: 530
RIOR APPLICATION DATA.
APPLICATION NUMBER: US 125627
FILING DATE. 25-NOV-1987
PRICH APPLICATION DATA.
RAPPLICATION NUMBER: US 160550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 258756
FILING DATE: 13-OCT-1988
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Wight, Christopher L. REGISTRATION NUMBER: 31,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 587-0606
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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AMINO ACID
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                                                                                                          OMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                            Washington
                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                     USA
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STREET: 1
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25;
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(215) 575-6000
(215) 575-6015
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                                        TELEX: 866172
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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RIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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MOLECULE TYPE: protein
US-08-924-376-2
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Best Local Similarity
Matches .25; Conserva
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US-08-685-212-2
  TELEPHONE:
                      TELEFAX:
                                                                                                  LENGTH:
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DB 4;

Score 66.5; Pred. No. 12;

9.18;

Query Match Best Local Similarity

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434 EDIVEVINENVKKSRRLIIILVRETSGFSWLGG--SSEEQIA-MYNALVQDGIKVVLLEL 490
18 EEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLPSSEFQISVVDC 77
                                                                                            78 OPVHD-EATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWK 127
                                                                                                                                           --GPQSAKTRFWK 532
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Debets, Johannes Eduard Maria
                                                                                                                                           491 EKIQDYEKMPESIKFIKOKHGAIRWSG----DFTQ
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING NAME OF THE OFFICE OFFI
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14-OCT-1998
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15-APR-1998
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10-AUG-1998
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Antonius
Sana, Theodore R.
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TTORNEY/AGENT INFORMATION:
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University of Pittsburgh of the Commonwealth System of Higer Educati
FNTION: Gene Transfer For Treating a Connective
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APPLICANT: University of Pittsburgh of the Commonwealth
APPLICANT: University of Pittsburgh of the Commonwealth
APPLICANT: System of Higher Education
TITLE OF INVENTION: Gene Transfer For Treating a Connective Tissue of a
TITLE OF INVENTION: Mammalian Host
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434 EDIVEVINENVKKSRRLIIILVRETSGFSWLGG--SSEEQIA-MYNALVQDGIKVVLLEL 490
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                                                                  TITLE OF INVENTION: Gene Transfer For Treating a Connective TITLE OF INVENTION: a Mammalian Host NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSE: Eckert Seamans Cherin & Mellott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       491 EKIQDYEKMPESIKFIKQKHGAIRWSG-----GPQ-----GPQSAKTRFWK 532
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UURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02414
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9.1%; Score 66.5; DB 5;
Best Local Similarity 22.5%; Pred. No. 12;
Matches 25; Conservative 20; Mismatches 53;
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1700 Market Street Suite 3232
                                                                                                                                                          SEE: Eckert Seamans Cherin & Mellott: 1700 Market Street Suite 3232 Philadelphia
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLOSPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Application PC/TUS9402414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Gould, Jr., Lewis F. REGISTRATION NUMBER: 25,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTORNEY/AGENT INFORMATION:
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(215) 575-6015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT: Kang, Richard
ITLE OF INVENTION: Gene Transfer For Treating a Connective Tissue of
ITLE OF INVENTION: Mammalian Host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 EDIVEVINENVKKSRRLIIILVRETSGFSWLGG--SSEEQIA-MYNALVQDGIKVVLLEL 490
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                                                                                                                        18 EEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLPSSEFQISVVDC 77
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                                                                         Indels 13;
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                                                                                                                                                                                                              78 QPVHD-EATPSOTTVLVVICGSVKFEGNKORDFNONFILTAQASPSNTVWK 127
                                                                                                                                                                                                                                              Length 569;
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Eckert Seamans Cherin & Mellott
1700 Market Street Suite 3232
                           9.1%; Score 66.5; Di
ilarity 22.5%; Pred. No. 12;
Conservative 20; Mismatches
                        Score 66.5;
Pred. No. 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  June 7, 1995
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08466932A
Patent No. 6413511
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glorioso, Joseph C.
Evans, Christopher H.
Robbins, Paul D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
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REGISTRATION NUMBER: 25,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (215) 575-60
(215) 575-6015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 22.5
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             URRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: 'protein
US-08-466-932A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                           Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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PCT-US94-02414-2
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single
                                          TYPE: amino acid
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                                                        STRANDEDNESS:
                                                                                               MOLECULE TYPE:
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LENGTH: 1871
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                                                                                                                   12-08-694-869-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434 EDIVEVINENVKKSRRLIIILVRETSGFSWLGG--SSEEQIA-MYNALVQDGIKVVLLEL 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEFVNVYYTTMDKRRKLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLPSSEFQISVVDC 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       491 EKIQDYEKMPESIKFIKOKHGAIRWSG----DFTQ-----GPQSAKTRFWK 532
                                                                                                                                                                                                                                                                                                                                                                            Length 569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schwegman, Lundberg, Woessner & Kluth,
                                                                                                                                                                                                                                                                                                                                                                     Cuery Match 9.1%; Score 66.5; Best Local Similarity 22.5%; Pred. No. 1; Matches 25; Conservative 20; Mismatch
APPLICATION NUMBER: PCT/US96/08899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08694869
Patent No. 5994123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
URRENT APPLICATION DATA:
                                                                                                   25,05
                                                                                                             REFERENCE/DOCKET NUMBER: 11
ELECOMMUNICATION INFORMATION
TELEPHONE: (215) 575-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 6
ELECOMMUNICATION INFORMATION
                                    CLASSIFICATION:
TTORNEY/AGENT INFORMATION:
NAME: Gould, Jr., Lewis F.
REGISTRATION NUMBER: 25,05
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amino acid
                                                                                                                                                                            (215) 575-6015
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REGISTRATION NUMBER: 3
                                                                                                                                                                                               TELEX: 866172
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 569 amino acid
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                                                                                                                                                                                                                                                                                                                   protein
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MEDIUM TYPE: Diskett
COMPUTER: IBM COMPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE:
PCT-US96-08899-2
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1181 IASIKANEYLOAEAEEILVATSEQEFINRSF - MSKNKRLLEEMKEQGYMGEDTLAHWNK 1238
                                                                                                                                                                                                                                                                                                 1239 NQIKCKIELRNPDLIIKDKPQTLLNIQKKEAMRKHIDALLERKVIRPSKSPHRTNAFIVE 1298
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                                                                                                                         1 MASVDFKTYVDQ-----ACRAAEEFVNVYYTTMDKRRRLLSRL----YMGTATLV-WNG 49
                                                                                                                                                                                                                                         ---TPSQTTVLVVI 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 NAVSGQESLSE---FFEMLPSSEFQISVVDCQPVHDEA-----TPSQTTVLVVI 95
                                                              Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 27;
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      Length 1871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLE OF INVENTION: Sugarcane bacilliform virus promoter 
ILE REFERENCE: 600.369US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- ACRAREEFVNVYYTTMDKRRLLSRL-
                                                                                                                                                                                                                                            50 NAVSGQESLSE---FFEMLPSSEFQISVVDCQPVHDEA-----
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      DB 2;
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Best Local Similarity 22.8%; Pred. No. 89;
Matches 28; Conservative 19; Mismatches
                                                              19; Mismatches
   Score 65.5; Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER FILING DATE: 1996-08-09
EARLIER APPLICATION NUMBER: PCT/IB97/01338
EARLIER FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/349,546
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SARLIER APPLICATION NUMBER: US 08/694,869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: sugarcane bacilliform virus .
US-09-349-546-1
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Patent No. 6429303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09349546 Patent No. 6093569.
Query Match 8.9%;
Best Local Similarity 22.8%;
Matches 28; Conservative 1
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Gaps
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Polynucleotides Encoding Members of the Human
Lymphocyte Activation Antigen B-7 Family and
Polypeptides Encoded Thereby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 NI---DAQP--KDKDPEQGHFLWIAAVLVMFVVFCGMVSFKTLRKRKKKQ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TTVLVVICGSVKFEGNKQRDFNQ 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 EEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          f: Guegler, Karl J.
f: Yue, Henry
INVENTION: HUMAN NUCLEIC ACID METHYLASES
                         FILE REFERENCE: 15966-562 (CURA-62);
FILE REFERENCE: 15966-562 (CURA-62);
CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
PRIOR APPLICATION NUMBER: 60/172909
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENTH: 329
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Herewith
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Corley, Neil C.
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NAME: CERRONE, MICHAEL C
REGISTRATION NUMBER: 39,
REFERENCE/DOCKET NUMBER:
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TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      URRENT APPLICATION DATA:
APPLICATION NUMBER: US,
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                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Fells catus
US-09-651-200-18
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Best Local Similarity
Matches 30; Conserv
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67 ASLDFKRYVTDR-RLAETLAQIYLGKPSRPPHLLLECNPGPGILTQALLEAGAKVVALES 125
                                                                                                                                                                                                                                                                                                                                                     126 DKTFIPHLESLGKNLDGKLRVIHCDFFKLDPRSGGVIKPPAMSSRGLFKNLGIEAVPWTA 185
                                                                                                                                                                                                                                                                                                              ----QPVHDEATPSQT 89
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                             2 ASVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMG----TATLVWNGNAVSGQES 57
                                                                                                                                                                                   20;
                                                                                                                                       Length 396;
                                                                                                                                                                                 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 90 TVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIASDCF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                           ----ALWKLAYDLY 212
                                                                                                                                                                                   17; Mismatches
                                                                                                                                                                                                                                                                                                              58 LSEFFEMLPS----SEFQISVVDC-
                                                                                                                                                                                     35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           186 DIPLKVVGMFPSRGEKR---
                                                        LIBRARY: THP1A2S08
SLONE: 2757184
                                                                                                                                            Query Match
Best Local Similarity
Matches 35; Conserva
STRANDEDNESS:
                                                                                 ; CLONE: ;
US-09-082-310-2
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Search completed: March Job time : 6.85349 secs

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                                                                                                      March 4, 2003, 14:58:57; search time 3.35122 Seconds (Without alignments) 1761.695 Million cell updates/sec
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Sequence 3, Ap
Sequence 2, Ap
Sequence 160,
Sequence 6, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13,
Sequence 14,
Sequence 12,
Sequence 15,
                                                                                                                                                                                                               732
1 MASYDFKTYYDQACRAAEEF......PSNTVWKIASDCFRFQDWAS 140
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Sequence 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ptodata/2/pubpaa/US10_NEW_PUB.pep:
ptodata/2/pubpaa/US10_PUBCOMB.pep:
ptodata/2/pubpaa/US60_NEW_PUB.pep:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters
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                                                                                                                                                                                                                                                                                                                           188354 seqs, 42170167 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein – protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications_AA
                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                               Title:
Perfect score:
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                                                                                                                  Run on:
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5977 5613 5893 131 120 120 12,	Sequence 4, Appli Sequence 5, Appli Sequence 1374, Ap Sequence 5, Appli Sequence 671, Ap Sequence 641, Appli Sequence 2, Appli Sequence 2, Appli Sequence 128, Ap Sequence 128, Appli Sequence 128, Appli
US-09-738-626-5977 US-10-116-048-4 US-09-738-626-6613 US-09-138-626-6613 US-09-815-242-15898 US-09-321-9878-2 US-09-800-729-155 US-09-765-272-120 US-09-765-272-120 US-09-78-813-2 US-09-78-813-2 US-09-78-626-5144	US-09-981-447-1 US-10-157-447-2 US-09-758-269-6 US-09-925-300-1374 US-09-829-318-5 US-09-828-302-641 US-09-881-853-2 US-09-881-853-2 US-09-928-307A-2 US-09-928-307A-2 US-09-928-307A-2 US-09-928-307A-2 US-09-928-307A-2 US-09-928-301-1238 US-09-928-301-1238 US-09-928-301-1238 US-09-25-301-1238
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257 2471 13441 13441 2150 2165 1040 1040 929	00000000000000000000000000000000000000
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## ALIGNMENTS

ö LOCATION: (10)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids 09-764-864-1181 of the naturally occurring L-amino acids OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids FFEMLPSSEFQISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQAS 120 1 MASVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSE 60 25 MASVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSE 84 ö Length 164; Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1181 LENGTH: 164 TYPE: PRI APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17 Indels Query Match 100.0%; Score 732; DB 10; Best Local Similarity 100.0%; Pred. No. 1.3e-76; Matches 140; Conservative 0; Mismatches 0; Sequence 1181, Application US/09764864 Patent No. US20020132753A1 LOCATION: (2) OTHER INFORMATION: Xaa equals any ORGANISM: Homo sapiens NAME/KEY: SITE NAME/KEY: SITE

Gaps

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PPLICANT: Chen, Wensheng
ITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                     82 TNCHTKIRHVDAHATLND-GVVVQVMGLLSNNNQALRRFMQTFVLAPEGSVANKFY-VHN 139
                                                                                                                                                                          71 QISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIAS 130
                                                                                                                          25 EFVRQYYTLINQAPDMLHRFYGKNSSYVHGGLDSNGKPADAVYGQK---EIHRKVMSQNF 81
                                                                                      --NAVSGQESLSEFFEMLPSSEF
                                        57; Indels
                   0.00051;
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                                      21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: Aeomica-X-1
UURRENT APPLICATION NUMBER: US/09/864,761
UURRENT FILING DATE: 2001-05-23
                     Pred. No.
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PLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LING DATE: 2001-01-30
PLICATION NUMBER: PCT/US01/00669
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LING DATE: 2001-01-30
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                                                                                 19 EFVNVYYTTMDKRRLLSRLYMGTATLVWNG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LING DATE: 2001-01-30
PLICATION NUMBER: PCT/US01/00667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICATION NUMBER: PCT/US01/00661
ILING DATE: 2001-01-30
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FILING DATE: 2000-02-04
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PPLICATION NUMBER: US 09/632,366
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PLICATION NUMBER: US 60/236,359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/234,687
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILING DATE: 2000-08-03
PPLICATION NUMBER: GB 24263.6
                   28.38;
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                                        Conservative
                Best Local Similarity
Matches 36; Conser
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|140 DIFRYQD 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-301-977
85 FFEMLPSSEFQISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQAS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPSSEFQISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 477;
                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFRENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEO ID NOS: 1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 977, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
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79.1%; Score 579; DB 10;
Best Local Similarity 75.7%; Pred. No. 4.9e-59;
Matches 103; Conservative 21; Mismatches 12;
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                                                                                                                                                                                                              Sequence 1180, Application US/09764864
Patent No. US20020132753A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID.NOS: 1694
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 977
                                                                                           145 PSNTVWKIASDCFRFQDWAS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1180
LENGTH: 162
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 VWKIASDCFRFQDWAS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 VWKIASDCFRFQDWSS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-09-764-864-1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                           GENERAL INFORMATION
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122 TYLSQEC-GGHPFVTQLYTHFHDQ----ARIYF-VIGLVENGDL---GESLCHFGSFDML 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 TSKFFASEILTGLQFLHDNKIVHRDMKPDNVLIQKDGHILITDFGSAQAFGGLQLSQEGF 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 TDANQASSRSSDSGSPPPTRFYSDEEEENTARRITFVGTALYVSPEMLADGDVGPQTDIW 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 TYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEF--FEML 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 PSSEFQISVV-----DCQPVHDEATPSQTT-----VLVVICGSVKFEGNKQ---
                                                       FITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR PITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Mismatches 59;
                                                                                                  FILE REFERENCE: 00786/351004
CURRENT APPLICATION NUMBER: US/09/205,658
CURRENT FILING DATE: 1998-12-03
EARLIER APPLICATION NUMBER: 08/857,076
EARLIER FILING DATE: 1997-05-15
EARLIER FILING DATE: 1997-07-07
EARLIER FILING DATE: 1997-07-07
EARLIER FILING DATE: 1998-05-15
EARLIER FILING DATE: 1998-05-15
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 328
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 67;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09840707A Patent No. US20020077276A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Caenorhabditis elegans US-09-205-658-159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.2%;
Best Local Similarity 22.6%;
Matches 43; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 KSLSEAFENLGKRSLEAGRCLPKSDSSSSLPKTNPTHSATRPOOTSDLHV------QGN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---CQPVHDEATPSQTTVLVVI 95
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                                                                                                                              EXPRESSED IN HEART, SIGNAL = 0.97
EXPRESSED IN BT414, SIGNAL = 1.3
EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
EXPRESSED IN ADULT LIVER, SIGNAL = 0.98
EST. HUMAN HIT: BEE69162.1, EVALUE 1.00e-109
SWISSPROT HIT: Q03414, EVALUE 3.30e+00
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                                                                                                                                                                                                                                                                                                                                Length 291
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                                                                                                                                                                                                                                                                                                                                                                                Indels
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URRENT FILING DATE: 2002-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.4%; Score 68.5; DB 12;
19.7%; Pred. No. 12;
tive 27; Mismatches, 48;
                                                                                                                                                                                                                                                                                                                                                                                25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: SITE
; LOCATION: all Xaa positions
; OTHER INFORMATION: Xaa-unknown amino acid residue
US-10-042-417-52
                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                              Score 69; DB 10
Pred. No. 4.1;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -TSHQSGFLKTSTSKITSTAWK 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-5
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PATENTIN VOT: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09205658
0010029617A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 52, Application US/10042417
Patent No. US20020123082A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 SSGIFRKS-----VSPSKTL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 KORDFNONFILTAQASPSNTV 125
                                                                                                                                                                                                                                                                                                                              7 Match 9.4%;
Local Similarity 29.6%;
nes 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 FEMLPSSEF----QISVVD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 19.7%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 159, App
Patent No. US2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -09-205-658-159
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LENGTH: 590
                                                                                                                                                                                                                                                                                                                              Query Match
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1,

Gaps

72;

Indels

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-- CASPSNTVW 126

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APPLICANT: Fredeking, Terry M.
APPLICANT: Fredeking, Terry M.
APPLICANT: Ignatyev, George M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
FILE REFERENCE: 24891-301C
CURRENT APPLICATION NUMBER: US/09/840,707A
PRIOR APPLICATION NUMBER: 09/562,979
PRIOR FILING DATE: 2000-04-27
PRIOR PELICATION NUMBER: 60/198,210
PRIOR APPLICATION NUMBER: 60/198,210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Interleukin-1 receptor, Type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 66.5;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DATABASE ACCESSION NUMBER: P14778/GenBank
DATABASE ENTRY DATE: 2001-08-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.1%;
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Best Local Similarity
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--- DCQPVHDEATPSQTT-----VLVVICGSVKFEGNKQRDFNQN 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173. TSKFFASEILTGLQFLHDNKIVHRDMKPDNVLIQKDGHILITDFGSAQAFGGLQLS-QEG 231
                            8 TYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEF--FEML 65
EEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLPSSEFQISVVDC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFFLICANT: Choi, InSoo
TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline
TITLE OF INVENTION: CTLA-4 Nucleic Acid and Polypeptides
FILE REFERENCE: 54954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 636;
                                                                                78 QPVHD-EATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWK 127
                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                   PDICANT: 099, SCOTT.
ITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR ITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS ILE REFERENCE: 00786/351004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.1%; Score 66.5; D
ilarity 28.1%; Pred. No. 23;
Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/303,510A
                                                                                                                                                                                                                                                                                                                                                                                                                         G DATE: 1998-12-03
CATION NUMBER: 08/857,076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LING DATE: 1997-05-15
PLICATION NUMBER: 08/888,534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-07-07
APPLICATION NUMBER: US98/10080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUMBER OF SEQ ID NOS: 1998-05-15
NUMBER OF SEQ ID NOS: 328
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 1999-04-30
EARLIER APPLICATION NUMBER: 60/083,869
EARLIER FILING DATE: 1998-05-01
                                                                                                                                                                                                                                   Sequence 160, Application US/09205658 Patent No. US20010029617A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09303510A Patent No. US20020028208A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Caenorhabditis elegans US-09-205-658-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Collisson, Ellen W. APPLICANT: Hash, Stephen M. APPLICANT: Choi, InSco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0028208A1
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Best Local Similarity
Matches 36; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 PSSEFQISVV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 FILTAQAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 FIDANQAS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Feline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                           Gaps
                                               18 EEFVNVYYTTMDKRRKLLSRLYMGTATLVWNGNAVSGOESLSEFFEMLPSSEFQISVVDC 77
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Glorioso, Joseph C.
Evans, Christopher H.
Robbins, Paul D.
TITLE OF INVENTION: Gene Transfer for Studying and Treating
a Connective Tissue of a Mammalian Host
          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 569;
                                                                                                                                                              78 QPVHD-EATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 018484-002280US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.1%; Score 66.5; DB 10;
22.5%; Pred. No. 20;
tive 20; Mismatches 53;
          53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICATION NUMBER: US 08/381,603
ILING DATE: 27-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ION NUMBER: US 07/963,928
ATE: 20-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILLING DATE: 08-MAR-1993
PPLICATION NUMBER: US 08/183,563
             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/731,175 FILING DATE: 05-Dec-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein SEQ ID NO: 2: 05-09-731-175-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATION NUMBER: 08/924,777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09731175 Patent No. US20020098168A1
          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF
             25;
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Best Local S:
Matches 25,
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               Matches
                                                                                                                                                                                                                                              RESULT 8
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20;

39; Indela

14; Mismatches

Score 65; Pred. No.

Length 612;

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55 QESLSEFFEMLP----SSEFQISVVDCQPVHDEA-----TPSQTTVL----VVICGS- 98
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                                                                     Query Match
Best Local Similarity 27.7%;
Matches 28; Conservative 1
, ORGANISM: Vigna unguiculata
US-09-758-269-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE
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Matches 35; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 ENSTTKYDTVMKKSQNNVTELYNVSISLPF---SVPEAHNVSVFCALKLETLEMLLSLPF 234
                                                                                                                                                                                     178 ENSTIKYDIVMKKSONNVIELYNVSISLPF---SVPEAHNVSVFCALKLETLEMLLSLPF 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----FEMLPSSEF 70
                                                                                              Indels 24; Gaps
                                                                                                                                               18 EEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEF-----FEMLPSSEF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 24;
                                                 Length 329;
                                                                                                                                                                                                                                                                      235 NI---DAQP--KDKDPEQGHFLWIAAVLVMFVVFCGMVSFKTLRKRKKKQ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---TTVLVVICGSVKFEGNKQRDFNQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---TTVLVVICGSVKFEGNKQRDFNQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLE OF INVENTION: Recombinant Virus Expressing Foreign DN TLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, TLE OF INVENTION: Feline Interferon-gama And Uses Thereof. LE REFERENCE: 54957-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITLE OF INVENTION: TRANSCENIC PLANTS CARRYING NEOXANTHIN ITLE OF INVENTION: CLEAVAGE ENZYME GENE ILE REFERENCE: 3914-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 EEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEF-
                                                                                                42;
                                                 Query Match

8.9%; Score 65; DB 10;
Best Local Similarity 27.3%; Pred. No. 14;
Matches 30; Conservative 14; Mismatches 42
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PRIOR APPLICATION NUMBER: 2001-01-12
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: JP 2000-010056
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 65;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRENT APPLICATION NUMBER: US/09/303,040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRENT FILING DATE: 1999-04-30
RLIER APPLICATION NUMBER: 60/083,870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: IUCHI, SATOSHI
APPLICANT: KOBAYASHI, MASATOMO
APPLICANT: SHINOZAKI, KAZUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARLIER FILING DATE: 1998-05-01
JMBER OF SEQ ID NOS: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.9%;
Best Local Similarity 27.3%;
Matches 30; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barbara J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 QISVVDCQPVHDEATPSQ---
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US-09-303-040-6
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       0S-09-303-210-6
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332 QKPYLKYFRFSPDGVKSPDVEIPLKEPTMMHDFAITENFVVVPDQQVVFKLTEMITGGSP 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Yue, Henry INVENTION: HUMAN NUCLEIC ACID METHYLASES
                                                     99 VKFEGNKQRDFNQNFILTAQASPSNTV-WKIASDCFRFQDW 138
                                                                                                       392 VVYDKNKTSRFG---ILHKNAKDANAMRWIDAPDCFCFHLW 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.7%; Score 64; DB 9;
ilarity 21.3%; Pred. No. 23;
Conservative 17; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0520 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/575,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/155,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/082,310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: CERRONE, MICHAEL C
                                                                                                                                                                                                                                                                                                                                APPLICANT: Hillman, Jennifer
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Publication No. US20020192787A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     Corley, Neil C. Guegler, Karl J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
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37 DKTFIPHLESLGKNLDGKLRVIHCDFFKLDPRSGGVIKPPAMSSRGLFKNLGIEAVPWTA 196
                                                                                                      126 DKTFIPHLESLGKNLDGKLRVIHCDFFKLDPRSGGVIKPPAMSSRGLFKNLGIEAVPWTA 185
                                                              ----OPVHDEATPSOT 89
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APPLICANT: TRIMNELL, MARY
TITLE OF INVENTION: NUCLECTIDE SEQUENCES MEDIATING MALE FERTILITY AND
TITLE OF INVENTION: METHOD OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50;
                                                                                                                                                                                                                                                                                                                                              GERERAL INFOGRATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62; Indels
                                                                                                                                              90 TVLVVICGSVKFEGNKORDFNONFILTAQASPSNTVWKIASDCF 133
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                                                                                                                                                                                        -- ALWKLAYDLY 212
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; Pred. No. 24;
17; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FILE REFERENCE: PHI 1147; CURRENT APPLICATION WHEHOD OF USING SAME; CURRENT APPLICATION NUMBER: US/10/058,566; CURRENT FILING DATE: 2002-01-28; NUMBER OF SEQ ID NOS: 8; SOFTWARE: PATENTIN VEF. 2.1; SEQ ID NO 8; LENGTH: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 LSEFFEMLPS----SEFQISVVDC------
                                                                                                                                                                                                                                                                                               Sequence 1057, Application US/09925301 Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/10058566 Publication No. US20020183274A1 GENERAL INFORMATION:
                                                              58 LSEFFEMLPS----SEFQISVVDC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 21.3%;
Matches 35; Conservative 1
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197 DIPLKVVGMFPSRGEKR---
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                                                                                                                                                                             : : | | | |:
186 DIPLKVVGMFPSRGEKR--
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US-09-925-301-1057
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; TYPE: PRT
; GrGANISM: Sorghum sp.
US-10-058-566-8

Query Match

Query Match

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Query Matches

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Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Pepride #11392 enc Protein #8807 enco

Human brain expres Peptide #7972 enco Peptide #11845 enc Human peptide enco Human sorting nexi

Human bone marrow

Human protein sequ Novel signal trans Novel human secret Human novel polype Human novel polype

polypeptide polypeptide colon cancer

Human Human Human

Drosophila melanog Human TRAF four as Lung cancer associ Amino acid sequenc Human ovarian anti

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Human Human

Human protein sequ SNEXN protein #2.

ORF2906 ORFX ORF2906 ORFX ORF3067

Drosophila Human MDDT

Guegler KJ;

2616 2611 2033

Score

Result ş 1554.5 1062 397.5 397.5

Perfect score:

Title:

Sequence:

OM protein

Run .on:

Minimum DB Maximum DB

Searched:

Database :

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Human; protein transport molecule; PTAM; diagnosis; cytostatic; antiarthritic; antiasthmatic; immunosuppressant; antiarteriosclerotic; antiallergic; antidiabetic; antilipaemic; antirheumatic; osteopathic; dermatological; antianaemic; antipsoriatic; hepatotropic; antigout;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiinflammatory; antiHIV; protein transport regulator; cancer; immune disorder; cell proliferative disorder; secretory disorder; utticaria; allargy; abnormal vesicle trafficking; asthma; autoimmune haemolytic anaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein transport molecule (PTAM) SEQ ID NO:3.
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AAM37808
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AA013502
AA013507
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Gorgone GA, Baughn MR, Patterson C;
                                                                                                                                                    AAM64876
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19-JUN-2000 (first entry)
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Drosophila melanog
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Arabidopsis thalia
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1559.740 Million cell updates/sec
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                                                                                                                                                                                                                             2620
1 MAMEREPPPLGDGKPTDFED......TQQQLIKYWEAFLPEAKAIA 519
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                                                                                                                                March 4, 2003, 14:50:41; Search time 44.3388 Seconds
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                 GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                              908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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AAB94707
AAW77095
AAW77094
ABB59331
AAG13370
AAG13369
                                                                                           protein search, using sw model
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length: 2000000000
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cytostatic, antiarthritic, antiasthmatic, immunosuppressant, antiarthritic, antiallergic, antidiabetic, antilipaemic? antiallergic, antidiabetic, antilipaemic? antitier antistement osteopathic, dermatological, antianemic, antipsoriatic, hepatotropic, antigout, antifilammatory and antimity activities, and regulate protein transport. PTAM proteins and antigonists are useful for perventing or treating a disorder associated with decreased or increased expression or activity of PTAM. PTAM polynucleotides are useful for diagnosing conditions associated with PTAM, comprising detecting PTAM by forming a hybridisation complex, preferably after PCR amplifying the biological sample. Diseases prevented, treated or diagnosed include cell proliferative disorders such as cancers, immune disorders, secretory disorders and other conditions associated with abnormal vesicle a targeting or delivery mechanism for bringing pharmaceutical agents into cells or tissues expressing PTAM and for diagnosis of PTAM-related disorders. PTAM, its catalytic or immunogenic fragments are useful for drug screening using libraries of compounds. PTAM polynucleotides are useful for generating hybridisation probes useful in mapping the trafficking, such as allergies, asthma, urticaria and autoimmune haemolytic anaemia. Anti-PTAM antibodies may be used as antagonists, as New human protein transport-associated polypeptide and polynucleotide useful for diagnosis, prevention and treatment of cell proliferative and secretory disorders such as leukemia, cystic fibrosis AAA08035 to AAA08042 encode the human protein transport-associated molecules (PTAMs) given in AAY82317 to AAY82324. The PTAMs have cytostatic, antiarthritic, antiasthmatic, immunosuppressant, naturally occurring genomic sequences Claim 1; Page 62-63; 75pp; English. WPI; 2000-256642/22. N-PSDB; AAA08037. 

519 AA; Sequence DB 21; Length 519; Indels 100.0%; Score 2620; DB 21; 100.0%; Pred. No. 4.7e-198; Mismatches ô Conservative Similarity Matches 519; Query Match Best Local S

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1 MAAEREPPPLGDGKPTDFEDLEDGEDLFTSTVSTLESSPSSPEPASLPAEDISANSNGPK 60

PTEVVLDDDREDLFAEATEEVSLDSPEREPILSSEPSPAVTPVTPTTLIAPRIESKSMSA 120 1 MAAEREPPPLGDGKPTDFEDLEDGEDLFTSTVSTLESSPSSPEPASLPAEDISANSNGPK 60 19 硆 õ

PVIFDRSREEIEEEANGDIFDIEIGVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSV 180 PVIFDRSREEIEEERANGDIFDIEIGVSDPEKVGDGMNAYMAYKVTTKTSLSMFSKSEFSV 121

KRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRRAALE

RYLQRTVKHPTLLQDPDLRQFLESSELPRAVNTQALSGAGILRMVNKAADAVNKMTIKMN 300 241 õ

SRALSQLAEVEEKIDQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDA 301 361

**ESDAWFEEKQOOFENLDOOLRKLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTAL** 

301

**QITLLKKREAEAKMMVANKPDKIQQAKNEIREWEAKVQQGERDFEQISKTIRKEVGRFEK** 421

361

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ERVKDFKTVIIKYLESLVQTQQQLIKYWEAFLPEAKAIA 519 

4.81

ERVKDFKTVIIKYLESLVQTQQQLIKYWEAFLPEAKAIA 519 481

RESULT 2 AAB95444

AAB95444 standard; Protein;

AAB95444;

(first entry) 26-JUN-2001

Human protein sequence SEQ ID NO:17891

Human; primer; detection; diagnosis; antisense-therapy; gene therapy.

Homo saptens

EP1074617-A2.

28-JUL-2000; 2000EP-0116126.

99JP-0300253. 2000JP-0118776. 2000JP-0183767. 27-AUG-1999; 11-JAN-2000; 02-MAY-2000;

2000JP-0241899 09-JUN-2000;

(HELI-) HELIX RES INST

Saito K, , Otsuki Nagai K, nıkawa T, Hayashi K, Wakamatsu A, Nagai K Nishikawa Sugiyama T, Ota T, Is Ishii S,

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length to EDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

8; SEQ ID 17891; 2537pp + CD ROM; English. Claim

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a complementary strand of a pering set least 15 nucleotides and the complation of the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length without any specialised methods. AAH03166 to AAH13628 and AAH18731 to AAH18742 represent human cDNA sequences. AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification 

Score 2620; DB 22; Pred. No. 4.7e-198; ; Mismatches 0; ö 100.0%; Conservative Similarity Best Local Sim: Matches 519; Query Match Best Local

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MAAEREPPPLGDGKPTDFEDLEDGEDLFTSTVSTLESSPSSPEPASLPAEDISANSNGPK 60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTEVVLDDDREDLFAEATEEVSLDSPEREPILSSEPSPAVTPVTPTTLIAPRIESKSMSA
                                                                                                                                                    PVIFDRSREEIEEEANGDIFDIEIGVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSV
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                MAAEREPPPLGDGKPTDFEDLEDGEDLFTSTVSTLESSPSSPEPASLPAEDISANSNGPK
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Otsuki T;
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Sugiyama T, Wakamatsı
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11-JAN-2000; 2000JP-0118776
02-MAY-2000; 2000JP-0183767
09-JUN-2000; 2000JP-0241899.
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The present invention describes primer sets for synthesising 5602
[11]-length cDNAs defined in the specification. Where a primer set
[12] comprises: (a) an oligo-dT primer and an oligonucleotide complementary
[12] comprises: (a) an oligo-dT primer and an oligonucleotide complementary
[13] complementary strand of a polynucleotide which comprises one of
[13] complementary strand of a polynucleotide with comprises one of
[13] complementary strand of a polynucleotide with comprises a 5'-end
[13] sequence and an oligonucleotide comprising a sequence complementary to the
[13] complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to a
[14] sequence and an oligonucleotide comprises a 1-end sequence complementary to a
[15] coligonucleotide which comprises a 1-end sequence complementary to a
[16] coligonucleotide which comprises a 1-end sequence where the
[17] coligonucleotide comprises a 1-end sequence, where the
[18] coligonucleotide comprises a 1-end sequence withose defined in
[18] coligonucleotide comprises a 1-end sequence is selected from those defined in
[18] coligonucleotide comprises a 1-end sequence is selected from those defined in
[18] consideration. The primers are useful for synthesising polynucleotides,
[18] consideration and/or diagnosis of the abnormality of the proteins encoded by
[18] coligonal colig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
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Pred. No. 9.7e-198;
1; Mismatches 0;
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99.8%;
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PVIFDRSREEIEEEANGDIFDIEIGVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length DDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs.
                                                                                                         detection; diagnosis; antisense therapy; gene therapy
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Pred. No. 2.4e-197;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashi K, Saito K, Ya
A, Nagai K, Otsuki T;
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                                                                      Human protein sequence SEQ ID NO:15700.
                                                                                                                                                                                                                                                                                                                                                                                                                                 sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
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                                                                                                                                                                                                                                                                                                       27-AUG-1999; 99JP-0300253
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                     2000EP-0116126
                                   (first entry)
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Best Local Similarity 99.6
Matches 517; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Isogai T,
                                                                                                         Human; primer;
                                                                                                                                                                                                                                                     28-JUL-2000;
                                                                                                                                             Homo sapiens
                                   26-JUN-2001
                                                                                                                                                                            EP1074617-A2
                                                                                                                                                                                                                                                                                      29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Ota T, IS
Ishii S,
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AAB94707
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PTEVVLDDDREDLFAEATEEVSLDSPEREPILSSEPSPAVTPVTPTTLIAPRIESKSMSA 120 

61 61

1 MAAEREPPPLGDGKPTDFEDLEDGEDLFTSTVSTLESSPSSPEPASLPAEDISANSNGPK 60 

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Sorting nexins (SNX) have the ability to bind an intracellular domain of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an activated cell surface receptor expressed on a cell and direct translocation of the receptor to a lysosome in the cell. The nucleic acids encoding SNX are useful for the down-regulation of cell surface receptors for degradation when they are no longer required to carry out signal. The nucleic acids can be used to express the protein in a cell
                                                                                  SRALSQLAEVEEKIDQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDA 420
                                                                                                                                                                                                                                                                                                                               QITLLKKREAEAKMVANKPDKIQQAKNEIREWEAKVQQGERDFEQISKTIRKEVGRFEK 480
                                                                                                                                                                                                                                                                                                                                                                                                               RYLQRTVKHPTLLQDPDLRQFLESSELPRAVNTQALSGAGILRWVNKAADAVNKMTIKMN 300
                                                                                                                                                                                                                          ESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTAL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding sorting nexin proteins - used for recombinant production and regulating expression of the protein, especially in treating unregulated cell growth e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nexin; intracellular domain; cell surface receptor; lysosome; down-regulation; cancer.
                                                             KRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRRAALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        where expression is desired e.g. where cancer is caused by up-regu
of receptors. Antisense constructs can be used to inhibit native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERVKDFKTVIIKYLESLVQTQQQLIKYWEAFLPEAKAIA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Column 29-34; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW77095 standard; Protein; 451 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      where expression is desired e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0625322.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-505652/43,
N-PSDB; AAV48249.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; sorting
translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                   TALSRALSQLAEVEEKIDQLRQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKW 349
                                                                                                                                                                                                                                                                                                                                                     477
                                                                                                                                                                                                                                                                                                                                                                  111 FSVK-RFTDFLGLHTTLDTTYLHVVIFVATSSRKSIVGMTKVKVGKEDSSSTEFVEKRRA 169
                                                                                                                                                                                                                                                                                                          TALSRALSQLAEVEEKIDQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKW 417
                                                                                                                                                  51.MSAPVIFDRSREEIEEEBANGDIFDIEIGVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSE 110
                                                                                                                                                                        FSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRRA 237
                                                                                   DDREDLFAEATEEVSLDS-----PEREPILSSEPSPAVTPVTPTTLI---APRIESKS 117
                                                                                                                             MSAPVIFDRSREEIEEEANGDIFDIEIGVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSE 177
                                                                Gaps
                                                                                                 nexin; intracellular domain; cell surface receptor;
                                                                                                                                                                                                                                                                                                                                                     EDAOITLLKKREAEAKMWVANKPDKIQOAKNEIREWEAKVQOGERDFEQISKTIRKEVGR
                                        Length.451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              not specified, encoded by TYT
                                                                                                                                                                                                                                                                                                                                                                                                 FEKERVKDFKTVIIKYLESLVQTQQQLIKYWEAFLPEAKAIA 519
                                                                                                                                                                                                                                                                                                                                                                                                            Score 2033; DB 19;
Pred. No. 7.7e-152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lysosome; down-regulation; cancer
                                                             7; Mismatches
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115
/note= "Xaa not spe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW77094 standard; Protein; 522 AA.
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                                         77.6%;
90.0%;
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protein
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                                                               Conservative
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                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sorting nexin 1.
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translocation;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1996;
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                                                    Best Local Sim
Matches 416;
 expression
                      Seguence
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                                                                                                                             118
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                                                                                                                                                                                                                                        170
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an activated cell surface receptor expressed on a cell and direct translocation of the receptor to a lysosome in the cell. The nucleic acids encoding SNX are useful for the down-regulation of cell surface receptors for degradation when they are no longer required to carry out signal. The nucleic acids can be used to express the protein in a cell where expression is desired e.g. where cancer is caused by up-regulation of receptors. Antisense constructs can be used to inhibit native expression of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTKTSLSMFSKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVÖMTKVKVGKE 224 [[::|||:||:||:||||||||||||||||| TTQTSLPLFRSKQFAVKRRFSDFLGLYEKLSEKHSQNGFIVPPPPEKSLIGMTKVKVGKE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acids encoding sorting nexin proteins - used for recombinant on and regulating expression of the protein, especially in unregulated cell growth e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GDGKPTDFEDLEDGEDLFTSTVSTLESSPSSPE--PASLP 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -TLIXLPPQEATNSSKP---QPTYEELEEEGEDQFDLTVGITDPEKIGDGMNAYVAYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSSSTEFVEKRRAALERYLQRTVKHPTLLQDPDLRQFLESSELPRAVNTQALSGAGILRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 4785.
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1554.5; DB 19
Pred. No. 5.2e-114;
8; Mismatches 99;
                                                                                      Column 23-28; 25pp; English
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59.6%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity.
                                                                                                                                                                                                                                                                                                                                                                         Sequence 522 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 319;
                                                  treating
                                                                                           Claim 3;
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Best Local
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368 ENRGRFELANRADKLDQAQQEVDEWQGKVQRCQQQFDDISAEIKREMERFELTRVKDFKV 427
                                     489 VIIKYLESLVQTQQQLIKYWEAFLPEAKAI' 518
                                                             428 NIKYIEDQMAHQQQIVSYWEAFAPFAREI 457
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                                                                                                                                                                     AAG13370 standard; Protein; 554
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                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                          AAG13370;
                                                                                                                                                     AAG13370
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTLLODPDLROFLES-SELPRAVNTQALSGAGILRMVNKAADAVNKMTIKMNESDAWFEE 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 ATEEVSLDSPEREPILSSEPSPAVTPVTPTTL - . IAPRIESKSMSAPVIFDRSREEIEEE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 ANGDIFDIEIGVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSVKRRFSDFLGLHSKL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 KITEVESLDANLQKLHNAMKSLVTSRRELSLLTGLVAKSAAMLSTCEEHTGLSRALSNLA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 DFEDLEDGEDLFTSTVSTLESSPSSPEPASLPAEDISANSNGPKPTEVVLDDDREDLFAE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EVESPEHTRDFAEVDINNGAATGSEDEEEEVPA------PGSVTLDRNESDLF-- 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to an isolated nucleic acid detection reagent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 4785; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.5%; Score 1062; DB 22;
43.9%; Pred. No. 3e-75;
tive 89; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                 Myers EW;
                                                                                                                                                                                                                                                                 L1 PWD,
                                                                                                                               23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                     23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 43.9%
Matches 224; Conservative
                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates
                                                                                                                                                                                                                                                                 Adams M,
                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75
                                                                                                                                                                                                                            (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                      N-PSDB; ABL03434.
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                                                     MO200171042-A2.
                                                                                                                                                                                                                                                                 Wenter JC,
                                                                                          27-SEP-2001
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
Arabidopsis thaliana protein fragment SEQ ID NO: 12840.
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9905-0139453.
9905-0139454.
9905-0139455.
9905-0139456.
9905-0139457.
9905-0139459.
9905-0139460.
9905-0139460.
                                                                                                99US-0139463.
99US-0139750.
99US-0139763.
99US-0139817.
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990S-0140353.
990S-0140354.
990S-0140695.
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90S-0145085
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9US-0142390
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99US-014514
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PR 11-AUG-1999 99UG-0148684.

PR 12-AUG-1999 99UG-014426.

PR 20-AUG-1999 99UG-014426.

PR 20-AUG-1999 99UG-014426.

PR 22-AUG-1999 99UG-0149922.

PR 23-AUG-1999 99UG-0149922.

PR 23-AUG-1999 99UG-0149922.

PR 22-AUG-1999 99UG-014992.

PR 27-AUG-1999 99UG-0150866.

PR 27-AUG-1999 99UG-0150866.

PR 27-AUG-1999 99UG-015086.

PR 27-AUG-1999 99UG-0151330.

PR 21-AUG-1999 99UG-0151330.

PR 22-SEP-1999 99UG-0151330.

PR 22-SEP-1999 99UG-0155139.

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PR 21-AUG-1999 99UG-015676.

PR 21-AUG-1999 99UG-01566.

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PR 21-AUG-1999 99UG-015676.

PR 21-AUG-1999 99UG-01566.

PR

Query Match
15.2%; Score 397.5; DB 21; Length 554;
Best Local Similarity 25.8%; Pred. No. 1e-22;
Matches. 149; Conservative 93; Mismatches 215; Indels 121; Gaps

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SLDSPEREPILSSEPSPAVTPVTPTTLIAPRIESKSMSAPVIF----DRSREEIEEEANG 137

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99US-0132486
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398 SRFTRE-LNSQTVKHLDTLHDYLGLAMAVQGAFADR-----SSALLTVQTLLSELSSL 449
                                                                                                                                                                                                                                                                                                            ---NKPDKIQQAKNEIREWEAKVQQGERDFEQISKTIRKEVGRF 478
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                                                                                                                                      278 ASSVEVVQPGRGGRDFLRMFKELRQSVSNDWGGSKPPVVEEDKEFLEKKEKMYDLEQQII 337
                                                                                                                                                                                                                   322 KLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTAL----SRA--LSQLAEVEEKI 374
                                                                                                                                                                                                                                          338 NASQQAESLVKAQQDMGETMGELGLAFIKLTKFENEEAVFNSQRARANDMKNLATSAVKA 397
                                                                                                                                                                                                                                                                 375 DQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITL-----LKKR 428
                                                                                                                                                                      -----GAGILRMVNKAADAVNK----MTIKMNESDAWFEEKQQQFENLDQQLR 321
                                                      107 OSSDSLSRSPSSLSSDYIKITVSNPOKEQEATNSMIPGGSTYITYQITTRINLSDYGGSE
                                                                                                                         ALERYLORTVKHPTLLQDPDLRQFLES-SELPRAVNTQALS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 12839
                                                                                                                                                                                                                                                                                                                                                           479 EKERVKDFKTVIIKYLESLVQTQQQLİKYWEAFLPEAK 516
                                                                                                                                                                                                                                                                                                                                                                         ::|| || :: : : | ::: | ::: | 510 DRERRADFLNMMKGFVANQVGYAEKIANVWTKVAEETR 547
AAG13369 standard; Protein; 571 AA
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99US-0123548.
99US-0125788.
99US-0126264.
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415 SRFYRE-LNSQTVKHLDTLHDYLGLMMAVQGAFADR-----SSALITVQTLLSELSSL 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 FSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRRA 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----IEIGVSDPEKVGDGMNA-----YMAYRVTTKTSLSMFSKSE 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 EDGEDLFTSTVSTLESSPSSPEPASLPAEDISANSNGPKPTEVVLDDDREDLFAEATEEV 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.2%; Score 397.5;
25.8%; Pred. No. 1.1e
ive 93; Mismatches
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AAG13368
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AC AAG13368;
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99US-0162142
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Best Local Similarity 25.89
Matches 149; Conservative
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99US-0147
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                    on; signal transduction pathway; metabolic pathway; genetic mapping; gene expression control; promoter;
Arabidopsis thallana protein fragment SEQ ID NO: 12838.
                                                                                                                            2000EP-0301439
                    Protein identification;
hybridisation assay; gentermination sequence.
                                                            Arabidopsis thalfana
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                         356 NASOQAESLVKAQQDMGETMGELGLAFIKLTKFENEEAVFNSQRARANDMKNLATSAVKA 415
                                                                                                                                                        375 DQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITL-----LKKR 428
                                                                                                                                                                                 416 SRFYRE-LNSQTVKHLDTLHDYLGLMMAVQGAFADR-----SALLTVQTLLSELSSL 467
                                                                                                                                                                                                                                     429 EAEA-KMMVA------NKPDKIQQAKNEIREWEAKVQQGERDFEQISKTIRKEVGRF 478
                                                                                                                                                                                                                                                              -GAGILRMVNKAADAVNK----MTIKMNESDAWFEEKQQQFENLDQQLR 321
                                                                           322 KLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTAL----SRA--LSQLAEVEEKI 374
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528 DRERRADFLNMMKGFVANQVGYAEKIANVWTKVAEETR 565
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Matches 146; Conservative 94; Mismatches 208;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                      ESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTAL 360
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                                                                                                                                                           VKVGKEDSSSTEFVEKRRAALERYLQRTVKHPTLLQDPDLRQFLE-SSELPRAVNTQALS 277
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                               SREEIEEEANG------GMNAY 159
---YIEPPSY-ADVIFSP 95
                                                                                                                                                                                                                                                                                                             FDENSDSEINGTEDNSLHSQFSDSLSRSPSSSSSDYIKITVSNPQKEQEISNSIVGGNTY
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 PADSDPLLAPSSYEDFRSSFSSKPI-SSDNS---
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nilarity 24.5%; Pred. No. 2.7e-20;
Conservative 94; Mismatches 217.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                         373 KIDQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEA 432
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                                                                                                                                                                                                                                                              Length 314;
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RR 16-JUL-1999; 9908-0144086.
RR 19-JUL-1999; 9908-014431.
RR 11-JUL-1999; 9908-014431.
RR 11-JUL-1999; 9908-014431.
RR 12-JUL-1999; 9908-014431.
RR 22-JUL-1999; 9908-014501.
RR 23-JUL-1999; 9908-014301.
RR 23-JUL-1999;
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262 LESSELP----RAVNTQAL-SGAGILRMV----NKAADAVNKMTIKMNESDAWFEEKQQQ 312
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Best Local Similarity 30.6%; Pred. No. 6.1e-19;
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Search completed: March 4, 2003, 14:58:35 Job time: 47.4817 secs

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OM protein - protein search, using sw model

Run on:

March 4, 2003, 14:53:52; Search time 23:3475 Seconds (without alignments) 2137.006 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-763-902B-3 2620 1 MAMEREPPPLGDGKPTDFED......TQQQLIKYWEAFLPEAKAIA 519

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	- 14	hypothetical prote			~		_	-	_	_	_	hypothetical prote	MVP1 protein - yea	centromere protein		le va	(1	pole b	F15K9.3	w	cal b	e golg	>	٠,	_	_	۳.	pothetical pro	related to MDM1 pr	
SUMMARIES	ΙD	G02522	T31063	T48483	T08691	S66952	T39046	S56808	T42515	S67656	T26610	T20971	T20978	S53033	S28261	688551	T50295	T39068	S26710	D86165	C96829	T22976	T40731	5130	1107	S51303	2113	381	T46337	497	
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<b>៷៷៷៷៷៷៷៷៷៷៷៷៷</b> <b>៙៙៸៸៸៸៸៸៷៰៷៰៷៰៷៰៷</b>	151.5	149.5	148 147.5 147.5	147.5 147 147	146.5 146.5 146
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## ALIGNMENTS

RESULT 1

	ASKYL  ASKYL  I :  SEKHS  DPDLR  DPDVR  III:  DOLHC
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RESULT 3  T48483  Hypothetical protein T28J14.60 - Arabidopsis thaliana C.Specias: Arabidopsis thaliana (mouse-ear cress) C.Specias: Arabidopsis thaliana (mouse-ear cress) C.Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C.Accession: T48483  R.Bevan, M.: Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Submitted.to the Protein Sequence Database, April 2000 A.Reference number: 224493 A.Reference number: 244483 A.Sccssion: T48483 A.Recielle type: DNA A.Residues: 1-554 ABEV> A.Residues: 1-554 ABEV> A.Residues: 1-554 CBEV> C.Genetics: Columbia; BAC clone T28J14	Map posi Introns: Note: T2 Ouery Ma Best Loc Matches 8	82 SLOSPEREPLISSESPAVTPVTPTLIAPRIESKSMSAPVIFDRSREEIEEEANG 137  [	238 ALERYLORTUKHPILLODPDLRQFLES-SELPRAVNTOALS	338 NASQUAESLYKAQQDMGETMGELGLAFIKLTKFENEEAVENSORARANDWKNLATSAVKA 397 375 DQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRWKCWQKWEDAQITLLKKR 428 :::  :  :  :    :    :      :	m m
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Oy 405 GVFDHRWKCWQKWEDAQITLLKKREAEAKMMVANKPDKIQQAKNEIREWEAKVQQGERDF 464	Kifulton, L.; Gattung, S.  Submitted to the EMBL Data Library, September 1999.  A; Description: The sequence of C. elegans. cosmid C05D9.  A; Reference number: 220960  A; Accession: T31063  A; Status: preliminary; translated from GB/EMBL/DDBJ  A; Molecule type: DNA  A; Molecule type: DNA  A; Residues: 1472 <ful> A; Cross references: EMBL: U64605; PIDN: AAB04589.1  A; Experimental source: strain Bristol N2 C; Genetics: A; Map position: X  A; Introns: 7002; 115/3: 169/3: 296/3: 455/3</ful>	hetical protein C05D9.1 5, DB 2; Length 472; 5,6e-37; ches 178; Indels 33; Gaps EVSLDSPEREPILSSEPSPAVTPVTPT 106  ::	OY 107 TLIAPRIESKSMSAPVIEDRSREEIEEEANGDIFDIEIGVSDPEKVGDG 155		OY 452 EWEAKVOQGERDFEDISKTIRKEVORFEKERVKDFKTVIIKYLESLVOTOQQLIKYWEAF 511  Db 404 DIVQKMDQLEQHFIELSKAIREEVARFDADRKQDMKKMLVEYMESMIHTHTELLHLWEKF 463  QY 512 LPEAKAI 518  L      Db 464 EPEANNI 470

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C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08691
R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
                                                       Gaps
                                                                                                                                                                                        SREPILSSEPSPAVTPVTPTTLIAPRIESKSMSAPVIF----DRSREEIEEEANG 137
                                                                                                                                                                                                                                 -----YADVIFSPFDDISEINGSEDGHS 106
                                                                                                                                                                                                                                                                                                                -----IEIGVSDPEKVGDGMNA-----YMAYRVTTKTSLSMFSKSE 177
                                                                                                                                                                                                                                                                                                                                                                               RESDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRRA 237
                                                                                                                                                                                                                                                                                                                                                                                                            RRLVAHPVIRNSDELKVFLQAQGKLPLATSTDVASRMLDGAVKLPKQLFGEGGG 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQPGRGGRDFLRMFKELRQSVSNDWGGSKPPVVEEDKEFLEKKEKMYDLEQQII 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITL-----LKKR 428
                                                                                             LFTSTVSTLESSPSSPEPASLPAEDISANSNGPKPTEVVLDDDREDLFAEATEEV 81
                                                                                                                                      TKSNVNG-DKSNSNYRSA-----MSTLFDSRHPSIVVTPADSDPLFAPPSYYS 60
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                                                    Indels 121;
Score 398.5; DB 2;
Pred. No. 1.2e-14;
2; Mismatches 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tein DKF2p564F052.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFKTVIIKYLESLVQTQQQLIKYWEAFLPEAK 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || :: :: :: |
DFLNMMKGFVANQVGYAEKIANVWTKVAEETR 547
                                                                                                                                                                                                                                      SKPNGGDRVSSYLEPPS----
                                                92;
  15.2%;
larity 26.0%;
Conservative 9
                          milarity
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324

381

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nypothetical phox domain containing protein – fission yeast (Schizosaccharomyces pomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-401 <GEN>
A;Cross-references: EMBL:298981; PIDN:CAB11735.1; GSPDB:GN00066; SPDB:SPAC6F6.12
A;Experimental source: strain 972h-; cosmid c6F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Schizosaccharomyces pombe
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 LQEILSR--MNEDCVVPPLPAKH-----KLEYIKGGRFSDNFINRAKLLNRYITRCALH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTLLQDPDLRQFLESSE-----LPRAVNTQALSGAGILRMVNKAADAVNKMTIKMN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 PVLHQSPHFIAFLENPNWNNYVRFFIQPKLNNTSKL------DEISDSLLNAFSKLK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTAL 360
                                                                                                                                                       61 LLGAEDAAEVLKNGGIDAESHKGFWSISFSSLPKYNEADEFFIEKKQKIDELEDNLKKLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 IEEEANGDIFDIEIGVSDPEKVGDG-MNAYMAYRVTTKTSLSMFSKSEFSVKRRFSDFLG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 LHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRRAALERYLQRTVKH 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 SRALSQLAEVEEKID-----QLHQEQAFADFYMFSELLSDYIRLIAAVKGV--FDHRMK 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               413 CWQKWEDAQITLLKKREAEAKMWVANKPDKIQQAKNEIREWEA-----KVQQGERDFE 465
                                                                                                                                                                                                                                                         382 AFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKRREAEAKMMVANKPD 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 SIQFDRLASLDQALDVPIESIQNALQQTGTEYANLTEKLT---LLLDTIKDVESYAHSLK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --DQKQQDVEALQEYSAKLSLERDKISSGGSNGF 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                     1 MESMLKKICQDPVLQKDKDFLLFLTSDDFSSESKKRAFLTGSGAINDSNDLSEVRISEIQ
                                                                                                                        284 -------MVNKAADAVNK---MTI-----KMNESDAWFEEKQQQFENLDQQLRKLH
                                                                                                                                                                                                                                                                                                                                                                       SLOETLIMGVMLDDYIRSLASVKAIFNQRSKLGYFLVVIENDMNKKHSQLGKLGQNIHSE
                                                                                                                                                                                                                            325 VSVEALVCHRKELSANTAAFA----KSAAMLGNSEDHTALSRALSQLAEVEEKIDQLHQEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: T39046
R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood,
submitted to the EMBL Data Library, September 1997
A;Reference number: 221797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 401;
                         LERYLORTVKHPTLLQDPDLRQFLESSELPRAVNTQA-LSGAGILR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 9.3%; Score 243.5; DB 2; Local Similarity 23.5%; Pred. No. 2.6e-06; les 97; Conservative 77; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 EEPTEFDIQRDHVQQFMFGISNLEGSIQKLLRLEKALES-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----ELLKRR
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298 KECIELWETF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502 QQLIKYWEAF 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: SPDB: SPAC6F6.12
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A; Introns: 44/3; 90/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: T39046
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Experimental source: strain S288C
                                                                                                                                                                                                                                                                             17;
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Bohn, C.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Dang, D.V.; Valens, M.
Dmitted to the Protein Sequence Database, July 1996
Reference number: S66929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Saccharomyces cerevisiae
Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 06-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --LHV-- 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 SASEEDLVDTLKDVASCIDRCCK-----ATEKRMSGLSEA--LLPVVH---- 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEAKMM----VANKP 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 -EYVLYSEML------MGVMKRRDQI-QAELDSKVEVLTYKKADTDLLPEEIGKLE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKIQQAKNEIR-EWEAKVQQGERDFEQISKTIRKEVGRFEKERVKDFKTVIIKYLESLVQ 499
                                                                                                                                                                                                                                                                                                                         53 SANSNGPKPTEVV-LDDDREDLFAEATEEVSLDSPEREPILSSEPSPAVTPVTPTTLIAP 111
                                                                                                                                                                                                                                                                                                                                                                                                                        112 RIESKSMSAPVIFDRSREEIEEEBANGDIFDIEIGVSDPEKVGDGMNAYMAYRVTTKTSLS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 VASSMRGVKNRPEEFMEMNNFIELFSQKINLIDKISQRIYKEEREYFDEMKEYGPIHILW 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SVEALVCHRKELSANTAAFAKSAAMLGNSEDHTALSRALSQLAEVEEKIDQLHQEQAF 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- RWKQNMQNDIKLAFTDMAEENIH 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                       ---PTSPLSMI-- 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 MFSKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEF
                                                                                                                                                                                                                                                                        Mismatches 171; Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .40;
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                                                                                                                                                                                                                          Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ypothetical protein YOR069w - yeast (Saccharomyces cerevisiae)
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                                                                                                                           Experimental source: fetal brain; clone DKF2p564F052
                                                                                                                                                                                                                                                                                                                                                                       3 SSGSSALLQAEVLDLDEDEDDLEVFSKDASLMDMNSFSPMM--
                                                                                                                                                                                                                       Score 309; DB 2;
Pred. No. 7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 VNKMT-----IKMNESDAWFEEKQQQFENLDQQLRK-
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Cross-references: SGD:S0005595; MIPS:YOR069w
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                                                                                                                                                                                                                                                                           85;
                                                                                                    A; Cross-references: EMBL: ALO49989
                                                                                                                                                                                                                       Query Match
Best Local Similarity 22.9%;
Matches 113; Conservative 8
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A; Reference number: 216470
A; Accession: T08691
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                                              A; Molecule type: mRNA
A; Residues: 1-420 <DUE>
                                                                                                                                                                            A; Note: DKFZp564F052.1
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C; Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000 C; Accession: T42518 Rs. Tato, K.; Nakai, K.; Okayama, H.; Nojima, H. DNA Res. 4, 363-369, 1997 A; Title: Identification of open reading frames in Schizosaccharomyces pombe	Reference number: Accession: T42515 Status: prelimina: Solecule type: mR Residues: 1-295    Cross references: Experimental sour	Query Match 8.2%; Score 215.5; DB 2; Length 295; Best Local Similarity 23.3%; Pred. No. 5.9e-05; Matches 80; Conservative 64; Mismatches 124; Indels 75; Gaps	QY 131 IEEEANGDIFDIEIGVSDPEKVGDG-MNAYNAYRTKTSLSMFSKSEFSVKRRFSDFLG 18: 1: 1   1   1   1   1   1   1   1   1	OY 190 LHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRAALERYLQRTVKH 249	QY 250 PTLLQDPDLRQFLESSELPRAVNTGALSGAGILRMVNKAADAVNKMTIKMN 300   1   1   1   1   1   1   1   1   1	Qy 301 ESDAWPEEKQQQFENLDQQLRKLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTAL 360	Qy 361 SRALSQLAEVEEKIDQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMK	413 CWQKWEDAQITLLKKREAEAKWWVANKPDKIQQAKNEIREWEA 455 272	6 17	67656 ypothetical protein YDL113c - yeast (Saccharomyces cerevisiae) Alternate names: hypothetical protein D2305 Species: Saccharomyces cerevisiae	=	•	Cross references: Experimental sourc; Genetics: Gene: MIPS:YDL113c	tion: 4L 7.69 SOUNTER TOOK TOOK TOOK TOOK TOOK TOOK TOOK TOO	Matches 129; Conservative 109; Mismatches 222; Indels 204; Gap	Qy 16 TDFEDLEDGEDLFTSTVSTLESSPSSPEPASLPAEDISANSNGPKPTEVVLDDDR 70 :	
Oy 466 QISKTIRKEVGRFEKERVKDFKTVIIKYLESLVOTOQQLIKYWEAFLPEAKAI 518 	RESULT 7 S56808 hypothetical protein YJL036w - yeast (Saccharomyces cerevisiae) NyAlternate names: hypothetical protein J1244 C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 19-Apr-2002	C; Accession: S56808; S52482 R;Pohl, T.M.; Aljinovic, G. submitted to the Protein Sequence Database, September 1995 A; Reference number: S56793	:g1009446;	R;Sora, S.; Tiboni, O.; Sanangelantoni, A. submitted to the EMBL Data Library, February 1995 A;Reference number: S52482 A;Accession: S52482	A;MOLGGUIE TYPE: DNA A;Residues: 1-291,'PDQIERPETDRL',305-403,'QSYRILRKDT' <sor> A;Cross-references: EMBL:248229; NID:9683697; PIDN:CAA88260.1; PID:9683698 C;Genetics:</sor>	A;Gene: SGD:SNX4 A;Cross-references: SGD:S0003573 A;Map position: 10L	Query Match 8.7%; Score 228; DB 2; Length 423; Best Local Similarity 23.1%; Pred. No. 2e-05; Matches 107; Conservative 76; Mismatches 154; Indels 126; Gaps 21;	OY 125 DRSREEIEBEANGDIFDIEIGVSDPEK-VGDGMNAYMAYRVTTKTSLSMF 173	Qy 174SKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGK 223 :	OY 224 EDSSTEFVERRRAALERYLQRTVKHPTLLQDPDLRQFLESSELPRAVNTQALSGAGI 281	Qy 282 LRMVNKAADAVNKMIIKMNESDAWFEEKQQFENLDQQLRKLHVSV 327	Qy 328EALVCHRKELSANTAAFAKSAAMLGNSEDHTALSRALSGLA 368   :	Qy 369EVEEKIDQLHQEQAFADFYMFSELLSDYI	Qy 407 FDHRWKCWQKWEDAQITLIKKREAEAKMMYANKPDKIQOAKNEIREWEAKVQQGERDFEQ 466	467 ISKTIRKEVGRFF		RESULT 8

GSPDB:GN000

100 EDIEDDSEGLEFENGESNAETCKISLSGSINSMNGETSASEEFSVSNRKKSAKIHLEEAK 167 151 KVGDGM-NAYMAYRVTTKISLSMFSKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAP 209 161 :		8 &	122,
KVGDGM-NAYMAYRVTTKTSLSMFSKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAP :  :		ογ	
		අු	317
		0У.	373
LPSEGSGSVDLSLSVIHASVNNSDEKLIRHRIRMLTEFLN	1	d d	220
243 KIVANFILLUOPULKUPILES		& A	433 263
275 ALSGAGILRHVNKAADAVNKMIIKMNESDAWFEEKQQOFEN-LDQQLRKLHVSVEA 329 :  :  :    ::    ::    ::    337 PIPGSSSOLLINKESND-KKMDKREKSEPNIFONYKOVENILDALIVKVNDPTMFWUHD 395		8 8	485
38		RESULT 11	7.
MESELLSDYIRLIAAVKGVEDRAMKGWQKWEDAQITLLKKREAEAKMWAN		1209/1 hypothetic C;Species: C;Date: 15 C;Accessio	etic ies 1
439		R;White, S submitted A;Referenc A;Accessio	e, ted rengren
447 RNEIREWEAKVQQGERDFEQISKTIRK-EVGRFEKERVKDFKTVIIKYLESLVQTQQQLI 505         : :                 : :       568 KKEIEQLSESLEVTENDLEVISKVIKHYARQNL 627	*.	A;Stat A;Mole A;Resi A;Cros	us: cule dues
506 KYWE 509 :  : 628 EIWR 631		A; Experime C; Genetics A; Gene: CE A; Map posi	rime tics : Cl
10		A; Introns: 86/3; 2019	ons 201
cal protein Y37AlB.3 - Caenorhabditis elegans - Caenorhabditis elegans - Caenorhabditis elegans	2	· Query Ma Best Loc Matches	y Ma Loc
in 19 Oct 1999 # teat_cliange		οy	91
submitted to the EMBL Data Library, June 1998 A; Reference number: 220245		QQ	257
ion: T26610 :: preliminary: translated from GB/EMBL/DDBJ		Qy	145
1le type: DNA les: 1-361 <wil></wil>		qq	305
<pre>Cross-references: EMBL:AL023835; PIDN:CAA19488.1; GSPDB:GN00022; CESP:Y37AlB.3 Experimental source: clone Y37AlB</pre>		ογ	186
ICS: CESP:Y37A1B.3		qa	365
osition: 4 is: 47/3; 161/2; 196/1; 222/1; 277/3; 350/3		ογ	236
	-	අ <u>ධ</u>	425
; Conservative 68			, ,
146 VSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSVKRRFSDFLGLHSKLASKYLHVGY 203		·	478
		ογ	317
204 IVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRRAALERYLQRTVKHPTLLQDPDLRQFLE 263		qa.	538
:	•	ογ	377

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ition: 1
:: 24/1; 130/3; 172/2; 194/2; 206/1; 235/3; 297/3; 438/2; 497/3; 601/2; 737/3
9/3; 2044/3
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ss: 1.2241 (WHL>
references: EMBL:281063; PIDN:CAB02951.1; GSPDB:GN00019; CESP:F15D3.1
nental source: clone F15D3
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s: CaenorhabditIs elegans
15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
lon: 120971
S.
                                                                                                                                                                   KIDQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEA 432
                                                                                                                                                                                                                                                                                                  TVASRRITEALA--YTASE-----YHEIGQVFDAHTK-----NDMEPVL--ENLYSY 262
                                                                                                                                                                                                                                                                                                                                                                                                                 DQQLRKLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTALSRALSQLAEVEEKIDQ_376
----LPRAVNTQALSGAGILRMVNKAADAVNKMTIKMNESDAWFEEKQQQFENL 316
                                          CIDEKDWKNGKRRAEKDEYIGGA-----FLNCIIVPHQPLDP-----NNV 161
                                                                                                                           DOQL----RKLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTALSRALSQLAEVEE 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ...---YMAYRVTTKTSLSMFSKSEF-SVKRRFS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFLGLHSKLASKYLHVGYIV------PPAPEKSIVGMTKVKVGKEDSSSTEFVEKR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFESFMSSLIDSQDTVGRVLLRGQMLSNKSESEEKESIGANLHLVNTRWEALREQAMQE 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAALERYLQRTVKHPTLLQDPDL---RQFLESSELP-----RAVNTQAL----- 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| |:: : ||| :| |:||::||| OAVLQQQIH------LLQQSELDTISQWLDAAELEIESFGPLAADSSQALRQIELHTKF 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------SGAGILRWVNKAA-----DAVNKMTIKMNESDAWFEEKQQQFENL.316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | | ::: :: : | | | ADLLDKTNEVFENLSGWLAERENELMTGLKSAHHLENEEQ----VAQQVRRLQKTEEQLEQ 594
                                                                                                                                                                                                                                                                                                                                                                                KMMVANKPDKIQ---QAKNEIREWEAKVQQGERD----FEQISKTIRKEVGRFEKERVK 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILSSEPSPA-----VTPVTPTTLIAPRIESKSMSAPVIFDRSREEIEEEANGDIFDIEI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSSSSQKSGKSKRRREEQLAEFKSCIEQVLTWLLEAEDELTITQMPRVELASVRSQFS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHQEQAFADFYMFSELLSDYIRLI-----AAVKGVFDHRMKCWQKWED--AQI-----TL 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           latch 6.4%; Score 167; DB 2; Length 2241;
cal Similarity 21.3%; Pred. No. 0.43;
111; Conservative 86; Mismatches 181; Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 to the EMBL Data Library, October 1996
nce number: 219353
lon: T20971
preliminary; translated from GB/EMBL/DDBJ
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DMKSTMGTYLKKQAMFYQEV 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFKTVIIKYLESLVQTQQQL 504
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RESULT 13 S53033	MVPI protein - yeast (Saccharomyces cerevisiae) N.Alternate names: protein WM8270.06; protein YMR004w C.Species: Saccharomyces cerevisiae C.Species: Saccharomyces cerevisiae C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 30-Apr-1999 C.Accesion: S53033; S50223	553(	DEV.  DEV.  EMBL:248613; NID:9728645; PID:9728651; MIPS:YMR004w  ce: strain AB972  18, T.H.  fbl Data Library, October 1994	gene interacts with vrsi and i		Query Match 6.3%; Score 164.5; DB 2; Length 511; Best Local Similarity 21.5%; Pred. No. 0.079; Matches 105; Conservative 79; Mismatches 188; Indels 117; Gaps 22;	OY 32 VSTLESSPESSPEPASLPAEDISANSNGPKPTEVVLDDDREDLFAEATEEVSLDSPER 88	OY 89 EPILSSEPSPAVTPVTPLTLIAPRIESKSMSAPVIFDRSREEIEEEANGDIF 140	QY 141DIEIGVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKS-EFSVKRRFSDFLGL 190	QY 191 HSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRRAALERYLQRTVKHP 250  191 HSKLASKYLHVGYIVPPAPEKSIVGMTKVKGKEDSSSTEFVEKRRALERYLQRTVKHP 250  DD 180 REILLKRYPFRMIPELPPKRIGSQNADQL-FLKKRRIGLSRFINLVMKHP 228	QY 251 TLLQDPDLRQFLESSELPRAVNTQALSGAGILRAVNKAAD-AVNKMTIKMNESDAWFE 307	QY 308 EKQQQFENLDQQLRKLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTALSR 362	QY 363 ALSQLAEVEEKIDQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQI 422	QY 423 TLLKKREAEAKMAVANKPDKIQQAKNEIREWEAKVQQGERDFE 465	Oy 466 QISKTIRKE 474	RESULT 14 \$28261 centromere protein E - human N;Alternate names: centromere 312K protein; kinesin-related protein CENP-E
Db 595 EHASFVRLSQLSCELVGRLDDSNGAAANAVRLSLDSITQRWDNLVARIEEHGKTL 649	Oy 425 LKKREAEAKAMVANKPDKIQOAKNEIREWEAKVQOGERDFEQISK- 469  1	DD 702 SHELEPLODWSEKFEVSRKKDDIRKMANTCQEKLIQIKEQ 741	RESULT 12 T20078 T0078  C.Species: Caenorhabditis elegans	R;White, S. submitted to the EMBL Data Library, October 1996. A;Reference number: 219353 A;Accession: T20078 A;Status: preliminary; translated from GB/EMBL/DDBJ	A; MOJECULE 1-776: (MIL> A; Cross-references: EMBL: 281063; PIDN: CAB02958.1; GSPDB: GN00019; CESP: F15D3.9 A; Experimental source: clone F15D3 C; Genetics:	A;Gene: CEST:12D2.5 A;Map position: 1 A:Inirons: 24/1; 130/3; 172/2; 211/1; 240/3; 302/3; 443/2; 502/3; 606/2; 742/3; 828/2; 9 064/3	Query Match 6.4%; Score 167; DB 2; Length 2261; Best Local Similarity 21.3%; Pred. No. 0.43; Matches 111; Conservative 86; Mismatches 181; Indels 142; Gaps 23;	Qy 91 ILSSEPSPAVTPVTPTTLIAPRIESKSMSAPVIFDRSREEIEEEANGDIFDIEI 144 :   :  :  :  :  :  :  :  :  :  :  :  :	QY 145 GVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSEF-SVKRRFS 185	Qy 186 DFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKR 235	OY 236 RAALERYLORTVKHPTLLQDPDLRQFLESSELPRAVNTQAL 276	QY 277SGAGILRMVNKAADAVNKMTIKMNESDAWFEEKQQFENL 316   :	OY 317 DQQLRKLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTALSRALSQLAEVEEKIDO 376	OY 377 LHOEGAFADFYMFSELLSDYIRLIAAVKGVFDHRWKCWQKWEDAQITL 424	OY 425 LKKREAEAKMYANKPDKIQOAKNEIREWEAKVQOGERDFEQISK-469 1 :  :  :  :  :  :  :  :  :  :  Db 655 VKSGKADVKQVQESQNEQKEQPASSEGLSTDTEGEEQKNOLVDKFLLHISKL 706	OY 470TIRKEVGRFEKERVK-DFKTVIIKYLESLVQTQQQ 503 ::          ::       ::  DD 707 SHELEPLQDWSEKFEVSRKKDDIRKWMNTCQEKLIQIKEQ 746

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Search completed: March Job time: 27.3475 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQORKIFSLIQEKNELQOMLESVIAEKEQLKTDLKENIEMTIENQEELRLLGDELKKQQE 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----LQEKQQQLLNVQEEMSEMQ--KKINEIENLKNELKNKELTLEHMETER 1181
Species: Homo sapiens (man)
Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRSREEIEEEEANGDIFDIEIGVSDPEKVGDGMNAYMAYRV-----TTKTSLSMFSKS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   866 TELSYKTOELOEKTREVOERLNEMEQLKEQLENRDSPLOTVEREKTLITEKLOOTLEEVK 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                926 TLTQEKDDLKQLQESLQIERDQLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS 985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---LLSELKSLPSEV 756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               660 TTYKOMENDIOLYOSOLEAKKKMOVDLEKELOS---AFNEITKLTSLIDGKVPKDLLCNL 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 DRE----DLFAEATEEVSLDSPEREPILSSEPSPAVTPVTPTTLIAPRIESKSMSAPVIF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 TDFEDLEDGEDLFTSTVST-----LESSPSSPEPASLPAEDISANSNGPKPTEVVLDD 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1182 LELAQKLNENYEEV-KSITKE-RKVLKELQKSFETERDHLRGYIREIEATGLQTKEEL 1237
                                                                                                                                                                                                                                   Cross-references: EMBL:215005; NID:929864; PIDN:CAA78727.1; PID:929865
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                                                                 Ven, T.J.; L1, G.; Schaar, B.T.; Szllak, I.; Cleveland, D.W. sture 359, 536-539, 1992
Title: CENP-E is a putative kinetochore motor that accumulates just Reference number: S28251; MUID:93024922; PMID:1406971
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                                                                                                                                                                                                                                                                                                                                                      Superfamily: centromere protein E; kinesin motor domain ho; Keywords: ATP; coiled coil; microtubule binding; mitosis; 7:35/Domain: kinesin motor domain homology «KWOT>; 86-93/Region: nucleotide-binding motif A (P-loop); 486-2183/Domain: coiled coil *status predicted «COI>; 92/Binding site: ATP (Lys) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 EFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184;
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Similarity 18.7%; Pred. No. 0.74;
23; Conservative 102; Mismatches 1
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                                                                                                                                                                                                                                                                                                              GDB:361164; OMIM:117143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           717 ELEGKITDLOKELNKEVEENEALREEVI----
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                                                                                                                                                                                                                                                                                                                                          Map position: 4q24-4q25
                                                                                                                                                                                           Molecule type: mRNA
Residues: 1-2663 <YEN>
                                               Accession: S28261
                                                                                                                                                                                                                                                                                                              Cross-references:
                                                                                                                                                                       Accession: S28261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Sim
Matches 123;
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A;Cross-references: GB:chr_III; PIDN:CAA81607.1; PID:93878558; GSPDB:GN00021; CESP:M0
                                                                                                                                                                                                   investigating bio
                                                                                                                                                                                            A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Reference number: A5000; MUD1:99069613; PMID:981916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                               C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNPPIDEKEKLSRLQH 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 IEDENELETPLVET----RIMPLP-----NDLNANFSNKNSTTTFVEPETPKSPTKKSOK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 VSLDSPEREPILSSEPSPAVTPVTPTLIAPRIESKSMSAPVIFDRSREEIEEEANGDIF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVG-----KEDSSSTEFVEKRRAALERYLQRTVKHPTLLQDPDLRQFLE 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LQAALANDCDHRNQMLTKEISSL 668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIKSRVSLLPPPAPKAPQKENKEGGEMTETPRRTITKTPLKTVNAKAKTSPTPPVERQ-- 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEDGEDLFTSTVSTLESSPSSPEPASLPAEDISANSNGPKPTEVVLDDDREDLFAEATEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 M----EEKPVVKKKEEPAAPPPPFFFPVKQKAPSKHQ---LMMEQLKASIEAEKTKPKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 DIEIGVS-----DPEKVGDGMNAYMAYRVTTKTSL-SMFSKSEFS----VKRRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KKERKPL---YVAPPAKERVEKEKKIPSKPVVSPPTTAEKKPVVSSIPSTSSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 163.5; DB 2;
; Pred. No. 0.19;
94; Mismatches. 207;
Caenorhabditis elegans
                                                                                                                               elegans Sequencing Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          457 SKGPFPTSSFAGGKLQGPRKTSSSSTTTSAKKQ
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Best Local Similarity 20,1%
Matches 115; Conservative
                                                                                                                            R; anonymous, The C. elegans
Science 282, 2012-2018, 1998
   [imported]
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                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                      A; Accession: G88551
                                                                                                   C; Accession: G88551
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GenCore version 5.1.3	17 18 19 21 21	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3000	33 33 33 33	35	3.3.7	) 4 4 4 4 0 0 11 01 18 4	45	RESULT 1 091021 ID 0910 AC 0910 DT 01-D	•			DR Inte DR Pfam DR Pfam SQ SEQU	Best Lo Matches Qy 1		Db 61
d 5 a 666 s	GenCore version (c) 1993 - 2003	<ul> <li>protein search, using sw model</li> <li>March 4, 2003, 14:53:32; Search time 35.5568 Se (without alignments)</li> <li>3007.543 Million cell</li> </ul>	US-09-763-902B-3 2620 1 MAAEREPPPLGDGKPTDFEDTQQQLIKYWEAFLPEAKAIA	: BLOSUM62 Gapop 10.0 , Gapext 0	seqs, 206047115	of hits satisfying chosen parameters:	ength: 20000000 ength: 20000000 Minimum Match Maximum Match Listing first	SPTREMBL_21:*  1: SP_archea.*  2: Sp_bacteria:*  3: Sp_fung1:*  4: Sp_human:*	خ		17: Sp_Doctering.  No. is the number of results predicted by greater than or equal to the score of the store dy analysis of the total score of	SUMMARIES	Match Length DB ID	\$23.4 580 3 Q9C2E4 Q962e4 n 16.4 402 10 Q9FG38 Q9Fg38 15.6 396 10 Q94CW4 Q94CW4 Q94CW4 15.2 554 10 Q9LYQ3	10.1 5/6 10 Q9FGH8 Q9FGH8 12.3 57 10 Q941X3 Q941X3 10.0 449 5 Q8T083 Q8T083 G999 417 5 Q9NKJ6 Q9NKJ6 10.0 417 5 Q9NKJ6	9.9 228 6 Q9BEC2 Q9be62 macaca 9.8 336 4 Q8WV04 homo se

Q9cz03 mus musculu	014243 schizosacch	Q91y12 mus musculu	Q9nes0 caenorhabd1	Q8rxm2 arabidopsis	Q07528 saccharomyc	Q9xxg1 caenorhabdi	Q91vh2 mus musculu	Q9p779 schizosacch	Q9ncc3 drosophila		O912r2 mus musculu	O96ng4 homo sapien	Snm O	Q9csc2 mus musculu	Q9d0a6 mus musculu		Q8tck9 homo saplen	ยาเร	O8wug9 homo sapien		Q91sb9 arabidopsis	O9tw65 caenorhabd1	Q9tyg9 caenorhabdi	Q99m52 mus musculu	Q99kq6 mus musculu	Q9urw7 schizosacch	Q9h2g2 homo sapien	09zvt8 arabidopsis	
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9.4	9.3	8.7	8.2	7.7	7.6	7.5	7.4	7.3	7.3	7.2	7.1	7.0	6.8	6.7	6.7	9.9	9.9	.9.9	6.5	6.4	6.4	6.4	. 6.4	6.3	6.3	6.2	0.9	0.9	
245	243.5	229	214.5	201	200	195.5	193.5	191	190	187.5	186.5	182.5	178.5	175	175	173.5	173.5	172	169.5	167.5	167	167	167	165.5	164	163	158.5	157.5	
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	SNX2.		
	Mus m		
	Eukar	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Rodentia: Sciuroquathi: Muridae: Murinae: Mus.	
	NCBI		
_	[7]		
	SEQUE	SEQUENCE FROM N.A.	
	CETT	DEPENDENCE:	
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_	Submi	Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.	
	EMBL;	EMBL; BCU06960; AAHU6960.1;	
	E CO	TOTOLOGICAL STATE	
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	ner	TROUBLES SOLLING HEXTH.	
	, Hall	FIGHT FEOUNDS TO THE TOTAL TO T	
	riam;	SOLUTING_NEXTH; I.	
	SEQUE	ENCE 519 AA; 58453 MW; 15CCUAA64E831729 CRC64;	
Ö	Query Match		
Be	st Loc	cal Similarity 97.9%; Pred. No. 4e-136;	
Жа	Matches	508; Conservative 4; Mismatches 7; Indels 0; Gaps	Ω.
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			(
_	7	MAAEREPPPLGDVKPTDFEELEDGEDLFTSTVSTLESSPSSPEPASLPAEDISANSNGSK 60	<b>-</b>
	61	PTEVVLDDDREDLFAEATEEVSLDSPEREPILSSEPSPAVTPVTTLIAPRIESKSMSA	120
_	. 19		120
	121	PVTENBSRETEEFANGDIEDTEIGVSDPRKVGDGMNAVMAVBATETSTSMESKSFESV	180
		THE DESCRIPTION OF THE DESCRIPTI	3

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                                                           KRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRRAALE 240
                                                                                                                                                         92 LSSEPSPAVTPVTPTTLIAPRIESKSMSAPVIFDRSREEIEEEANGDIFDIEIGVSDPEK 151
KRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRRAALE 240
                                                                                                                                       RYLQRTVKHPTLLQDPDLRQFLESSELPRAVNTQALSGAGILRMVNKAADAVNKMTIKMN 300
                                                                                                                                                                                                                   ESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTAL.360
                                                                                                                                                                                                                                                                                             SRALSOLAEVEEKIDOLHOEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-TESTIS;
Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
Tarao K., Suzuki Y., Sugano S.;
"Isolation of novel full-length cDNA clones from macaque testis cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 ESSPSSPEPAS-LPAEDISANSNGPKPTEVVLDDDRE--DLFAEATEEVSLDSPEREPI 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGDGMNAYMAYRVTTKTSLSMFSKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       libraries.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.8%; Score 1514; DB 6:62.9%; Pred. No. 2.1e-77
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70; Mismatches
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NCBI_TaxID=9541;
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Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
R.A. Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gacler R.F.,
R.A. Adams M.D., Celliker S.E., Holt R.A., Robkins R.A., Galle R.F.,
R.A. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R.A. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
R.A. Brandon R.C., Rogers Y.H.C., Blazej B.G., Change M., Pfeliffer B.D.,
R.A. Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
R.A. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
R.A. Ballew R.M., Basu A., Baxendale J., Bayraktearoglu L., Beaaley E.M.,
R.A. Ballew R.M., Basu D.A., Barman B.P., Bhandari D., Bolshakov S.,
R.A. Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
R.A. Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
R.A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
R.A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
R.A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R.A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn R.,
R.A. Harris N.L., Harvey D., Heinan T.J., Hernande J.R., Hernande J.R., Hernande J.R., Hernande J.R., Hernande J.R., Hernande J.R., Match B., Kallush F., Karpen G.H., Ke Z., Kenlison J.A.,
A. Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A. Malshina N.V., Mobarry C., Morledo M.P., Morberson D.,
R.A. Melson D.R., Milshina N.V., Mobarry C., Morledo R., Sandeler F., Shen H.,
R. Reinert K., Semington K., Sanders R.D., Puri V., Resse M.G.,
R. Reinert K., Semington R., Sanders R.D., Smith T.,
R. Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Salith T.,
                                                                                                                                                                                                                287 NHRKELAPNTAQFAKSLAMLGSSEDNTALSRALSQLAEVEEKIEQLHQEQANNDFFLLAE 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEAKMWVANKPDKIQQAKNEIR 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHRKELSANTAAFAKSAAMLGNSEDHTALSRALSQLAEVEEKIDQLHQEQAFADFYMFSE 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EWEAKVOOGERDFEQISKTIRKEVGRFEKERVKDFKTVIIKYLESLVOTQOQLIKYWEAF
SIVGMIKVKVGKEDSSSIEFVEKRRAALERYLQRTVKHPILLQDPDLRQFLESSELPRAV
                                                                                    SLIGMTKVKVGKEDSSSAEFLEKRRAALERYLQRIVNHPTMLQDPDVREFLEKEELPRAV
                                                                                                                                                                        272 NTOALSGAGILRMVNKAADAVNKMTIKMNESDAWFEEKOOOFENLDOOLRKLHVSVEALV
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Last sequence update)
Last annotation update)
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Consortium.";

ode C. elegans: a pl elegans Sequencing

cosmid C05D9."; EMBL/GenBank/DDBJ databases

EMBL/GenBank/DDBJ databases

BFFB40F307F2AF60 CRC64;

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MEDLINE-99069613; PubMed-9851916;
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472 AA; 54107 MW;
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                                                                                                                                                                                                                               Fulton L., Gattung S.;
"The sequence of C. elegans
Submitted (JUL-1996) to the
                                                            "Genome sequence of the nema
investigating biology. The C
Science 282:2012-2018(1998).
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"Direct Submission.
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                          SEQUENCE FROM N.A
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Q9C2E4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVESPEHTRDFAEVDINNGAATGSEDEEEVPA-------PGSVTLDRNESDLF-- 48
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang 2.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I.,
Zheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X., Smith H.G
Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
Science 287:2185-2195(2000)
EMBL, AE003579; AAF511091:
FlyBase; FBgn0031534; CG2774.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                       Pfan, PF00787; PX; 1.
SMART; SM00312; PX; 1.
SEQUENCE 458 AA; 52195 MW; 85ABCAA1F1349128 CRC64;
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Last annotation update)
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Rhabditidae, Peloderinae, Caenorhabditis
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|NIKYIEDQMAHQQQIVSYWEAFAPFAREI 457
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01-WAR-2001 (TrEMBLrel. 16, Last seq
01-70N-2002 (TrEMBLrel. 21, Last anno
Hypothetical 54.1 kDa protein
C05D9.1.
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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Mac.
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09GYJ9;
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274 QALSGAGILRMYNKAADAVNKMTIKMNESDAWFEEKQQQFENLDQQLRKLHVSVEALVCH 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 AALSSFGVKKIFKNFQVVFSKMAFHMEEGDRWFEQVQSQVDELDEALRKLYTVTETLVAS 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 RRDMATSGEOLGKALSMLAACEESTSLSRALSSLTDVTENVSAVYGKQAEVDNSKFSESI 343
                                                                                                                              47 LPAEDISANSNGPKPTEVVLDDDREDLFAEATEEVSLDSPEREPILSSEPSPAVTPVTPT 106
                                                                                                                                                                                                                                                      107 TLIAPRIESKSMSAPVIFDRSREEIEEEANGD------IFDIEIGVSDPEKVGDG 155
                                                                                                                                                                                                                                                                                                                                                                          156 MNAYMAYRVTTKTS-LSMFSKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIV 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEAK--MMVANKPDKIQQAKNEIR 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 GMTKVKVGKEDSSSTEFVEKRRAALERYLQRTVKHPTLLQDPDLRQFLE-SSELPRAVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EWEAKVOOGERDFEOISKTIRKEVGRFEKERVKDFKTVIIKYLESLVOTOOOLIKYWEAF
                                                                                                                                                                                                                                                                                        Length 472;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Related to vacuolar protein sorting-associated protein VPS5.
                                                                  Indels
      DB 5;
                                                                  Matches 174; Conservative 102; Mismatches 178;
                                                                                                                                                                          2 LSEEDVHINSYAGRIVAVM-:-EQPDLFSDCDEINLGNED--
      30.7%; Score 803.5; DB 5 35.7%; Pred. No. 1.6e-37;
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273 223

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Pfam; PF00787; PX; 1
SMART; SM00312; PX;
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                                                                                                            [1]
SEQUENCE FROM N.A.
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                                                                                                                                                     STRAIN-COLUMBIA;
                                                                                NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                          InterPro;
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                                             Sordariomycetes;
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; Pred. No. 9.9e-27;
82; Mismatches 224; Indels 89
                                                                                                                                                       Hoheisel J., Brandt P., Fartmann B.,
                                                                                                                                                                                                                                                                 German Neurospora genome project;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR001683; PX.
InterPro; IPR001683; PX.
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SEQUENCE 580 AA; 64100 MW; 311F73EP889C7E2F CRC64;
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Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariales; Sordariaceae; Neurospora.
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9G6.210,
Neurospora crassa.
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                                                                                  NCBI_TaxID=5141;
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                                                                                                            Rosidae;
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Arabidopsis thaliana (Mouse-ear cress). Embryophyta; Tracheophyta; Eukaryota; Vifidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosice eurosids II; Brassicales; Brassicales; Arabidopsis.
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Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 16.4%; Score 428.5; DB 10; Best Local Similarity 29.8%; Pred. No. 1.5e-16; Matches 115; Conservative 76; Mismatches 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492 KYLESLVQTQQQLIKYWEAFLPEAKA 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP002030; BAB10207.1; -.
EMBL; AP002544; BAB10207.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46523 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP002030; BAB10207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR001683; PX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. NIPPONBARE;
Sasaki T.; Matsumoto T
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                           238
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                                                                                                                                                                                                                                                                                                                                                                                                283
                                                                                                                                                                                                                                                                                                                                                                                                                       231
                                                                                                                                                                                                                                                                                                                                     ---MVNKAADAVNKMTIKMNESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKELSAN 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAFAKSAAMLGNSEDHTALSRALSQLAEVEEKIDQLHQEQAFADFYMFSELLSDYIRLI 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 AAVKGVFDHRMKCWQKWEDAQITLLKKREAEA----KMMVANKPDKIQQAKNEIREWEAK 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457 VOOGERDFEQISKTIRKEVGRFEKERVKDFKTVIIKYLESLVQTQQQLIKYWEAFLPEAK 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiphantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicacae, Arabidopsis
                                                                                                                                                                                                                                RIESKSMSAPVIFDRSREEIEEEANGDIFDIEIGVSDPEKVGDGMNAYMAYRVTTKTSLS 171
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                          280 QSIKATMVDRANAFRQHHD----LFQQKEYKGVNLEKLKFVN-PDKFSELEAEL---TAD
                                                                                                                                                                                                                                                                                                                172 MFSKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LADFGKAIKLLGACEG-DSLEKVFSEVGSKSEMLSVKLQREADNLLFNFEEPLKDYVRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 SEEATKRFEHIVAVMNEELARFQEQKTADIGFAFHEFAKGQAKLAKDIADAWRGVLPKLE
                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes Rudd S., Legicke K., Mayer K.F.X.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                             232 VEKRRAALERYLQRTVKHPTLLQDPDLRQFLESSELPRAVNTQALSGAGILR----
                                                                                                                                              Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL163652; CAB87268.1;
InterPro; IPR001683; PX.
                                                          Pfam; PF00787; PX; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; UNKNOWN_1.
SEQUENCE 396 AA; 45390 MW; 3BD22A82EB75DDBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6C63A8823C4E75F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 62.2 kDa protein.
                                                                                                                                              ; Score 408; DB 10;
; Pred. No. 2.1e-15;
80; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      554 AA
               InterPro; IPR001683; PX.
InterPro; IPR000634; S/T_dehydrtse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62223 MW;
                                                                                                                                              15.6%; 27.6%;
AP003611; BAB63798.1;
                                                                                                                                                                                       Matches . 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    · PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al protein.
554 AA; 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00787; PX; SMART; SM00312; PX;
                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     517 A 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 A 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
  SO DR DR
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321
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                                                                                                                                                                                      82 SLDSPEREPILSSEPSPAVTPVTPTTLIAPRIESKSMSAPVIF----DRSREEIEEEANG 137
                                                                                                                                                                                                                                                                                   --IEIGVSDPEKVGDGMNA-----YMAYRVTTKTSLSMFSKSE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 ALEKYLRRLVAHPVIRNSDELKVFLQAQGKLPLATSTDVASRMLDGAVKLPKQLFGEGGG 277
                                                                                                                                      9
                                                                                            22 EDGEDLFTSTVSTLESSPSSPEPASLPAEDISANSNGPKPTEVVLDDDREDLFAEATEEV 81
                                                                                                                                                                                                                        -----YADVIFSPFDDISEINGSEDGHS
                                                                                                                                                                                                                                                                                                         -------GAGILRMVNKAADAVNK----MTIKMNESDAWFEEKQQQFENLDQQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 ASSVEVVOPGRGGRDFLRMFKELROSVSNDWGGSRPPVVEEDKEFLEKKEKMYDLEQQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NASQQAESLVKAQQDMGETMGELGLAFIKLTKFENEEAVFNSQRARANDMKNLATSAVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 EDGDPLTKSNVNG-DKSNSNYRSA-----MSTLFDSRHPSIVVTPADSDPLFAPPSYYS
                                                                                                                                                                                                                                                                                                                                                                           FSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTAL----SRA--LSQLAEVEEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITL------LKKR
                                              Indels 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.A., Barrell B.G., Saunders D., Harris D.
to the EMBL/GenBank/DDBJ databases.
  Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D8CC2B20CA3D09AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fung1; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
  DB 10;
                                              Mismatches 215;
Score 398.5; DB 1 Pred. No. 1.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKERVKDFKTVIIKYLESLVQTQQQLIKYWEAFLPEAK 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 396; DB 3;
Pred. No. 1.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALERYLORTVKHPTLLQDPDLRQFLES-SELPRAVNTQALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             510 DRERRADFLUMMKGFVANQVGYAEKIANVWTKVAEETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                        ESRSPRSKPNGGDRVSSYLEPPS----
                                              92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64230 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.1%;
22.1%;
15.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2001) to the EMBL; AL590182; CAC34987.1; InterPro; IPR001683; PX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 17, (TrEMBLrel. 17, (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sorting nexin-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood V., Rajandream M.A.,
Submitted (JAN-2001) to th
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAEA-KMMVA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00787; PX; ]
SMART; SM00312; PX;
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-972H-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-4896
                                                                                                                                                                                                                                                                                   DIFD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001
01-JUN-2001
01-OCT-2001
                                                Matches 150;
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| : ||||:|| |||:|| ||: :| || -- VESQVMQKQEFVEQRRVALEKYLRLSAHPVIRNSDELKVFLQVQGKLPLPMSTDVAS. 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNPQRTRANDMKNLATAAAVKASRPYRE-LNSQTVKHLDTLHEYLGMMMAVQGAFADRSSA 445
                                                                                                                                                                                                                                                                                                                                                                                                  96 FDENSDSEINGTEDNSLHSOFSDSLSRSPSSSSDYIKITVSNPQKEQEISNSIVGGNTY 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAYRVTTKTSLSMF-SKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --GAGILRMVNKAADAVNK----MTIKMN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTAL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEDKEFLEKKEKMHDLEQQIINASQQAESLVKAQQDMGETMGELGLAFIKLTKFENEEAV.386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLTVQTLLSELPSLQTRVEKLEAASSKVFGGDKSRIRKIEELKETIKVTEDAKNVAIKGY 505
                                                                                                                                                      DDDREDLFAEATEEVSLDSPEREPILSSEPSPAVTPVTPTTLIAPRIESKSMSAPVIFDR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 133; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 VKVGKEDSSSTEFVEKRRAALERYLQRTVKHPTLLQDPDLRQFLE-SSELPRAVNTQALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMLDGAVKLPKQLFGEGGASAVPVTEVGQPARGGRDLLRLFKELRQSVSNDWGGSKPPVV
GDGKPTDFEDL - - EDGEDLFTSTVSTLES - - SPSSPEPASLPAEDISANSNGPKPTEVVL
                                                                                                                                                                                                                                        52 PADSDPLLAPSSYEDFRSSFSSKPI-SSDNS-----YIEPPSY-ADVIFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : |::||:|| | |||||:||| | : | :|| | | :|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SRA--LSQLAEVEEKIDQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----WQKWEDAQITLLKKREAEAKMWVANKP--DKIQQAKNEIREWEAKVQQGERDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                         ---IEIGVSDPEKVGD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JUN-2001) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
GEOTHENCE 577 AA; 62866 MW; A3EF868B6BFCB31D.CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     506 ERIKENNRSEVERLDRERRADFWNWAKGEVVNQVGYAEKMGNVW 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
12.3%; Score 322.5; DB 10;
Best Local Similarity 22.9%; Pred. No. 2.1e-10;
Matches 127; Conservative 81; Mismatches 213;
                                                                             10 GGDHPLKISDVNGDTSNSGYRSAMSTLSNVRDPLSPPPT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA
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Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP003734; BAB68097.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B1088C09.3 protein.
B1088C09.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00787; PX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone: B1088C09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, streptophyta; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- IGVSDPEKVGDGMNAYMAYRVTTK-TSLSMFSKSEFSVKRRFSDFL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 AHPAAAPOSLTPFYIQVHDPHTVKEITKSHTVYSVSTRLEEHNOPSVSNVTVQRRYNDFA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KMNESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDH 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418 EDA--QITLLKKREAEAKMAVANKPDKIQQAKNEIREWEAKVQQGERDFEQISKTIRKEV 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSFSPSPIGATENPTIPNSEQTVDTLDAASSSAPNFTHTVSSASSQKQGSTSLTDTENQK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRRAALERYLQRTVK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 KFSEQDPILIEAKDTLDSLETQLKSVYHALLLSIDQRIQFASAIHDFGEAVGNLSLVDLE 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418 PTLSSKFDGLSQLQVELRFVQERKVAQDNLTLGTTLEEYIRYVESAKNAFTTRQKLWQTW 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                            95
                                                                                 EDGEDLFTSTVSTLESSPSSPEPASLPAEDISANSNGPKPTEVVLDDDRE---DLFAEAT 78
                                                                                                                                  478 OSSVQAVSRAKTQLEKCKKQAKSQQKSLPYLEEQYEKYRAKAADLEKEFSESTTLLKRDL
                                                                                                                                                                                                                                                                                                                         ETLTLDSAPLGPLQFSDAPSMAPENNRLEVGLNTKINPLKGSSPALNADFSANKPWISEV
                                                                                                                                                                                                                                                                                                                                                                                                           ----PSPAVTPVTPT----TLIAPRIESKSMSAP-VIFDRSREEIEEEANGDIFDIE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 TALSRALSQLAEVEEKIDQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-COLUMBIA;
Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 566;
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPTLLQDPDLRQFLESSEL-PRAVNTQAL--SGAGILRMVNKAADAVNKMT
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eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created).
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.0%; Score 367; DB 10;
24.5%; Pred. No. 6.6e-13;
1ve 94; Mismatches 217;
    241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              476 GRFEKERVKDFKTVIIKYLESLVQTQQQLIKYWEAFLPE 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              566 AA
        Mismatches
    112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity to sorting nexin.
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        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001683; PX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Structural analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 566 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00787; PX; SMART; SM0310. PV
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                                                                                                                                                                                                                                                EEVSLDS --
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Q9NKJ6
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------AVNTQALSGAGILR 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SANTAAFAKSAAMLGNSE------DHTALSRALSQLAEVEEKIDQLHQEQAF 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKIEIHLGTIYEYLETMTSVRNAFTDRANALLRVQSLSGDLFLLHTQAAKLESVSSRGMG 488
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                                                                                                                                                                                                                                               58 PSRPRPQSSP-----PPPGPAMVGADAESSAVVDAGEGHGDLALDSSSAASTDPL 107
                                                                                                      LSSEPSPAVTPVTPTTLI-------APRIESKSMSAPVIFORSREEIEEEANG 137
                                                                                                                                                                                                                                                                                                                                                      MVNKAADAVNKMTIKM-----NESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377 KATTGQLGMTFIKLAKFEKEQDTCNSQRKRAVDMSNFANAVINMSRSQTKLN-----
                                                                                                                                                                                                                ----VGDGMNAYMAYRVTTKTSLSMFSKSEFSVKRRFSDF
                                                                                                                                                                                                                                                                                                                       LGLHSKLASKYLHVGYIVPPAPEKSIV-GMTKVKVGKEDSSSTEFVEKRRALERYLQRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWE--DAQITLLKKREAEAKMMVAN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----KPDKIQQAKNEIREWEAKVQQGERDFEQISKTIRKEVGRFEKERVKDFKTVIIKYL
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21.3%; Pred. No. 4.3e-07;
ive 88; Mismatches 206; Indels 128;
PSSPEPASLPAEDISANSNGPKPTEVVLDDDREDL----FAEATEEVSLDS
                                                                                                                                                          LHPPPSPSSTPSSPTAIADHDAFIEEDGEDDSAPHVPSASDEAAPEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                      247 VKHPTLLQDPDLRQFL-----ESSELPR--
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                                                                                                                                                                                                                138 DIFDIEIGVSDPEK-----
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01-JUN-2002 (TrEMBLrel.
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AC 08108
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64 WYC--IVPPIPEKESV---QDKLGKLPRMVASAKETTASEGDLLEYRRISLRRFLQRLAY 118
                                                                                                                                                                                         1 SDALSEKEKV-----KFTVHTRTTLPGFSKKDNNVVRQHEEFVWLHDRIEENDDYAG 130
                                                                                                                                                                                                                                                                          243
                                                                                                                                                                                                                                                                                                                              131 YIIPPCPPRPDFDASREKLORLGEGEGNMTKEEFKKMKSELEAEYLATFKKTVAMHEVFL 190
                                                                                                                                                                                                                                                                                                                                                                                     QRTVKHPTLLQDPDLRQFLESSE----LPRAVNTQALSGAGILRMVNKAADAVNKMTIKM 299
                                                                                                                                                                                                                                                                                                                                                                                                                                            191 RRLASHPVFRVDQHLKVFLEYDQDLCAKPR--KKMAIFG-GFVKSLGKTTDEI-LLSATV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 NESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTA 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----EDSSSTEFVEKRRAALERYLQRTVK 248
                                                       142
                                                                                                                                                            EIGVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSVKRRFSDFLGLHSKLASKYLHVG 202
30
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NCBI_TaxID=5664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-FRIEDLIN, White J., Handley F., Vogt C., Robertson Wyler P.J., Slak E., Cawthra J., Handley F., Vogt C., Robertson McDonagh P., Ivens A., Nguyen D., Munden H., Stuart K.; Submitted (MAY-2000) to the EMBL/Genbank/DDBJ databases.
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                                                                                                           31 LATP---PATGGAPAPSGATNGSGSATSPDSSSSAPATPAVLGENALHVE
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Local Similarity 23.3%; Pred. No. 4.5e-07;
les 98; Conservative 77; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDVNDFFENELQFLTEYHGHLREAALRTEKMTQRHKDV --
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Interpro; IPR001683; PX.
Pfam; PF00787; PX; 1.
SMART; SM00312; PX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 I------NNGSKENGIHEEQDQEPQDLFADATVELSLDNIQN-----NQKKVPAKTLISLP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 PQEAP---NSSKHQP----TYEELEEEEQEDQFDLTVGITDPEKIGDGMNAYVAYKVTT 169
                                                                                                                       397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 AEDISANSNGPKPTEVVLDDDRE--DLFAEATEEVSLDSPEREPILSSEPSPAVTPVTPT 106
                                                                                                                                                                                                   RLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEAKMMVANKPDKIQQAKNEIREWEAKV 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AAEREPPPL------GDGKPTDFEDLEDGEDLFTSTVSTLESSPSSPEPAS--LP 48
                                                                                                                                                      ASAVSNFAASFGLLANGEEDAELRGAIEGVRDCGRKVADVYSKHADNESTRLVSTLSFYV
                                                                                                                                                                                                                                                                                                        355 AHLEEDLMGAEKTFSEEFVLFHENKQYDAKDMLKKFGMLELSFSESMKQEWDALRPMLES
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                                       -----VNKAADAVNKMTIKMNESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKEL
                                                                   GAAGGGGVSQTGAAYQSALTQEPVDEATWRATSEYIGELESNLKNMRNLLEALVDRHRRA
                                                                                                                       SANTAAFAKSAAMLGNSEDHTALSRALSQLAEVEEKIDQLHQEQAFADFYMFSELLSDYI
                                                                                                                                                                                                                            GMCAAVRETLNHMESAHQYLRNLQ---KKGQELQASAMRAQSANQV-QVQSELHEVNEQR
                                                                                                                                                                                                                                                                                 QQGERDFEQISKTIRKEVGRFEKERVKDFKTVIIKYLESLVQTQQQLIKYWEAFLPEAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 KTSLSMFSKSEFS----VKRRFSDFLGLHSKLASKYLHV--GYIVPPAPEKSIVG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca fascicularis (Crab eating macaque) (Cynomolgus monke).
Eukaryota, Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-FRONTAL LOBE LEFT;
Osdan N., Hidda M., Kusuda J., Tanuma R., Iseki K., Hirai M.,
Sizuki Y., Sugano S., Hashimoto K.;
Isolation of full-length cDNA clones from macaque brain CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 AA; 24827 MW; FEE036C502053BD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.9%; Score 259; DB 6; 32.2%; Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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InterPro; IPR005329; Sorting_nexin.
Pfam; PF03700; Sorting_nexin; 1.
Hypothetical protein.
SEQUENCE 228 AA; 24827 MW; FEE0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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01-JUN-2001 (TrEMBLrel. 17, Ca
01-JUN-2001 (TrEMBLrel. 17, La
01-JUN-2002 (TrEMBLrel. 21, La
Hypothetical 24,8 kDa protein.
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Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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09BE62
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RESULT 15 Q8WVD4

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----KGMVERFNDDFIETRRKALHKFLNRIADHPTLTFNEDFKIFLTAQAW--ELSSHKK 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 SPAVTPVTPTTLIAPRIESKSMSAPVIFDRSREEIEEEEANGDIFDIEIGVSDPEKVGDGM 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 NAYMAYRVTTKTSLSMFSKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGM 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 TKVKVGKEDSSSTEFVEKRRAALERYLQRTVKHPTLLQDPDLRQFLESSELPRAVNTQAL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 YFDEMKEYGPIHILWSASEEDLVDTLKDVASCIDRCCKA----TEKRMSGLSEALLPVV 271
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                                                                                                                                        Euteleostomi;
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID=9606;
                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00312; PX; 1.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
SEQUENCE 336 AA; 39207 MW; AAEOBE2FA7BF4616 CRC64;
                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.8%; Score 258; DB 4; L
llarity 24.5%; Pred. No. 4.4e-07;
Conservative 60; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4, 2003, 15:02:35
                                                                                                                                                                                                                                                                                                                           Submitted (DEC-2001) to the EMBL/GenE
EMBL, E0018105, AMH8105.1; ...
Interpro; IPR001005; Myb_DNA_binding.
Interpro; IPR001683; PX.
     Created)
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01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                  Similar to sorting nexin 7
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                                                                                                                 Homo sapiens (Human)
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les 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          completed: March
ne : 38,5568 secs
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Appli Appli Appli Appli Appli Appli Appl

Sequence

Sequence

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DDREDLFAEATEEVSLDS-----PEREPILSSEPSPAVTPVTPTTLI---APRIESKS 117
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                                      Sequence 2, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 3, A Sequence 33, Sequence 23, Sequence 23, Sequence 23, Sequence 23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gill, Gordon N.
APPLICANT: Kurten, Richard C.
APPLICANT: Cadena, Deborah L.
TITLE OF INVENTION: Sorting Nexins and Methods of NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
GOMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/625,322
FILING DATE: 01-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2033; DB 1;
Pred. No. 2.3e-160;
7; Mismatches 17;
                                                                    US-08-214-222-2.

US-08-46-8528-2.

US-08-247-4918-2.

US-08-247-4918-2.

US-08-127-498-23.

US-08-127-498-23.

US-08-137-4508-2.

US-09-73-820-2.

US-09-73-820-2.

US-09-154-7508-85
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JS-08-466-662-5
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1955
TELECOMMUNICATION INFORMATION:
TELEFRAN: (619,535-9001
TELEFRAN: (619) 535-9049
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08625322
Patent No. 5804412
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Matches 416
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                                                                                                                                                                                                                                                                                           US-09-763-902B-3
2620
1 MAAEREPPPLGDGKPTDFED......TQQQLIKYWEAFLPEAKAIA 519
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
                           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -467-852A-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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Maximum DB seq
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Gaps

	OY 2 AAEREPPPL	49 AEDISANSNGPKPTEVVLDDDREDLFAEATEEVSLDSPE	Db 68 I NNGSKENGIHEEQDQEPQDLFADATVELSLDSTQNNQKKVLAK 111 OY 105 PTTLIAPRIESKSMSAPVIFDRSREEIEEFANGDIFDIEIGVSDPEKVGDGMNAYMAYRV 164	Db 112 -TLIXLPPQEATNSKPOPTKEELEEEDGEDGFDLTVGTTDFEKIGDGMNAYVAYKV 167  Qy 165 TTKTSLSMFSKSFFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGWTKVKVGKE 224		22 2 2 2 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3	OY 285 VNKAADAVNKMTIKMNESDAWFEEKQOOFENLDQOLRKLHVSVEALVCHRKELSANTAAF 344	345					; Sequence 1, Application US/09310187A ; Patent No. 6358751	; GENERAL INFORMATION: ; APPLICANT: Benichou, Gilles : APPLICANT: Federaveve Process	; TITLE OF INVENTION: Involvement of Autoantigens in Cardiac ; TITLE OF INVENTION: Graft Rejection	; FILE REFERENCE: UCSF-090 ; CURRENT APPLICATION NUMBER: US/09/310,187A	; CURRENT FILING DATE: 1999-05-12; NUMBER OF SEQ ID NOS: 3	; SOFTWARE: FastSEQ for Windows Version 4.0		US-09-310-187A-1.	Query Match 5.7%; Score 149; DB 4; Length 1939; Best Local Similarity 18.1%; Pred, No. 0.002;	Matches	OY 19 EDLEDGEDLFTSTVSTLESSPESSPERASLPAEDISANSNGPKPTEVVLDDDREDLFAEAT 78    -	79 BEVGIDGDERPDIIGGBDGDAXMDVMMTTAANDAGAGAAAAA	. 1436 RSNAA	Qy 124FDRSREEIEEEANGDIFDIEIGVSD-PEKVGD-GMNAYMAYRVTKTSL 170	Db 1489 AYEESLEHLETFKRENKNLQEEISDLTEQLGEGGKNVHELEKV 1531
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	 MFSKSE 110	VEKRRA 237        VEKRRA 169	VNKMTI 297        VNKMTI 229		SEDH 289 WQKW 417 	KCWQKW 349 RKEVGR 477							٠						. •		,				,		. Gaps 8;
		FSVKRRFSDPIGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVERRRA        :      :   :	ALERYLQRTVKHPTLLQDPDLRQFLESSELPRAVNTQALSGAGILRWVKRADAVNKMTI 	AAFAKSAAMLGN	TALSRALSOLAET BENEGOGE ENLLOQUENTER SOVEALVCHRKELSANTAAFAKSAAMLGNSEDH TALSRALSOLAEVEEKIDOLHOEQAFADFYMFSELLSDVIRLIAAVKGVFDHRMKGWQKW 	AVKGVFDHRMKC RDFEQISKTIRK		519 451	•		f Using Same															th 52	Indels 39;
		KSIVGMTKVKV 	VNTQALŠGAGI               VNTQALSGAGI	VCHRKELSANT	VCHRRELSANI ELLSDYIRLIA 	ELLSDYIRLIA. REWEAKVQQGE)		FLPEAKAIA 51.              FLPEAKAIA 45.			Methods of	٠	Suite 700				Version #1.25								•	, DB 1; 2e-120;	66,
		FSYKRKFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEP        :      :   :         FSVK-RFTDFLGLHTTLPTTYLHVVIFVATSSRKSIVGMTKVKVGKEDSSSTEF	ALERYLORTVKHPTLLQDPDLRQFLESSELPRAVNTQALSGAGILRMVNKAADA 	KANESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKELSANTAAFAKSAAML	TALSRALSOLARE BENEGOGE ENLINGUER BRINS V BALNY, HEKKELSANTAAFAKSAAML TALSRALSOLAEVEEK IDOLHQEQAFADFYMFSELLSDY IKLIAAVKGVFDHRM 	TALSRALSQLAEVEEKIDQLHQEQAFADFYWFSELLSDYIRLIAAVKGVFDHRM EDAQITLLKKREABAKMMYANKPDKIQQAKNEIREWEAKVQQGERDFEQISKTI		FEKERVKJEKTVITKYLESSLOGTOOLIKWEAFLEEAKAIA 	25322		Sorting Nexins and	and Flores	4370 La Jolla Village Drive, in Diego			ble .	#1.0,	n: US/08/625,322 1996		1.5	P-UD 1955 ON:			-		Sco	78; Mismatches
	REEIEEEANGD	TGLHSKLASKY         :   TGLHTTLPTTY	KHPTLLQDPDLI 	EKQQQFENLDQ(              EKQQQFENLDQ(	AEVEEKIDOLHO IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	AEVEEKIDOLH( REAEAKMMVANK	REAEAKMMVANE	TVIIKYLESLV(                TVIIKYLESLVC	ation US/086	DRMATION: : Gill, Gordon N. : Kurten, Richard C.		ADDRESS: 25 Campbell and	La Jolla Vi	ornia	LE FORM:	Ξ.	Nisiem: PC-DOS/M Patentin Release Camion Dama.	UMBER: US/0 01-APR-1996	N: 435 INFORMATION:	Campbell, Cathryn A MATION NUMBER: 31,8	CKET NUMBER: ION INFORMATIC	9) 535-8949 80 ID NO: 2	TERISTICS:	o acid linear	protein	59.38;	vative
		1/8 FSVKRRFSDE        :    111 FSVK-RFTDE	238 ALERYLORTV 	298 KMNESDAWFE 		290 TALSRALSOL 418 EDAQITLLKK		4/8 FEKERVKDFK           410 FEKERVKDFK	SULT 2 -08-625-322-2 Sequence 2, Application US/08625322 Patent No. 5804412	GENERAL INFORMATION: APPLICANT: G111, G APPLICANT: Kurten,	APPLICANT: Cadena, TITLE OF INVENTION: NIMBER OF SPOITENCES:	SSEE	STREET: 4370 CITY: San Die	H.	ZIP: 92122 COMPUTER READABLE FORM: MEDIUM TYPE: Flores	COMPUTER: IBM PC	SOFTWARE: PC- SOFTWARE: Patentin Re	APPLICATION NUMBER: FILING DATE: 01-APP	# 7	NAME: Campbell, Cat. REGISTRATION NUMBER:	KEFEKENCE/DOCKET NUMBER: P TELECOMMUNICATION INFORMATION TELEDHONE: /610, 535-0001	92	SEQUENCE CHARACTERISTIC LENGTH: 522 amino ac	TOPOLOGY: lir	; MOLECULE TYPE: US-08-625-322-2	atch cal Simi	(ATC
			óy 2.	Oy 25		Oy 41		0y 4,	RESULT 2 US-08-625-322-2 Sequence 2, A Patent No. 58	GENE	TIL				COM		S	( <b>4 L</b>	, ATT	Z & 1	TEL	INFOR	Oas :	= £4	; MOL US-08-62	Query Match Best Local	9733

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us-09-763-902b-3.rai

20 DLEDGE       -		187 VASSSS		232 -ELELE	272	272 260 OFLESS			) 362 LEKELS	334 RKELS	422 AATLA	371 EEKID	: :::  482 KEELEC	431 EAKMIN	: ; 530 EKOAOI	478		0 0 0 .	RESULT 5	-08-470-950-4 Sequence 4, A	Patent No. 56	APPLICANT:		TITLE OF II NUMBER OF :	CORRESPONDI ADDRESSE	STREET: CITY: BO	STATE: 1	ZIP: 02:	MEDIUM T	OPERATIN	SOFTWARE CURRENT AP	APPLICAT FILING D	CLASSIFI ATTORNEY/A	REGISTRA REFERENC	TELECOMMON
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MTKVK	-LPRAVNTQALSGAGIL	EALVC	: I DDAVR	HOEOA	HSQNT	NKPDK	0SE	VOTOV	KKNME	-																			÷					Length 2101;	Indels
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VPPAPI	LESSE	DOOLR	OSLLKI	LAEVE	 LIETS	KREAE	KMESDI	KTVII	ODTSAHLERMKKNMEQTIKDLOHRL							CELL TY		₽ <u>.</u>						ston		,				٠		•		145; DB 1; No. 0.0047;	. seu
HVGYI	-RAALE-RYLQRTVKHPTLLØDPDLRQFLESSE	OFENL	OVKSL	-DHTALSRALSQLAEVEEKIDQLHQEQAFADFYMFSEL	LAEQE	) 	SLINQKKKMESDLTQL	SRVKDF : I	ODT			•						THIBEAULT					w	Patentin Release #1.0, Version #1.25 CATION DATA:	390			13	•					Score 145; Pred. No.	Mismatches 188;
LASKYI   	TLIODI	FEEKO	AAEAQI	TALSR	TERSE	KWEDA(	SI	GRFEKI					. 0689		Ω.	NOVEL MALIGNANT		ᅜ					compatible PC-DOS/MS-DOS	e #1.	US/08/466,39		R 0	MTP-01	¥					អដ	TO4;
FLGLHSKI 	TVKHP	ESDAW	:: HANRM	HQ	AVVEO	МКСМО		IRKEV	LKKE-	-			4 Application US/08466390		GARY	VEL M		HURWITZ	TEET	•		disk	patib	keleas 'A:	US/08	NOI	SDMUND R	SER:	- 7000	. 4:	S: scids		_	ິດເຕັ	
FESDFL	RYLOR	NOT DE	:::		LEELR	VFDHR		CISKT	MMAEE				on US		•		6	A, HU	H STREET		0	Floppy disk	25 :: P. P. B.	otin F	÷	435 FORMAT	ESO, E	I NUM	7) 248	ID NO	RISTIC nino a	r d	protein	-	rvacı.
SKSEFSVKRF :   :: -RKQLEVEK-	RAALE-	DAVNKA	:   :   3DLNEME	ALGNSE	T-04E	FAAVKÖ		SERDFE	AITDA?	610	1806		licati	562 ATION:	TOUKATLY, LIDGARD,	ENTION	DUENCE	TESTA,	125 HIGH STON	USA		DABLE E: F]	SYSTE	Pater ICATI	N NOW	TION: NT IN	CHER	DOCKE	(61)	R SEQ	ARACTERISTICS: 2101 amino acids	amino acid Y: linear		larit	Conservative
SMFSKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTE 	FVEKR1	hebon llraudee nu raeleknijaerdeerokanningk vuosidi soldabiikskus vi RavikaadavnkatikanesDaafeekOOOFENLDOOLRKLHYSVEALVCHRKELSANTA		AFAKSAAMLGNSE	IVERRNNLL-QAELEELRAVVEQTERSRKLAEQELIETSERVQLLHSQNT-	LSDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEAKMMVANKPDKIQQAKNEIRE		WEAKVOOGERDFEDISKIRKEVGRFEKERVKDFKTVIIKYLESLVOTOOOLIKYWEAFL	AEEKAKKAITDAAMMAEELKKE	FEAKAIA SIS	AEQIA		0-4 , App.	£ 8		22	NUMBER OF SEQUENCES	吕믑	T: 125 BOSTON	₹	02110	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy	COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS	SOFTWARE: Patentin Re CURRENT APPLICATION DATA	APPLICATION NUMBER: FILING DATE: 06-JUI	CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:	NAME: PITCHER ESQ, EDMUND REGISTRATION NUMBER: 27 R	RENCE/	TELEPHONE: (617) 248-7000	IELEFAN: (11) 248-71 INFORMATION FOR SEQ ID NO:	CE CHA	: ami .OGY:	MOLECULE TYPE:	Query Match Best Local Similarity	(co.
171 SM 532		283 RM		343 AF	1675 IV	393 LSI	1724			34 FIG	1800 DE	. 4	US-08-466-390-4 ; Sequence 4, A	RAL I	APPLICANT: APPLICANT:	TLE O	MBER	ADDRE	STREET: CITY:	STATE: .	ZIP:	MEDIUM	COMPU	SOFTWARE: JRRENT APP	APPL1 FILIN	CLASS	NAME:	REFER	TELEF	TELE	EQUENCE (	TYPE: TOPOL	MOLECULE T S-08-466-390-4	y Mate Local	nea
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                          SPEREPILSSEPSPAVTPVTPTLIAPRIESKSMSAPVIFDRSREEIEEEANGDI 139
                                                                                                          SSGNN--FLSGSPASPAGDILQT-----PQFQMRRL-----KKQLADERSNRD- 231
                                                                                                                                                                    GVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSVKRRFSDFLGLHSKLASKYL 199
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                                                                                                                                                                                                                                                                                            -----LEELRDKNESLTMRL--HETLKQCQDLK 303
                                                                                                                                                                                                                                                                                                                                       SELPRAVNTQALSGAGILRMVNKAA-----DAVNKMTIKMNESDAWFEEKQQQ 312
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EDLFTSTVSTLESSPSSPEPASLPAEDISANSNGPKPTEVVLDDDREDLFAEATE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYBGA-2
OFRATION:
INTOURATLY, GARY
F: LIDGARD, GRAHAM P
INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
INVENTION: INTERIOR NUCLEAR MATRIX
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PPLICATION DATA:
TION NUMBER: US/08/470,950
DATE: 06-JUN-1995
ICATION: 536
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R: IBM PC compatible
NG SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-C
TELECOMMUNICATION INFORMATION:
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598439
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NDENCE ADDRESS:
SEE: TESTA, HURWIT:
125 HIGH STREET
BOSTON
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Floppy disk

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Sequence 4, Application US/08195487
Patent No. 5783403
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                                                                                                                                                                                                                                                                                                                                                                                                                              187 VASSSSGNN--FLSGSPASPMGDILOT----PQFQMRRL-----KKQLADERSNRD- 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---MMQQRIDRLALLNEKQAAS-- 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 LEKELSAALQDKKCLEEKNEILQGKLSQLEEHLSQLQDNPPQEKGEVLGDVLQLETLKQE 421
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APPLICAMY: TOUKATLY, GARY
APPLICAMY: *LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                      Length 2101;
                                                                                                                                                                                                                                                              Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --AKSAAMLGNSEDH----
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STREET: 125 HIGH STREET
                                                                                                                                                                                                                   5.5%; Score 145;
Similarity 18.2%; Pred. No. (
35; Conservative 104; Mismatch
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Patent No. 5780596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 --FEKERVKDFKTVIIKYLESLVQ--
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2101 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 -ELELELAENRKLLTEKDAQIA-
                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-470-950-4
                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                           105;
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                                                                                                                                                                                                                   Query Match
Best Local S
Matches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                        80
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EVSLDSPEREPILSSEPSPAVTPVTPTTLIAPRIESKSMSAPVIFDRSREEIEEEANGDI 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---MMQORIDRLALLNEKQAAS-- 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----LEELRDKNESLIMRL--HETLKQCQDLK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -TEKSOMDRKINOLSEENGDLSFKLREFASHLOOLODALNELTEEHSKATQEWLEKQAQ 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEKELSAALQDKKCLEEKNEILQGKLSQLEEHLSQLQDNPPQEKGEVLGDVLQLETLKQE 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 AATLAANNTOLOARVEMLETERGOGEAKLLAERGHFEEEKOOLSSLITDLOSSISNLSOA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEKIDQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEELEQASQAHGARLTAQVASLTSELTTLNATI-------QQQDQELAGLKQQAK 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKGAGLAGTLOQQEGASOGLRHQVEQLSSSLKQKEQOLKEVAE--KQEATRQDHAQQLAT. 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 DLEDGEDLFTSTVSTLESSPSSPEPASLPAEDISANSNGPKPTEVVLDDDREDLFAEATE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QFLESSELPRAVNTQALSGAGILRMVNKAA-----DAVNKMTIKMNESDAWFEEKQQO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---REIRFLELOK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2101;
SOFTWARE: Patentin Release #1.0, Version #1.25
UURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 104; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHEDGLNLNEDLENFLOKAPVPSTCSSTFPEELSPPSHQAK --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , DB 1;
0.0047;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 145;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --FEKERVKDFKTVIIKYLESLVQ---
                                                                                                                                                                                                                          27,829
                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: MI
FELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                    TTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND
REGISTRATION NUMBER: 27,82
                                                                                     06-JUN-1995
N: 424
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                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PLEPKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 105; Conserv
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                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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GENERAL INFORMATION:

COMPUTER READABLE FORM:

02110

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---- DAVNKMTIKMNESDAWFEEKQQQ 312
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                                                                                                                   ---TQQQL 504
                                                                                                                                                         588 AAEEREASLRERDAALKOLEALEKEKAAKLEILOOOL 624
                                                                                                                                                                                                                                                                                                                                                                                                                                          & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 145;
Pred. No. (
482 KEELEQASQAHGARLTAQVASLTSELTTLNATI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08/483,924
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
                                                                                                                                                                                                                                                      Sequence 4, Application US/08483924
Patent No. 5882876
                                                                                                                     478 --FEKERVKDFKTVIIKYLESLVQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.5%; Sc
Best Local Similarity 18.2%; Pr
Matches 105; Conservative 104;
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NAME: PITCHER ESQ, EDMUND R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 -ELELELAENRKLLTEKDAQIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 125 HIGH STREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               URRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE
                                                                                                                                                                                                                                       US-08-483-924-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-483-924-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -TALSRALSQLAEV 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEKIDQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----REIRFLELOK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 EVSLDSPEREPILSSEPSPAVTPVTPTTLIAPRIESKSMSAPVIFDRSREEIEEEANGDI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDIEIGVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSVKRRFSDFLGLHSKLASKYL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 HVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRRAALERYLQRTVKHPTLLQDPDLR 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LEELRDKNESLTMRL--HETLKQCQDLK 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----VSVEALVCH 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 LEKELSAALQDKKCLEEKNEILQGKLSQLEEHLSQLQDNPPQEKGEVLGDVLQLETLKQE 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 180; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 DLEDGEDLFTSTVSTLESSPSSPEPASLPAEDISANSNGPKPTEVVLDDDREDLFAEATE 79
                                     NOVEL MALIGNANT CELL TYPE MARKERS OF THE INTERIOR NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2101;
                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 5.5%; Score 145; DB 1; L
Best Local Similarity 18.2%; Pred. No. 0.0047;
Matches 105; Conservative 104; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 DHEDGLNLNEDLENFLOKAPVPSTCSSTFPEELSPPSHOAK--
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                                                                                                               3: TESTA HURWITZ & THIBEAULT
53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                 RIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/901,701
                                                                                                                                                                                                                                                                                                                                URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,487
                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                    IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 -ELELELAENRKLLTEKDAQIA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-195-487-4
                                                                            NUMBER OF SEQUENCES: (
                                                                                                                                                                                                                                   OMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                   ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                USA
                                                                                                                                                      BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                            02109
                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                              FILING
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--- MMQORIDRLALLNEKQAAS-- 271
--- QQQDQELAGLKQQAK 529
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                                                                                                                                                        530 EKOAQLAQTLQQQEQASQGLRHQVEQLSSSLKQKEQQLKEVAE--KQEATRQDHAQQLAT 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVSLDSPEREPILSSEPSPAVTPVTPTTLIAPRIESKSMSAPVIFDRSREEIEEEANGDI 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRRAALERYLORTVKHPTLLQDPDLR 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TILE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE TILE OF INVENTION: INTERIOR NUCLEAR MATRIX
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                                                                                      EAKMMVANKPDKIQQA----KNEIREWEAKVQQGERDFEQISKTIRKEVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.25
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271	259	303	312	361	333 421	370	481	430	229	477				•						•				}							•		
Db 232 -ELELELAENRKLLTEKDAQIA	A 1000 HVGYTVEHENSSTORMENSSSORENSSSORE OF SOLUTION OF	272PLEPKE	260 QFLESSELPRAVNTQALSGAGILRMVNKAADAVNKMTIKMNESDAWFEEKQQQ	Teksomdrkinglseengdlsfklrefashloolodalnelteehskatgewlekoao	QY 313 FEVSVEALVCH	Qy 334 RKELSANTAAFAKSAAMLGNSEDHTALSRALSQLAEV	DD 422 AATLAANNTQLQARVEMLETERGQQEAKLLAERGHFEEEKQQLSSLITDLQSSISNLSQA	371 EEKIDQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREA :   ::	482 KEELEQASQAHGARLTAQVASLTSELTTLNATIQQQDQELAGLKQQAK	OY 431 BAKWMYANKPDKIOQAKNEIREWEAKVOGGRDFEOISKTIRKEVGR D:: : : : : : : : : : : : : : : : : : :	478FEKERVKDFKTVIIKYLESLVQTQQQL 504	DD 588 AAEEREASLRERDAALKQLEALEKEKAAKLEILQQQL 624		3		Leslie	; APPLICANT: VIKSTIOM, KATEN L. ; TITLE OF INVENTION: TRANSGENIC MODEL FOR HEART FAILURE MITMORD OF CENTRANDE.	OF SECTENCES: 3 20NDENCE ADDRESS:	" ∺	9 2	r: U.S.A. 30203	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk	ER: IBM PC compatible ING SYSTEM: PC-DOS/MS-DOS	E 5	; APPLICATION NUMBER: US/08/938,105 ; FILING DATE:	CLASSIFICATION: ATTORNEY/AGENT INFORMATION:	NAME: Crook, Wannell M.	REFERENCE/DOCKET NUMBER: 3595-4 TRIECONMINICATION INFORMATION	TELEPHONE (303) 863-9700 TELEFAX: (303) 863-0223	CHAR	TYPE: amino acids TYPE: amino acid	YPE:	

Score 143.5; DB 4; Length 1886; Pred. No. 0.0054;

5.5%;

Query Match Best Local Similarity

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Identifying Pathogenic Markers In A Sample
                                                                                                                                                                                                                                                                                                                                                                                             -----EEAEASLE 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1502 HEEGKILRAQLEFNQIKAEIERKLAEKDEEMEQAKRNHLRVVDSLQTSLDAETRSRNEAL 1561
                                                                                         --VEAVNAKCSSLEKTKHRLQNEIEDLMYDVE 1382
                                                                                                                                                                                              1383 RSNAAAAALDKKQRNFDKILAEWKQKYEES-----QSELESSQKEARSLSTELFKLKN 1435
                                                                                                                                                                                                                                                                                1622 IVERRNTLL-QAELEELRAVVEQTERSRKLAEQELIETSERVQLLHSQNTSLINQKKKMD 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1738 TIKDLOHRLDEAEQIALKGGKKOLOKLEARVRELENELEAEOKRNAESVKGMRKSERRIK 1797
                                                                                                                                                                                                                                                                                                                                             171 SMFSKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTE 230
                                                                                                                                              79 EE----VSLDSPER--EPILSS-----EPSPAVTPVTPTTLIAPRIESKSMSAPVI---- 123
                                                                                                                                                                                                                                               124 ------FDRSREEIEEEANGDIFDIEIGVSD-PEKVGD-GMNAYMAYRVTTKTSL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                              231 FVEKR--RAALE-RYLQRIVKHPILLQDPDLRQFLES-----SELPRAVNTQALSGAGIL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 RMYNKAADAVNKMTIKMNESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKELSANTA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343 AFAKSAAMLGNSE------DHTALSRALS--QLAEVEEKIDQLHQEQAF----- 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384 ADFYMFSELLSDYIRLI-----AAVKGVFDHRMKC--WQKWED--AQITLLKKREAE 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432 AKMAVANKPDKIQQ-----AKNEIREWEAKVQQGERDFEQISKTIRKEVG--RFEKERVK 484
  Gaps
                                                EDLEDGEDLFTSTVSTLESSPSSPEPASLPAEDISANSNGPKPTEVVLDDDREDLFAEAT 78
201; Indels 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1798 ELTYQTEEDKKNLVR-LQDLVDKLQLKVKAYKRQAEEAE 1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       485 DF-----KTVIIKYLESLVQTQQQLIKYWEAFLPEAK 516
  Conservative 113; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            And Methods For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09104324B
Patent No. 6232460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanson, No. 6232460man D.
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                                                                                                                                                                                                                                                                                                                                                                                 | | :::||
1436 AYEESLEHLETFKRENKNLOEE-
                                                                              OPERATING SYSTĖM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wordperfect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTORNEY/AGENT INFORMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New 10103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SULT 12
3-09-104-324B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE
Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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189 VPTVSLKVSESVIDVKTTMESISNTSTOSLTAETKDIALEPKEOKHEDROSNTPSPPVST 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 DFQKLTESCCSSDAFERIDSFSVQSLDSRSVSEINSDDELSGK----GYALVPIIVNSST 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEKSIVGMTKVKVGKEDSSSTEFVEKRRAALERYLQRTVKHPTLLQDPDLRQFLESSELP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TPINEGOTVLDKVAEQCEPAESQPEALSEK----EDVCKTVEFLNEKLEKREAQLL 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALVCHRKELSANTAAFAK-SAAMLGNSEDHTALS----RALSQLAEVEEKIDQLHQEQAF 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384 ADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQ-----KWEDAQIT-LLKKREAEAKMMVA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KEIKNIKEELATRINSSETADLLKEKDEQIRGLMEEGEKLSKQQLH 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NK-----PDKIQQAKNEIREWEAKVQQGERDFEQISKTI--RKEVGRFEKERVKDFKTV 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 EREPPPLGD----GKPTDFEDLEDGEDLFT----STVSTLESSP---SSPEPASLPAED 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 FSSGISTISDIEVLDHESVISESSASSRQETIDSKSSLHLMQTSFQLLSASACPEYNRLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAVNTQALSGAGILRMVNKAADAVNKMTIKMNESDAWFEEKQQQFENLDQQLRKLHVSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SL---SKEKALLEEAFDNLKDEMFRVKEESSSISSLKDEFTQRIAEAEKKVQLACKERDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 ISAN-----SNGPKPTEVVLDDDR-----EDLFAEAT------EEVSLDSPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 PKSKTVESAEGK -- SEEVNETLVIPTEEAEMEESGRSAT -- PVNCEOPDI --- LVSS ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.0%; Score 131.5; DB 5; Length 1093; Best Local Similarity 19.2%; Pred. No. 0.024; Matches 118; Conservative 103; Mismatches 234; Indels 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGLHSKLASKYLHVGYIVPP---
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                                                                                                                                     Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                        29,775
SR: UTFD270PCT
                                                                                                                                  SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03077
FILING DATE: 19930331
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/07/862,025 FILING DATE: April 2, 1992 ATTORNEY/AGENT INFORMATION:
                                                  MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                   Kammerer, Patricia A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FELECOMMUNICATION INFORMATION TELEPHONE: 713-787-1540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1093 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 713-749-2679
                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---VSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTALSRALSQLAEVEE-KIDQLHQE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEAKMMVANKP 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 RAAHSF-----VVTEFETTVCSLEELLRTEQQ-------RLEKNEDQLKILTM--- 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 VTPTTLIAPRIESKSMSAPVIFDRSREEIEEEANGD---IFDIEIGVSDPEKVGDGMNAY 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 :-----ESKLQENRKIIEAQRKAIQELQFGNEKVSLKLEEGIQENKDLIKENNAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 M----AYRVTTKTSLSMFSKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 MTKVKVGKEDSSSTEFVEKRRALERYLORTVKHPTLLODPDLROFLESSELPRAVNTOA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 KOVSLLLIQITEKENKMKDLTFLLEESRDKVNQLEEKTKLOSENLKOSIEKOHHLTKELE 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----EEDLQIATKTICQLTEEKETQMEESNKA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 -ELOKKSSELEEMTKLTNNKEVELEELKKVLGEKETLLYEN---KOFE----KIAEELKG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SN-----GPKPTEVVLDDDREDLFAEATEE-----VSLDSPEREPILSSEPSPAVTP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 EPPPLGDGKPTDFEDL----EDGEDLFTST----VSTLESSPSSPEPASLPAEDISAN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 KPQTLG-GDSTFFKSFNKCTEDDLEFPFAKTNLSKNGENIDSDPALQKVNFLPVLEQVGN 82
                                                                                                                                                                                                                                                                                                                                                                                                      Indels 147;
                                                                                                                                                                                                                                                                                                                                           5.1%; Score 134.5; DB 4; Length 976; 18.7%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application PC/TUS9303077
GENERAL INFORMATION:
APPLICANT: &Board of Regents, The University of Texas System
APPLICANT: Gaynor, Richard B.
APPLICANT: Wu, Foon Kin
TITLE OF INVENTION: PROTEIN CELLULAR FACTOR USEFUL FOR
TITLE OF INVENTION: REGULATING GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276 LSGAGILRMVNKAADAVNKMTIKMNES----DAWFEEKOQOFENLDQOLRKLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 SDCHYQEGLKDSDLENSEGLSRVFSKLYKEAEKIKKWKVSTEAELRQK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 RHLCNLLKETCARSAEKTKKYEYEREETROVYMDLNNI-----
                                                                                                                                                                                                                                                                                                                                                                                                   Matches 103; Conservative 101; Mismatches 200;
                             LUD 5491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arnold White & Durkee
REGISTRATION NUMBER: 30,946
REFERENCE/POCKET NUMBER: LC
TELECOMMULCATION INFORMATION
TELEPHONE: (212) 318-3000
                                                                               TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                              326 DIKVSLQRSVSTQKAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P.O. Box 4433
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 FQELRVQAENS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:|:|| :|
463 TEQELIGLLQA 473
                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                      US-09-104-324B-4
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--DRVRQEEDGRHQEEERV---KRDAEEKRRQEEGYYSRLEAERRRQHEEAARRLLE 1682
                       1631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1216 ----EQTPPPRPEAYPIPTQTYTREYFTFPASKSQDRMAPVQNQWPNYEEKPHMHTESDH 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : || | || : : | : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----ELQNKGDRTAEESDRLRKLMLEWQFQKRLQESKQKDEDDDE-- 1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1272 ASIAIQRVTRSQEELREEKVYQLERHRVESGMDRKCDSDMWINQSSSVESSTSSQEHLNH 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1332 SSKSVTPASTLTKSGPGRWKTPAAVLPTPVAVSQPIRTDLPPPPPPPPPAHYTSDFDGISM 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SVKRRFSDFLGLHS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSSEPSPAVTPVT -- - PTTLIAPRIESKSMS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 KLASKYLHVGYIVPP----APEKSIVGMTKVK-----VGKEDSSSTEFVEKRRAAL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -ORTVKHPTLLQDPD---LRQFLESSELPRAVNTQALSG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---LSRALSQLAEVEEKIDQLH 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 QEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEAKMMVAN 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439 KPDKIQQAKNEIREWEAKVQQGERDFEQISKTIRKEVGRFEKERVKDFKTVIIKYLE 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 AGILRMVNKAADAVNKMTIKMNESDAWFE-----EKQQQFENLDQQLRKLHVSVEALVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1503 ITISKEELSSGDSLS-----PDPWKRDAREKLEKQQQMHIVDMLSKEIH---
                                                                                                                                                                                                                                                                                                                                                                                                              PLICANT: OBAISHI, HITOSHI
"LE OF INVENTION: ACTIN FILAMENT-BINDING PROTEIN "L-AFADIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1167 DDRLMKNRADHRSSPNVANQPPSPGGKSPYTSGTAAKITSVSTGNLCTE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDGKPTDFEDLEDGEDLFTSTVSTLESSPSSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KVGDGMNAYMAYRVTTKTSLSMFSKSEF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.0%; Score 130.5; DI
8.6%; Pred. No. 0.062
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                                                                                                                                                                                                             Sequence 1, Application US/09157420 Patent No. 6180760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US, CURRENT FILING DATE: 1998-09-21
                                                                                                                                                                                                                                                                                                     TAKAI, YOShimi
NAKANISHI, Hiroyuki
MANDAI, Kenji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.0
                 490 IIKYLESLVQTQQQ 503
                                                 || | |:|: |::
625 - IKKLNSMVERQEK 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 122; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1392 DLP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 ERYL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-157-420-1
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90 KLEAINKELNENYYKLODGIDALEKEKEDLKTTLAKTTKENEISEASRKGLSRDLEASRT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423 TLLKKREAEAKMMVANKPDKIQQAKNEIREWEAKVQQGERDFEQISKTIRKEVGR-FEKE 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KYQKLETDHQALEAKHQKLEADY-QVSETSRKGLSRDLEAS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 GAGFANQTEVRADEAKKMEVKESEKESQYKTLALRGENADLRNVNAKYLEKINAEEEKNK 89
                                                                                                               TITLE OF INVENTION: No. 5352588el Immunoglobulin A Binding Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 AKKELEAKHOKLEA--ENKKLTEGNOVSE-----ASRKGLSN--
                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 482 RVKDFKTVIIKYLESLVQTQQQLIKYWEAFLPEAKAIA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 REANKKVT----SELTQAKAQL----SALEESKKLS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 128.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4, 2003, 15:06:08
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/813,584A
                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 GAGILRMVNKAADAVNKMTIKMNESDAWF
Sequence 3, Application US/07813584A Patent No. 5352588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45:
                                                                                                                                                                                 s: Kittie Murray
98 Cutter Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.98;
llarity 22.78;
Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19911224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                       NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                           STREET: 90 TIME Great Neck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Job time: 24.9926 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 QFENLDQQLR--
                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                            11021
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

Title: Perfect score: Sequence:

2620 1 MAAEREPPPLGDGKPTDFED.....TQQQLIKYWEAFLPEAKAIA 519 US-09-763-902B-3

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188354 seqs, 42170167 residues Searched: . Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SUMMARIES

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

		æ				
Result No.	Score	Query .Match	Query Score .Match Length DB	DB	ID	Description
	327	12.5	99	9	US-09-864-761-42106	Sequence 42106, A
7	323.5	12.3	422	δ	US-10-114-893-71	Sequence 71, Appl
m	306	11.7	61	6	US-09-764-868-993	Sequence 993, App
4	248	9.5	414	10	US-09-925-302-706	Sequence 706, App
Ŋ	248	9.5	414	10	US-09-927-738-8	Sequence 8, Appli
φ	165	6.3	278	σ	US-09-764-868-1051	Sequence 1051, Ap
7	160	6.1	198	10	.US-09-927-738-7	Sequence 7, Appli
σο	139	5.3	606	О	US-09-925-299-988	Sequence 988, App
თ	139	5.3	606	10	US-09-925-299-988	Sequence 988, App
10	138.5	5.3	1805	σ	ם	Sequence 73, Appl
11	136	5.2	241	10	US-09-925-302-619	Sequence 619, App
12	135	5.2	. 294	10	US-09-927-738-9	Sequence 9, Appli
13	134	5.1	856	, 10	US-09-815-242-11489	Sequence 11489, A
. 14	134	5.1	1013	6	US-10-076-622-553	Sequence 553, App
15	134	5.1	1013	12		Sequence 553, App
16	132.5	5.1	1884	1,0		
17	132:5	5.1	1907	10		
18	132	5.0	1002	σ	US-10-076-622-475	Sequence 475, App
9	132	r.	1002			Segmence 475. App

Sednence 4/2, App		-	Sequence 275, App	Seguence 17, Appl	Sequence 16, Appl	Seguence 565, App	Sequence 565, App	Sequence 573, App	Seguence 573, App	Sequence 2, Appl1		Sequence 2, Appli		'n	Sequence 1, Appl1	Seguence 5, Appli	Sequence 73, Appl		Seguence 859, App	O1	Sequence 911, App	Sequence 911, App	Αb	Sequence 811, App	Sequence 5192, Ap
L2 US-10-007-805-475	9 US-10-076-622-493	L2 US-10-007-805-493	10 US-09-764-898-275		9 US-09-820-843A-16	9 US-10-076-622-565	12 US-10-007-805-565	9 US-10-076-622-573	12 US-10-007-805-573	9 US-09-927-597-2	9 US-09-927-597-4	10 US-09-950-046A-2	9 US-09-819-104A-5	9 US-09-742-096-3	9 US-09-882-774-1	9 US-09-742-096-5	9 US-09-893-519A-73	10 US-09-784-249-2	9 US-09-925-299-859	10 US-09-925-299-859	9 US-09-925-299-911	10 US-09-925-299-911	10 US-09-946-805-4	9 US-09-764-868-811	10 US-09-815-242-5192
					1616 9	1341 9	1341 1	1349 9	1349 1	1945 9	1979	1164 1	2462	1786	619	630	888	496	758	758 1	1242 9	1242 ]	1043	276	854
2.0	5.0	5.0	5.0	5.0	5.0	4.9	4.9	6.4	4.9	4.9	4.9	4.9	4.9	4.9	4.8	4.8	4.8	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7
132	132	132	130.5	130.5	130	129.5	129.5	129.5	129.5	129	129	128.5	128	127.5	126.5	125.5	125.5	124	124	124	124	124	123.5	123	123
20	21	22	23	24	. 25	. 26	27	28	29	30	31	32	. 33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO GENE EXPRESSION ANALYSIS BY MICROARRAY ION NUMBER: PCT/US01/00666 PCT/US01/00669 LICATION NUMBER: PCT/US01/00668 PCT/US01/00664 CON NUMBER: US 60/236,359 (TE: 2000-09-27 NUMBER: US 60/180,312 ON NUMBER: US 60/207,456 Application US/09864761 ION NUMBER: GB 24263.6 -05-26

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208 APEKSIVG-----ATKVKVGKEDSSSTEPVEKRR-------AALERYLORTVK 248
                                                                                                                                                                                                                                                                                                                               111 APTKPDFDGPREKMOKLGEGEGSMTKEEFAOMKQELEAEYLAVFKKTVSSHEVFLQRLSS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps .
                                                                               88 REPILSSEPSPAVTPVTPTTLIAPRIESKSMSAPVIFDRSREEIEEEANGDIFDIEIGVS 147
                                                                                                                                                                                                                       148 DPEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                    171. HPVLSKDRNFHVFLEYDQDLSVRRKNTKEMFG-GFFKSVVKSADEVLFTGVK--EVDDFF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 EQEKNFLINYYNRIKDSCVKADKMTRSHKNVADDYIHTAACLHSLAL----EEPTVIKKY 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 LLKKREAEAKMMVANKPDKIQQAKNEIREWEAKVQQGERDFEQISKTIRKEVGRFEKERV 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --DKARLKSKDVKLAEAHQQECCQKFEQLSESAKEELINFKRKRV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 EEKQQQFENLDQQLRKLHVSVEALVCHRKELS---ANTAAFAKSAAMLGNSEDHTALSRA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 LSQLAEVEEKIDQLHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQIT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 KRRESDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSSTEFVEKRRAALE 240
                                                                                                                                       ----IDIPDALS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 HPTLLQDPDLROFLESSE--LPRAVNTQALSGAGILRMVNKAADAVNKMTIKMNESDAWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prior application data removed – refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
IITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
          25.8%; Pred. No. 2.9e-15; ive 83; Mismatches 178;
                                                                                                                                  9 RRPLLESRVAMAAVPELLQQQEEDRSKLRSVSVDLNVDPSLQ-
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100.0%; Pred. No. 3.5e-15;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/764,868 CURRENT FILING DATE: .2001-01-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 993, Application US/09764868 Patent No. US20020168711A1 GENERAL INFORMATION:
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SEQ ID NO 993
LENGTH: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61; Conservative
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ORGANISM: Homo sapiens
       Local Similarity
les 117; Conserv
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                                                                                                                                                                                                                                     59 ERDKV----
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US-09-925-302-706
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APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6000-10A
FURENT APPLICATION NUMBER: US/10/114,893
EURRENT FILING, DATE: 2002-04-02
EARLIER APPLICATION NUMBER: 09/413,232
EARLIER FILING DATE: 1999-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 LSANTAAFAKSAAMLGNSEDHTALSRALSOLAEVEEKIDQLHQEQAFADFYMFSELLSDY 396
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OTHER INFORMATION: EST_HUMAN HIT: BE280479.1, EVALUE 2.00e-24
OTHER INFORMATION: SWISSPROT HIT: Q60396, EVALUE 5.10e-01
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EXPRESSED IN LUNG, SIGNAL = 2.5
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100.0%; Pred. No. 1.4e-16;
ive 0; Mismatches 0;
APPLICATION NUMBER: PCT/US01/00670
                                                                  PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEO ID NOS: 49117
                       FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
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owman, Michael R.
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SOFTWARE: Patentin Ver.
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JS-10-114-893-71
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
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                                                                                                                                                                                                         125 DRSREEIEEEANGDI---FDIEIGVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSVK 181
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                                                                                                                                                                                                                                                                                       24 DRGLKAINVDLQSDAALQVDISDALSERDKV-----KFTVHTKSSLPNFKQNEFSVV 75
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                              Length 414;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
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Pred. No. 0.00022;
5; Mismatches 111; Indels
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                              Score 248; DB 10;
Pred. No. 5.7e-10;
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Best Local Similarity 21.9%;
Matches 70; Conservative 5
                                  9.5%;
                                                                                                                          Conservative
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                                                                              Similarity
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                                                                                                                      92;
                                       Query Match
Best Local S
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TITLE OF INVENTION: Composistions and Methods of modulating TGF-B Signaling
FILE REFERENCE: 17633/1082
CURRENT APPLICATION NUMBER: US/09/927,738
CURRENT FILING.DATE: 2001-08-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEAKMMVANKPDKIQQAKNEIREW 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DKARAKNKDVLQA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 DRSREEIEEEBANGDI---FDIEIGVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSVK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----YLQRTVKHPTLLQDPDLRQFLESSELPRAVNTQALSGAG-- 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 RRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGK----EDSSSTEFVEKRRA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 DRGLKAINVDLQSDAALQVDISDALSERDKV-----KFTVHTKSSLPNFKQNEFSVV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 RKELSANTAAFAKSAAMLGNSEDHTALSRALSQLAEVEEKIDQLHQEQAFADFYMFSELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
CANT: Rosen et al. OF INVENTION: Nucleic Acids, Proteins and Antibodies REFERENCE: PA104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.5%; Score 248; DB 10;
ilarity 22.9%; Pred. No. 5.7e-10;
Conservative 74; Mismatches 170;
                                                                                                        CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 KYYLRESQAAKDLLYRRSRSLVDYENANKAL-
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
JS-09-925-302-706
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Best Local Similarity
Matches 92; Conserva
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FEATURE:
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454

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52
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TITLE OF INVENTION: Composistions and Methods of modulating TGF-B Signaling
FILE REFERENCE: 17633/1082
CURRENT APPLICATION NUMBER: US/09/927,738
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/119786
PRIOR PPLICATION NUMBER: PCT/US00/03561
PRIOR FILING DATE: 1999-02-11
PRIOR FILING DATE: 2000-02-11
                                                                                                                     182 RRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGK----EDSSSTEFVEKRRA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPA 208
                                                                                                                                                                                     PEKSIVGMIKVKVGKEDSSSTEFVEKRRALERYLORTVKHPILLODPDLROFLESSELP 268
                                                                                                                                                                                                                                                                                  269 RAVNTQALSGAGILRMVNKAADAVN-----KMTIKMN-----ESDAWFEEKQQQFENLD 317
                                                                                                                                                                                                                                                                                                                              ----SFSGSDVQNKLKESAQCVGDEFLNCKLATRAKDFLPADIQAQFAISRELIRNIY 242
SSEPSPAVTPVTPTLI----APRIESKSMSAPVIFDRSREEIEEEANGDIFDIEIGVSD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 DRSREEIEEEBANGDI---FDIEIGVSDPEKVGDGMNAYMAYRVTTKTSLSMFSKSEFSVK 181
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                                         SDLPTPQA--IEPQAIVQQVPAPSRMQMPQGNPLLLSHTLQELLAR---DTVQVEL---I 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 160; DB 10;
Pred. No. 0.00031;
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Publication No. US20030040617A9
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                             318 QQLRKLHVSVEALVC--HRK 335
                                                                                                                                                                                                                                                                                                                                                                                                        11 | 1 | 1 | 243 NSFHKLRXRAERIACAGHRQ 262
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SOFTWARE: Patentin version 3.1
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LENGTH: 19
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-299-988
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Best Local Similarity 20.3%; Pred. No. 0.077;
Matches 119; Conservative 102; Mismatches 260; Indels 104;
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APPLICATION NUMBER: PCT/US00/05883
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                                                         APPLICATION NUMBER: 60/124,270
FILING DATE: 1999-03-12
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                                   2000-03-08
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Db 182 AERSPNO Qy 52 ISANSNG       Db 242 ADABANQ Qy 109 IAPRIES Db 299 YLPYKTL Qy 165 TTKTSLS	Db 355 EEEERLL Qy 225 DSSSTEE Db 400 LVAREDE Qy 282 LRWVNKA Qy 282 LRWVNKA Qy 341 TAAFAKS Qy 341 TAAFAKS Oy 349 LIAAVKG		RESULT 10 US-09-820-843A-73 Sequence 73, Ap Publication No.; GENERAL INFORMA TITLE OF INVER TITLE OF INVER TITLE OF INVER CURRENT APPLIC CURRENT APPLIC CURRENT APPLIC SEQ ID NO 73 LENGTH. 1805 COGRANISM N. FENGTH: 1805 COGRANISM N. FENGTH: 1805 COGRANISM N. FENGTH: 1805 COGRANISM N. FENGTH: 1805 COGRANISM N. FENGTH: PRT ORGANISM: M. COGRANISM: M. COG	Query Match Best Local Sim' Matches 82; Oy 167 KTSLSME Db 629 KETLDQI Oy 220 KVGK
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511 AAAFEKQVLQLQASHRESEEALQKRLDEVSRELCHTQSSHA 399 LIAAVKGVFDHRMKCWQ	Db 686 AEQACKEKLHSLTQAKEESEKQLCLIEAOTMEALLALPELSVLA 730  RESULT 9 US-09-925-299-988 ; Sequence 988, Application US/09925299 ; Patent No. US20020055627A1 ; GENERAL INFORMATION: ; APPLICANT: ROSEN et al. ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies ; FILE REFERENCE: PA102 ; CURRENT APPLICATION NUMBER: US/09/925,299 ; CURRENT FILING DATE: 2001-08-10 ; PRIOR PILING DATE: 2001-08-10 ; PRIOR FILING DATE: 2001-08-10 ; PRIOR FILING DATE: 2000-03-08 ; PRIOR FILING DATE: 2000-03-08		J. DOCATION: (41) COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (47) COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (48) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (52) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (63) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (63) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids LOCATION: (63) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (125) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (125) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE	ORNATION: Xaa equals any of the naturally occurring L-amino act SITE (851) ORNATION: Xaa equals any of the naturally occurring L-amino aci ORNATION: Xaa equals any of the naturally occurring L-amino aci 5.3%; Score 139; DB 10; Length 909; Similarity 20.3%; Pred. No. 0.077; Length 909; Conservative 102; Mismatches 260; Indels 104; Gaps

3 AEREP--PPLGDGKPTDFEDLE----DGEDL--FTSTVSTLESSPS---SPEPASLPAED

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ouncil of Scientific and Industrial Research
ENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PRO
ENTION: USEFUL AS ANTI-INFECTIVES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OLTKS-FEGER------LINQREHKELVASVEKQKEILGKKLQDFSQTSL 676
                                                                                                                                                                                                                                                                                                                                                        AADAVNKMTIKM-NESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKELSAN 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKLQSSEAEVRSKCEELSGLHGQLQEARAENSQLTERIRSIEALLEAGQARDAQ 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 KVGK---EDSSSTEFVEKRRAALERYLQRIVKHPTLLQDPDLRQFLES----SELPRAV 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         677 NASKNLAEREMAIKFKEKEIEATEKQLLNDVNNAEVIQ-ADLAQLNQERSELQNA- 734
                                                                                                                                                                                                                                        SMFSKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKE 224
                                                                                                                                                                                                                                                                              ----EKAKAAAGEAKVKKQ 399
                                                                                                                                                                                                                                                                                                                             FVEKRRAALERYLORTVKHPILLODPDLRQFLESSELPRAVNTOAL---SGAGI 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAAML -- GNSEDHTALSRALSQLAEVEEKIDQLHQEQAFADFYMFSELLSDYIR 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVLQLQASHRESEEALQKRLDEVSR----ELCHTQSSHASLRADAEKAQEQQQ 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVF-----DHRMKCWQ------KWEDAQIT-----LLKKREAEAKM 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKIQQAKNEIREWEAKVQQGERDFEQISKTIRKEVGRFEKERVKDFKTV---- 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
GPKPTEVVLDDDREDLFAEATEEVSLDSPEREPILS---SEPSPAVTPVTPTTL 108
                                                                                                                                                 SKSMSAPVIFDRSRE----EIEEEANGDIFDIEIGVSDPEKVGDGMNAYMAYRV 164
                                                                                                                                                                                LVSTVGSMVFNEGEAQRLIEILSEKAGIIQDT---WHKATOKGDPV-AILKRQL
                                                                                                                                                                                                                                                                                                                                                                                                                                               --DALNQATSQVESKQNAELAKLRQELSKVSKELVEKSEAVRQDEQQRKALEAK
                                                                                           Length 1805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYLESLVQTQQ------QLIKYWEAFLPEAKAIA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.3%; Score 138.5; DB 9; 21.8%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141;
                                                                                                                                                                                                                                                              : : : | : | : : | : | LATEQEDAAVAK--SKLRELNKEMAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATION NUMBER: US/09/820,843A NG DATE: 2001-03-30 DD NOS: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09820843A
5. US20030039963A1
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RMATION: gi|1045905
73
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Conservative
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; NAME/KEY: SITE
; LOCATION: (220)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-619
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INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377 LHQEQAFADFYMFSELLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEAKMMV 436
                                                                                                                                                                                                                                                                                 170 LSMFSKSEFSVKRRFSDFLGLHSKLASKYLHVGYIVPPAPEKSIVGMTKVKVGKEDSSST 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 EFVEKRRAALERYLORTVKHPTLLODPDLRQFLESSELPRAVNTQALSGAGILRMVNKAA 289
35 -----KQRIADFHNDSLKKINEYELSLQKRLQELQTLEANQKQHSYQNQAYF 781
                                                             --QLRKLHVSVEALVCHRKELSANTAAFAKSAAMLGNSEDHTALSRALSQLAEVEEKIDQ 376
                                                                                                            782 EGELDKLNREKQAFLNLRKKQTMEVDAIKQRL----SDKHQALN---MQQAELDRKTHE 833
                                                                                                                                                                                                                                                      A-----NKPDKIQQAKNEIREWEAKVQQGERDFEQISKTIRKEVGRFEKERVKDFKTV 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 APRIESKSMSAPVIFDRSREEIEEEANGDIFDIEIGVSDPEKVGDGMNAYMAYRVTTKTS 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---SFSGSDVQNKLKESA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 SPQSNADAAGNPLLLSHTLQELLAR---DTVQVEL---IPEKKGLFLK-HVEYEVSSQ-- 77
                                                                                                                                                                                         Indels 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 DAVN-----KMTIKMN-----ESDAWFEEKQQQFENLDQQLRKLHVSVEAL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 OCVGDEFLNCKLATRAKDFLPADIQAQFAISRELIRNIYNSFHKLRXRAERI 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 619, Application US/09925302
Patent No. US20020044941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.2%; Score 136; DB 10;
21.1%; Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 EFIEARRALKRFVNLVARHPLFSEDVVLKLFL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR PLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SEQ ID NO 619
                                                                                                                                                                                                                                                                                                                                               490 IIKY -- LESLVQTQQQL 504
                                                                                                                                                                                                                                                                                                                                                                                              941 EAKQRELDKLAEKNNOV 957
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Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-09-925-302-619
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                                                             319
                                                                                                                                                                                                                                                      437
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RESULT 12

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APPLICANT: Wang, Tongwen
TITLE OF INVENTION: Composistions and Methods of modulating TGF-B Signaling
FILE REFERENCE: 17633/1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344 FAKSAAMLGNSEDHTALSRALSQLAEVEEKIDQLHQEQAFADFYMFSELLSDYIRLIAAV 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGVFDHRMKCWQKWEDAQITLLKKREAEAKMMVANKPDKIQQAKNEIREWEAKVQQGERD 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- DKARAKNKDVLQAETSQQLCCQK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 MVNKAADAVNKMTIKMNESDAWFEEKQQQFENLDQQLRKLHVSVEALVCHRKELSANTAA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.2%; Score 135; DB 10; Length 2
21.0%; Pred. No. 0.031;
tive 55; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TILE OF INVENTION: Identification of Essential Genes in TLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 EKRRAALERYLQRTVKHPTLLQDPDLRQFLESSELPRAVNTQALSGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEQISKTIRKEVGRFEKERVKDFKTVIIKYLE 495
                                                                                                                                                                                                                                                                                                                                                                                        US-09-927-738-9
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CURRENT FILING DATE: 2001-03-21
                                                                  CURRENT APPLICATION NUMBER: US/09/927,738
                                                                                                                                            PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: PCT/US00/03561
PRIOR FILING DATE: 2000-02-11
                                                                                              CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/119786
PRIOR FILING DATE: 1999-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11489, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATION NUMBER: 60/191,078
DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIOR FILING DATE: 2000-05-26
RIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITLE OF INVENTION: Prokaryotes ILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto, Robert T
Xu, H. Howard
                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 KDLLYRRSRSLVDYENANKAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zyskind, Judith W
Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 21.09
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                             LENGIH: 294
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--TLESSPSSPEPASL 47

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48 PAEDISANSNGPK---PIEVVLDDDREDLFAEATEEVSLDSPEREPILSSEPSPAVTPVT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 --DGLLKATCGMKVSIPTKALELKDMQTFKAEPPGKPSAFEPATE-MQKSVPNKALELKN 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --- MSAPVIFDRSREEIE-EEANGDIFDIE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 IGVSDPEKVGDGM---NAYMAYRVTTKTSLSMFSKSEFSVK----RRFSDFLGLHSKLA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 -- EGSPGK--DGLLKANCGMKVSIPTK-ALELMDMQTFKAEPPEKPSAFEPAIEMQKSVP 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449 --NGKLEESPDNDGFLKSPCRMKVSIPTKALE---LMDMQTFKAEPPEKPSAFEPAIEMQ 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          504 KSVPNKALELKNEQTLR---ADQMFPSESKQKNVEENSWDSESLRETVSQKDVCVPKATH 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               635 KWEQELCSVRLTLNQEEEKRRNADILNEKIREELGRIEEQHRKELE--VKQQLEQALRIQ 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 RKELSANTAAFAKSAAMLGNSEDHTALSRALSQLAEVE--EKIDQLHQEQAFADFYMFSE 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 LLSDYIRLIAAVKGVFDHRMKCWQKWEDAQITLLKKREAEAKMMVANKPDKIQQAKNEIR 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----KMEQMKK----KFCVLKKKLSEAKEIKS-----QLENQKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 ---VNKAADAVNKMTIKMNESDAWF--EEKQQQFENLDQQLRKLHVSV-EALVC----H
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                                                                                                                                                                                                                                                                          Indels 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---KISGKLEDSTSLSKILDTVHSCERARELOKDHCEORTG---
                                                                                                                                                                                                                   Length 1013;
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                                                                                                                                                                                                                                                                        204;
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                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                   Ouery Match 5.1%; Score 134; DB Best Local Similarity 20.1%; Pred. No. 0.2; Matches 123; Conservative 102; Mismatches
  NUMBER OF SEQ ID NOS: 627
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 553
LENGTH: 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 553, Application US/10007805 Patent No. US20020150581A1
                                                                                                                                                                                                                                                                                                                               8 PPLGDGKPTDFEDLEDGEDLFTSTVS
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McNeill, Patricia D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              itcham, Jennifer L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harlocker, Susan L.
Hepler, William T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 PITLIAPRI --- ESKS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jiangchun
                                                                                                                                  ; ORGANISM: Homo saplens US-10-076-622-553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502 QQLIKYWEAFL 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   693 DIELKSVESNL 703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-10-007-805-553
                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.1%; Score 134; DB 10; Length 856; Best Local Similarity 18.8%; Pred. No. 0.16; Matches 104; Conservative 86; Mismatches 163; Indels 200;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 856;
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                                                               PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.05
SEQ ID NO 11489
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Publication No. US20030023036Al
FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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APPLICANT: Persing, David H.
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: AND DIAGNOSI
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APPLICANT: Houghton, Raymond L.
                                                                                                                                                                                                                                                                                                                          , ORGANISM: Helicobacter pylori
US-09-815-242-11489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 -- EGSPGK--DGLLKANCGMKVSIPTK-ALELMDMQTFKAEPPEKPSAFEPAIEMQKSVP 388
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                                                                                                                                                                                                                                                                                                                                                                        5.1%; Score 134; DB 12; Length 1013;
ilarity 20.1%; Pred. No. 0.2;
Conservative 102; Mismatches 204; Indels 182; Gaps
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER. FILLE REFERENCE: 210121.470210
CURRENT APPLICATION UNMER: U5/10/007,805
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 593
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 1013
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                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-805-553
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Job time : 15.4234 secs
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Matches 123;
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Perfect score: 3638
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ABG65631 AAY77575 AAM79264 AAM25756 AAB69076 AAW31732 AAW31733	AAM798 AAW798 AAW320 AAM788 ABG017 AAW320	ABB 59948 ABG 05856 AAM 4 09936 AAM 4 1000 ABG 20032 ABG 20032	AAM392 AAM392 ABB590 AAW022 AAW843 AAB711 AAB623 AAR728
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## ALIGNMENTS

Corley NC,

Lal P, Bandman O, Yue H, A, Baughn MR, Patterson C;

Tang YT, La Gorgone GA,

Novel human diagno

molecules (PTAMS) given in AAY82131 to AAY82324. The PTAMS have cytostatic, antiatheratic, immunosuppressant, antiatheratic, antiatheratic, immunosuppressant, antiatheratic selectic, antiatheratic, immunosuppressant, antiatheratic, osteopathic, dermatchogical, antiatherand.

Continheumatic, osteopathic, dermatchogical, antianaemic, antipsoriatic, epatectoropic, antigout, antiinflammatory and antianomists, and uncomparate protein transport. PTAM proteins and antagnoists are useful for requisite protein transport. PTAM proteins are useful for disponsing conditions associated with decreased or increased expression or activity of PTAM. PTAM polynucleotides are useful for disponsing conditions associated with PTAM, comprising detecting PTAM by forming a hybridisation complex, preferably after PCR amplifying the biological sample. Diseases prevented, treated or diagnosed include cell proliferative disorders such as cancers, immune disorders, secretory disorders and other conditions associated with abnormal vesicle trafficking, such as allergies, asthma, urticaria and autoimmune trafficking, such as allergies, asthma, urticaria and autoimmune attrafficking or delivery mechanism for bringing pharmaceutical agents into cells or tissues expressing PTAM and for diagnosis of PTAM related disorders. PTAM, its catalytic or immunogenic fragments are useful for drug screening using libraries of compounds. PTAM polynucleotides are useful for generating pharmic sequences.

Control of generating pharmic sequences or compounds. PTAM polynucleotides are useful for generating spenomic sequences. New human protein transport-associated polypeptide and polynucleotide useful for diagnosis, prevention and treatment of cell proliferative and secretory disorders such as leukemia, cystic fibrosis AAA08035 to AAA08042 encode the human protein transport-associated Claim 1; Page 65-67; 75pp; English. WPI; 2000-256642/22 N-PSDB; AAA08039. 

Seguence

100.0%; Score 3638; DB 21; Length 719; 100.0%; Pred. No. 1,9e-253; ive 0; Mismatches 0; Indels 0; Best Local Similarity 100. Matches 719; Conservative Query Match

1 MSVDKAELCGSLLTWLQTFHVPSPCASPQDLSSGLAVAYVLNQIDPSWFNEAWLQGISED 60 a ò

PGPNWKLKVSNLKMVLRSLVEYSQDVLAHPVSEEHLPDVSLIGEFSDPAELGKLLQLVLG 120 61 61 셤 CAISCEKKÖDHIQRIMTLEESVQHVVMEAIQELMTKDTPDSLSPETYGNFDSQSRRYYFL 180

121

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SEEAEEGDELQORCLDLERQLMLLSEEKQSLAQENAGLRERMGRPEGEGTPGLTAKKLLL 240 121 181 181 g ŝ g

LOSQLEGLQEENFRLESGREDERLRCAELEREVAELQHRNQALTSLAQEAQALKDEMDEL ç 요

ROSSERAGQLEATLTSCRRRLGELRELRROVRQLEERNAGHAERTRQLEDELRRAGSLRA 360 301 301 셤

QLEAQRRQVQELQGQRQEEAMKAEKWLFECRNLEEKYESVTKEKERLLAERDSLREANEE 420

361

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ROEELORHLEDANRARHGLETQHRLNQQQLSELRAQVEDLQKALQEGGKTEDAISILLK 540 481

RRYVDKARMVMQTMEPKQRPAAGAPPELHSLRTQLRERDVRIRHLEMDFEKSRSQREQEE 660 661 KLLISAWYNMGMALQQRAGEERAPAHAQSFLAQQRLATNSRRGPLGRLASLNLRPTDKH 719 RQEELQRHLEDANRARHGLETQHRLNQQQLSELRAQVEDLQKALQEQGGKTEDAISILLK RKLEEHLQKLHEADLELQRKREYIEELEPPTDSSTARRIEELQHNLQKKDADLRAMEERY 601 601 661 엄 ò ò

ABG10025 standard; Protein; 724

13-FEB-2002

Novel human diagnostic protein #10016

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Homo saplens.

40200175067-A2

11-0CT-2001.

30-MAR-2001; 2001WO-US08631

31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.

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(HYSE-) HYSEQ INC

Liu C, Drmanac RT,

WPI; 2001-639362/73 N-PSDB; AAS74212

mutations New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity 

Claim 20; SEQ ID No 40384; 103pp; English

The invention relates to isolated polynucleotide (1) and polypeptide (II) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed egenes. (1) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (1) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess blodiversity amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO and to produce other types of data and products dependent on DNA and

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Drosophila melanogaster
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                                                                        MSVDKAELCGSLLTWLQTFHVPSPCASPQDLSSGLAVAYVLNQIDPSWFNEAWLQGISED
                                                                                 PGPNWKLKVSNLKMVLRSLVEYSQDVLAHPVSEEHLPDVSLIGEFSDPAELGKLLQLVLG
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                                    DB 22; Length 724;
                                                     Indels
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                                                      14;
                                   Ouery Match 96.3%; Score 3503.5; DB 2 Best Local Similarity 97.4%; Pred. No. 9.3e-244; Matches 705; Conservative 0; Mismatches 14;
at ftp.wipo.int/pub/published_pct_sequences
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(ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176 ABL30511), expressed DNA
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                                                                                                                                                                                                                                                                                                                       Myers EW
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11-JUL-2000; 2000US-0614150.
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WO200171042-A2.
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                                         QLENKRLCRQEAADRERQEELQRHLEDANRARHGLETQHR-LNQQQLSELRAQVEDLQKA 523
                                                                              467 EAENKALREGGGG----QTALAQLLDDANKRCENLREQLKTANERILSLSHASQSDDPIL
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                                                                                                                                                                                                                                                                                                                     Human; receptor; dlagnostic; therapeutic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell proliferative disorder; Crohn's disease; lymphoma; leukaem
acquired immune deficiency syndrome; AIDS; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human diagnostic and therapeutic polypeptide (DITHP) #27.
                                                                                                                                                                                                                                                 ETNLSAREQEILVYDAKYRKCVEKAKEVIKSIDPRIASA---
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DSLLKERDNLREAVDELKCGQLSSN---
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(11) may be used to Liedt Lustices associated with ucticasous purperious corpression by rectifying mutations or deletions in a patient's genome, that affect the activity of the DITHPS, by expressing inactive proteins or supplementing the patient's own production of them. (1) and (11) may be used to treat diseases, for example, cell proliferative disorder. Crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma, club, action and acquired immune deficiency syndrome (AIDS), lymphoma, into a host cell and culturing the cell to express the protein. (1) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in heed of restorative therefore which patients may be in heed of restorative therefore which patients may be in heed of restorative transpars. (1) may also be used as antigens in the production of antibodies against DITHPs and in assays to identify modulators of DITHP expression and activity. The anti-DITHP antibodies and antagonists may also be used to down regulate expression and activity. The anti-DITHP antibodies and antagonists may also be used as antigens in a samily and activity. The anti-DITHP antibodies and antagonists may also be used to down regulate expression and activity. The anti-DITHP antibodies and antagonists may also be used to down regulate expression and activity. The anti-DITHP antibodies and anti-DITHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    associated with inappropriate DITHP expression. For example, (I) and (II) may be used to treat disorders associated with decreased polypeptide
                                                                                                                                                                                                         fones AL;
Daffo A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotides encoding diagnostic and therapeutic proteins, e.g. enzymes, hormones and receptors, useful in diagnostics and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and proteins involved in growth and development and receptors. (I) and II) may be used in the prevention, diagnosis and treatment of diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 CAVNCEQRQEYIQAIMMMEESVQHVVMTAIQELMSKESPVSAGNDAYVDLDRQLKK---T 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to polynucleotides (I) encoding diagnostic and therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and proteins involved in growth and development and receptors. (I) and proteins involved in growth and development and receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVDKAELCGSLLTWLQTFHVPSPCASP-QDLSSGLAVAYVLNQIDPSWFNEAWLQGISED 60
                                                                                                                         PA, Banville SC, Shah P, Chalup MS, Chang SC; Amshey S, Dahl CR, Dam TC, Daniels SE; V, Fong WT, Greenawalt LB, Hillman JL, Jones AM, Rosen BH, Russo FD, Stockdreher TK, Daffo DM, Lincoln SE, Jackson S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        also be used as diagnostic agents for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                presence of DTTHPs in samples (e.g. by enzyme linked immunosorbant. assay (ELISA)). AAU19415-AAU19625 represent human diagnostic and therapeutic (DITHP) polypeptides of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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48.9%; Pred. No. 4.8e-41;
Live 62; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; Page 414-415; 522pp; English
17-MAY-2000; 2000US-0205324
                                                                  (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                              Liu TF, Roseberry AM,
Wright RJ, Yap PE, Yu
Cohen HJ, Hodgson DM,
                                                                                                                                R, Spiro PA,
D'Sa SA, Ams]
E, Flores V,
                                                                                                                                                                                                                                                                                                                                                               2001-502867/55.
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Matches 135; Conserv
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Dufour GE,
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SEEAEEG----DELQQRCLDLERQLMLLSEEKQSLAQENAGLRERMGRPEGEGTPGLTA- 235 237 TEELNEALSAKEEIAQRCHELDMQVAALQEEKSSLLAENQVLMERLNQSDSIEDPNSPAG 296

KKLLLLOSQLEQLQEENFRLESGREDERLRCAELER 271 

297

236

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AAM78520 standard; Protein; 990

RESULT 6 AAM78520 (first entry)

06-NOV-2001

AAM78520

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forensic; gene therapy; chromosome mapping; signal peptide; probate a regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acids encoding human secreted proteins - obtained from cDNA libraries prepared from kidney, fetal kidney, dystrophic muscle, muscle and heart tissue
                                                                                                                                                                                                                                                                                                                              Human; secreted protein; EST; expressed sequence tag; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    reproductive hormone regulation; chemotactic; chemothrombolytic; anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                    Human 5' EST secreted protein SEQ ID NO: 562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 34; Page 615-616; 622pp; English.
                                                       AAY12249 standard; Protein; 105 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-IB01238
                                                                                                                                                                             (first entry)
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N-PSDB; AAX41082.
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                                                                                                               AAY12249,
RESULT 5
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Lacroix B;

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AAX40826 to AAX41093 represent 5' expressed sequence tags (ESTs) for human secreted protelns, and encode the proteins given in AAY01602 and AAX11994 to AAX12260, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and thereto proteins obtained may have cytokine activity, cell proliferation/differentiation activity, hemotopies is regulating activity, tissue growth requiating activity, reproductive hormone continuour inhibition activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into
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ö Query Match 14.2%; Score 516; DB 20; Length 105; Best Local Similarity 100.0%; Pred. No. 1e-29; Matches 102; Conservative 0; Mismatches 0; Indels 74 MVLRSLVEYSQDVLAHPVSEEHLPDVSLIGEFSDPAELGKLLQLVLGCAISCEKKQDHIQ 133 

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29;

Gaps

Indels 160; Length 990;

11.5%; Score 420; DB 22; ilarity 23.5%; Pred. No. 1.6e-21; Conservative 156; Mismatches 270;

Similarity

Best Local Sim Matches 180;

990 AA;

Sequence Query Match

Gaps

-- LSSGLAVAYVLNQIDPSWFNEAWLQGISEDPGP -63

LLTWLQTFHVPSPCASPQD----

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> RIMTLEESVQHVVMEAIQELMTKDTPDSLSPETYGNFDSQSR 175 134 61 ö

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM8323-AAM830302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The production of other cytokines in other cell populations. The peptides and polypeptides are useful in gene therapy, vaccines or peptide therapy The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, itssue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Мa
                                                                Human, cytokine, cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Asundi V, Zhou
Wang J, Zhang J, Ren F, C
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 3425-3427; 6221pp; English.
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Wang D, Wang J, Zh
Yang Y, Wejhrman T,
Human protein SEQ ID NO 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0654936
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N-PSDB; AAK51653.
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                                                    GCAISCEKKQDHIQRIMTLEESVQHVVMEAIQELMTKDTPDSLSPETYGN---FDSQSRR 176
                                                                                                                                                                                                                                                                                  373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             508 LONCONLSKDIMKEKAQLEKTIETLRENSERQIKILEQEN--EHLNOTVSSLRQRSQISA 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EELEPPIDSS-----TARRIEELQHNLQKKDADLRAMEERYRRYVDKARMVMQTMEPKQ 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKENELLOKKITULKITCEKIEA - - - LEQENSELERENRKLKKTLDSFKNLTFQLESLE 680
                           --SLRMHNLSILVRQIKFYYQETLQQLIMMS-LPNVLIIGKNPFSEQGTEEVKKLLLLLL 116
NWKLKVSNLKMVLRSLVEYSQDVLAHPVSEEHLPDVSLIGE--FSDPA--ELGKLLQLVL 119
                                                                              117 GCAVQCQKKEEFIERIQGLDFDTKAAVAAHIQEV-----THNQENVFDLQWME
                                                                                                                            ---TAKKLLLLQSQLEQLQEENFRLESGREDERLRCAELEREVA
                                                                                                                                                                                                                          ELQHRNQALTSLAQEAQALKDEMDELRQSSERAGQLEATLTSCRRRLGELRELRRQVRQL
                                                                                                                                                                                                                                         ---LRAQL-----EAQRRQVQELO
                                                                                                                                                                                                                                                                                                   GOROEEAMKAEKWLFECRNLEEKYESVTKEKERLLAERDSL-REANE----ELRCAQLQP
                                                                                                                                                                                                                                                                                                                                                                                                                        QSLTKTVEELRTTVDSVEGNASKI ------LKMEKENQRLSKKVEILENEIVQEKQS
                                                                                                           177 YYFLSEEAEEGDELQQRCLDLERQLMLLSEEKQS---LAQENAGL----RERMGRPEGEG
                                                                                                                                                                                             SPGMKRTESROHLSVELADAKAKIRRLRQELEEKTEO--LLDCKOELE-----OMEIELK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation;
vaccine; peptide therapy; stem cell growth factor; haematc
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       619 RPAAGAPPELHSLR---TQLRERDVRIRHLEMDFEKSRSQREQEEK 661
                                                                                                                                                                                                                                                                                                                                                                                              RGLTQADPSLDPTSTPVDNLAAEILPAELRETLLRLQLENKRL-
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03-FEB-2000; 2000US-0496914.

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAW18323-AAM80302) that exhibit activity elating to encoded polypeptides (AAW18323-AAM80302) that exhibit activity elating to expokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment of cancer, leukaemia, nervous system disorders, arthritis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 LKVSNLKMVLRSLVEYSQDVLAHPVSEEHLPDVSLIGE--FSDPA--ELGKLLQLVLGCA
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                                                                                                                                                                                                                                                                                    C, Cao Y,
Wang ZW;
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R,
                                                                                                                                                                                                                                                                                 ', Asundi V., Zhou P,
Zhang J, Ren F, Chen
', Goodrich R,
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                                                                                                                                                                                                                                                                                 Liu C, Drmanac RT,
Wang D, Wang J, 'Zh
Yang Y, Wejhrman T,
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                                                                                                           2000US-0663561
2000US-0693325
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N-PSDB; AAK52637.
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
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Zhao QA,
                                                                                                                                                                                                                                                                                                                                                Kue AJ,
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Matches
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(PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, cytokine, cell proliferation, cell differentiation, growth factor,
haematopolesis regulation, tissue growth, immunomodulator, activin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                         EPPTDSS-----TARRIEELQHNLQKKDADLRAMEERYRRYVDKARMVMQTMEPKQRPA 621
                               ---RERQEELQRHLEDANRARHGLETQHRLNQQQLSELRAQ 516
                                                        452 CONLSKDIMKEKAQLEKTIETLRENSERQIKILEQEN--EHLNOTVSSLRORSQISAEAR 509
                                                                                        517 VEDLQ----KALQEQGGKTEDAISIL-----LKRKLEEHLQKLHEADLELQRKREYIEEL 567
                                                                                                                                                                   ----LKMEKENORLSKKVEILENEIVOEKOSLON 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibin, chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; ell culture; drug screening; gene therapy; antinfiammatory; antiasthmatic; antiathritic; haemostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                                                                                                                                                                                                            622 AGAPPELHSLR---TQLRERDVRIRHLEMDFEKSRSQREQEER 661
                                                                                                                                                                                                                             SQLDBENLELRRNVESLKCASMKMAQLQLENKELESEKEQLKK 667
                                                                                                                                                                                                                                                                                                                                                                                                             Human hook2 protein homologue, SEQ ID NO:2585.
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                                                                                                                                                                                                                                                                                                                 ABB12215 standard; peptide; 169 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intifungal; vulnefary; antiulcer.
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27-APR-2000; 2000US-0560875.
401 TKTVEELRTTVDSVEGNASKI-
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N-PSDB; ABA09459.
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polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; anamaropotasis regulatory activity; itssue growth activity; immunomodulatory activity; activity is the inmunomodulatory activity activity changes activity changed activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or
                                                                                                                                                                                                                                                                                                                                                                thrombolytic activities; receptor or ligand activities; or may be involved in oncogenees; cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, heamatopoletic disorders (e.g., maploid or lymphoid cell disorders, inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures thromote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSVDKAELCGSLLTWLQTFHVPSPCASPQDLSSGLAVAYVLNQIDPSWFNEAWLQGISED 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  screening techniques. The present sequence represents a novel human polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.4%; Score 380; DB 22; Length 169; larity 97.2%; Pred. No. 1.2e-19; Conservative 2; Mismatches 0; Indels
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nes 69; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL0156-ABL30511), expressed DNA sequences (ABL016176-ABL30511), expressed DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : |:: ||| : | :| | : :|| | : :|| | :|| | :|| | :|| | :|| | :| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| | :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| 
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EDSLERLTPQS------MYTHILRLTKERDVMYLKWID------LACVETEMTASDN 217
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                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 552; 21pp + Sequence Listing; English.
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    EW.
        Myers
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    Li PWD,
        Adams M,
                                                                                   2001-656860/75.
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Matches 178;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes; polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in generating antibodies against it, detecting or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quantitating a polypetide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical mingding of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human
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644
                                                           600 ELEQYLEKSRQYELTKQKLYEIEARVSTYERENASLLKEVSKLKEGSEQKSVQLDDSINR 659
                                                                                                                                                                                                                         660 IDVQSKELQKLGKALEDSEQVHQKLVELEKQNQELA-SQRIIDQEMISTLRNDLVTGTLV 718
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                                                                                                                                                  KSRSQREQ-EEKLLISAWYNMGMALQQRAGEERAPAHAQSFLAQQRLA
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N-PSDB; AAS71389.
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                                                                               LMTKDTPDSLSPETYGNFDSQSRRYYFLSEEAEEG----DELQQRCLDLERQLMLLSEEK 208
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                                                                                                209 OSLAQENAGLRERMGRPEGEGTPGLTA-KKLLLLQSQLEQLQEENFRLESGREDERLRCA
                                                                                                                                                            SSLLAENQVLMERLNQSDSIEDPNSPAGRRHLQLQTQLEQLQEETFRFLLSAVD-----
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                                                       Indels 152;
                          DB 22; Length 320;
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                                       ; Pred. No. 5.3e-19.
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                         similarity 30.38;
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ELOKKRAIIEDLEPRFNNS 304
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                                                     Matches 133; Conservative
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320 AA
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breast-specific polypeptides (BSP). Also included are a method for chermining the BSNA in a sample, a vector comprising a BSNA, a host cell comprising the vector, a method for producing a polypeptide encoded by a BSNA, an anti-BSP antibody and a method for determining the presence of a BSP in a sample. The breast-specific nucleic acids, polypeptides and compositions comprising them are useful for identifying, diagnosing, monitoring, staging, identifying breast cancer, mammary tumour and non-cancerous disease states in breast tissue; for identifying breast tissue; for monitoring, identifying and/or designing agonists and cantagonists of the polypeptides; in gene therapy; in producing transgenic animals and cells; for producing engineered breast tissue for retarment and research; and as elements in an array or computer program for pattern recognition of breast disorders. The nucleic acids may be used as the state of the polypeptidisting nucleic acids in, and isolate hybridising nucleic acids from, both genomic and transcript-derived nucleic acids amples. The BSP protein of the present sequence is BSP protein of the present acids in an array or canging an immune the process against breast cancer. The present sequence is BSP protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1680 --LMQERAEEGKGPSKAQRGSLEHMKLILRDKEKEVECQQEHIHELQELKDQLEQQLQGL 1737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LLLSQREQEIVVLQQQ---LQEAREQGELKEQSLQSQLD 1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHI-----SLSPETYGNFDSQRR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 CRNLEEKYESVTKEKERLLAERDSLREANEELRCAQLQPRGLTQADPSLDPTSTPVDNLA 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HITODLERRDQELMLQKERIQ---VLEDQRTRQTKILDEDLEQIKLSLRERGRELTTQRQ
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specific nucleic acids (BSNA) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.3%; Score 339.5; DB 23; ilarity 23.7%; Pred. No. 3.1e-15; Conservative 114; Mismatches 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----DELQQRCLDLERQLML---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1591 SHSTVLARELQERDOEVKSQREQIEEL
he invention relates to breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 166; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2383 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177. YYFLSEEAEEG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1738 HRKVGETS---
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219 RERMGRPEGEGTPGLTAKKLLLLGSQLEQ----LQEENFRLESGREDERLRCAELEREVA 274
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2000US-0693325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-2000;
                                                                                                                                                                                                                                                        510 LSE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5-SEP-2000;
0-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-FEB-2000;
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20-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides human cytoskeletal proteins (HCYT) and nucleic acids encoding the proteins. The HCYT polypeptides can be expressed by standard recombinant methodology. The HCYT polypeptides, modulators and antibodies are useful for treating or preventing a disorder associated with decreased and increased expression or activity of HCYT in mammals. The polypeptides are also useful for diagnosing HCYT activity disorders such as cell proliferative, immunological, reproductive, developmental and nervous disorders. Sequences AAY77569-576 represent HCYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cytoskeletal proteins useful for diagnosing, treating preventing cell proliferative, immunological, reproductive, developmental and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---- QRQK 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reproductive; nervous disorder; cytostatic; immunosuppressive; anti-HT anti-diabetic; anti-Inflammatory anti-infertility; vasotropic; cardiant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 YYFLSEEAEEG------DELQQRCLDLERQLML-----LSEEKQSLAQENAGL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 DHI------QRIMTLEESVQHVVMEAIQELMTKDTPD-----SLSPETYGNFDSQSRR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 SNLKMVKRSLVEYSQDVLAHPVSEEHLPDVSLIGEFSDPAELGKLLQLVLGCAISCEKKQ 129
                                                                                                                                                                                protein; HCYT; cell proliferation; immunological;
                                                                                                                                                                                                                                                                                                                                                                                                                          Azimzai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; Length 2442;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Guegler KJ,
   : | | : | | : | | : | | : | | : | | : | | ----RLQAALRQTEAREIEWREKAQDLALS-LAQTKASVSS 2164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.3%; Score 339.5; DB 21; 23.7%; Pred. No. 3.2e-15; tive 114; Mismatches 224;
                                                                                                                                                       Human cytoskeletal protein (HCYT) (clone 1655208)
                                                                                                                                                                                                                                                                                                                                                                                                                         Yue H, Corley NC,
Baughn MR;
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                                                                               2442
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                                                                                                                                                                                                                                                                                                                                               98US-0155185.
98US-0160081.
98US-0155228.
                                                                             Protein;
                                                                                                                                                                                                                                                                                                                       99WO-US17167
                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 166; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-195297/17
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                                                                            AAY77575 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nervous disorders
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Patterson C,
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                                                                                                                                                                                                                                                Homo saptens
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19-AUG-1998;
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                                                                                                                                08-MAY-2000
                                                                                                                                                                                                                                                                                               10-FEB-2000
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                                                                                                        AAY77575;
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                  2129
                                                       RESULT 12
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cell differentiation; gene therapy;
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                                                                                ---LLLSQREQEIVVLQQQ---LQEAREGGELKEQSLQSQLD 1806
                                                                                                                                                                                                     1867 QARRLEEELAVEGRRVQALEEVL---GDLRAESREQEKALLALQQQCAEQAQEHE---VE 1920
                                                                                                                                                                                                                                                    390 CRNLEEKYESVTKEKERLLAERDSLREANEELRCAQLQPRGLTQADPSLDPTSTPVDNLA 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555 LELORKREYIEELEPPIDSSTARRIEE----LOHNL--OKKDADLRAMEERYRR----YV 604
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                                                                                                                                                                                                                                                                                                                                                    450 AEILPAELRETLLRLQLENKRLCRQEAADRERQEELQRHLEDANRARHGLETQHRLNQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- LRAQVEDLQKALQEQGGKTEDAISILLKRKLEEHLQKLHEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          605 DKARMVMQTMEPKQRPAAGAPPELHSLRTQLRERDVRIRHLEMDFEKSRSQREQEEKLLI
                                                   275 ELQ----HRNQALTSLAQEAQALKDEMDELRQSSER-AGQLEATLTSCRRLGELRELRR
                                                                                                                                                      330 OVROLEERNAGHAERTROLEDELRRAGSLRAQLEAORROVOELOGGROEEAMKAEKWLFE
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Zhang J, Ren F, Chen R, Wang 2W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytokine; cell proliferation; cell differentiation; vaccine; peptide therapy; stem cell growth factor; haemato tissue growth factor; immunomodilatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       665 SAWYNMGMALQQRAG-----EERAPAHAQSFLAQQRLAINS 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM79264 standard; Protein; 1203 AA
                                                                                                                                                                                                                                                                                                   1921 TRALODSW----LOAGAVLKERDGELEA--
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Wang J, 2
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Wang D,
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Zhao QA,
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us-09-763-902b-5.rag

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                      activity, tissue growth factor activity, immunomodulatory activity and activiny and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inflammation.
Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
(AAM80020) are omitted as the relevant pages from the sequence listing
                                                                                                                Nucleic acids encoding polypeptides with cytokine-like activities
Goodrich R;
                                                                                                                                                                                   Claim 20; Page 4327-4329; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  were missing at the time of publication
                                                                                                                                       useful in diagnosis and gene therapy -
Xue AJ, Yang Y, Wejhrman T,
                                            WPI; 2001-476283/51.
                                                                  N-PSDB; AAK52397
                                                                                                                                                                                                                                                                                                                                                                                                                                                       reatment of
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1203 AA; Sequence

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30;
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                                                                                                                                                                                                                                                                                                                                                                                                                 371 ELQGQRQEEAMKAEKWLFECRNLEEKYESVTKEKERLLLAERDSLREANEELRCAQLQPRG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 LQGISEDPGPNWKLKVSNLKMVLRSLVEYSQDVLAHPVSEEHLPDVSLIGEFSDPAELGK 113
                                                                                                                                              561 LEETSEETG-RWOSMFOKNKEDLRAT---KOELLOLRMEKEEMEE------ELGE 605
                                                                                                                                                                                                                               606 KIEVLQRELEQARASAGDTRQVEVLKKELLR-TQEELKELQA-----BRQSQEVAGRHRDR 660
                                                                                                                                                                                                                                                                                    174 --SRRYYFLSEEAEEGDELQQRCLDLERQLMLLSE--EKQSLAQENAGLRERMGRPEGEG 229
                                                                                                                                                                                                                                                                                                                                                                                    230 TPGLTAKKLLLLQSQLEQLQEEN--FR------LESGRE--DERLRCAELE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 REVAELQHRNQALT-----SLAQEAQALKDEMDELRQSSERAGQLEATLTSCRRLGE 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRE-LRROVROLEERNAGHAERTROLEDELRRAG-----SLRAQL----EAQRRQVQ 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              525 QEQGGKTEDAISILLKRKLEEHLQKLHEADLELQRKREYIEELEPPTDSSTARRJEELQH 584
                                                                                                                                                                                            114 LLQLVLGCAISCEKKQDHIQRIMTLEESVQHVVMEAIQELMTKDTPDSLSPETYGNFDSQ 173
                                                                                                                                                                                                                                                                                                                  / Match 9.3%; Score 338.5; DB 22; Length 1203; Local Similarity 24.4%; Pred. No. 1.5e-15; nes 175; Conservative 127; Mismatches 271; Indels 143; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTQ----ADPSLDPTSTPVDNLAAEI--LPAELRETLLRLQLENKRLCRQEAADRERQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         585 NLOKKDADLRAMEERYRRYVDKARWYWQTMEPKQRPAAGAPPELHSLRTQLRERDVRIRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1062 QAE -- EREKTVLOSTNRKLE -- - RKVKELSIQIEDEROHV -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQRHLEDANRARHGLE - - - - TQHRLNQQ - -
                             Best Local Sim
Matches 175;
       Query Match
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heumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction

infections, autoimmunity, genetic diseases, haematopoletic disorder

cardiac anaphylaxis,

neuropathology,

viral, bacterial

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AAM25966 to AAM99904 encode the human proteins given in AAM25255 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antinfinamatory: antinheumatic; antintiamatory: antinheumatic; cardiamusouppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; antibacterial; endocrine; cardiants antianaemic; antiaggregant; haemostatic; vulnerary: antiulcer; osteopathic; dermatological; antidalpergic; antiagmatic; antidabetic; cytostatic; neuroprotective; antidapressant; nootropic; antidabetic; cytostatic; neuroprotective; antidapressant; nootropic; antidabetic; cytostatic mumanostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroprotective, antidepressant, nootropic; antiparkinsonian; infection, immunostimulant; gene therapy; antisense therapy; vaccine; inflammation antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
1097 NDQKDQLSLRV--KALKRQVDEAEEEIERLDGLRKKAQREVEEQHEVNEQLQ---ARIKS 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antlinflammatory; antirheumatic; antiarthritic; immunosuppressive;
antibacterial; endocrine; cardiant; central nervous system; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genetic disease, haematopoletic disorder; platelet disorder; asthma, thromboytopaenia, osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; allerimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection
                                                                                                                                                                                 1152 LEKDSWRKASRSAAE----SALKNEGLSSDEEFDSVYDPSSIASLLTESNLQTSS 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; ulcer; HIV infection; human immunodeficiency virus;
                                                                                      645 LEMDFEKSRSQREQEEKLLISAWYNMGMALQQRAGEERAPAHAQSFLAQQRLATNS 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein sequence SEQ ID NO:1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 262; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             AAM25750 standard; Protein; 1879 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lang YT, Llu C, Drmanac RT;
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2000US-0488725.
2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurological disorder.
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N-PSDB; AAH99691.
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21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM25750;
                                                                                                                                                                                                                                                                                                                  RESULT 14
AAM25750
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SEQ ID NO:2

protein

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Human male enhanced antigen-2 (MEA-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1605 AAEEGRKQADLE---KEELAEELASSLSGRNALQDEKRRLEARIAQLEEELEEEOGNMEA 1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1662 MSDRVRKATOQAEQLSNELATERSTAQKNESARQQLERQNKELRSKLHEMEGAVKSKFKS 1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1722 TIAALEAKIAQLEEQVEQEAREKQAATKSLKOKDKKLKEILLQVEDERKMAEQYKEQAEK 1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1545 GRGGKAIKQLRKLQAQMKDFQRELEDARASRDEIFATAKENEKKAKSLEADLMQLQEDLA 1604
                                                                                                                                                                                                                                 EMRQKHAQAVQSLTEQLEQXKRAKANLDKNKQTLEKENTD-LAGELRVLGQAKQEVEHRM 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            507
                                                                                                                                                                                                                                                                                                                          LQSQLEQLQEENFRLESGREDERLRCAELEREVAELQHRNQALITSLAQEAQALKDEMD-- 298
     burns, ulcers
                                                                                                                                                                                                EKKQDHIQRIMTLEESVQH-----VVMEAIQELMTKDTPDSLSPETYGNFDSQSRRYYFL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                           --AERTR-QLEDELRRAGSLRAQLEAQRRQVQELQGQRQEEAMKAEKWLFECRNLEEKY- 397
                                   depression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ADLELQRKREYIEELEPPTDSSTA------RRIEELQHNLQKKDADLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----DVRIRHLEMDFEK -----SRSQREQEEKL ---LISAWYNMGMALQQRAGEER
                                                                                                                                                                                                                                                                                   --RELRROVROLEERNAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKLEKTKNRLQQEL---DDLVVDLDNQRQLVSNLEKKQR----KFDQLLAEEKNISSKYA
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                                                                                                                                                                                                                                                                                                                                                            ---LLQEESRQKLNVSTSLRQLEEERNSLQDQLDEE
                                                                                                                                                                                                                                                                                                                                                                                                                            MEAKQNLERHISTLNIQLSDSKKKLQDFASTVEALEEGKKRFQKEIENLTOQYEEKAAAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ADPSLDPTSTPVDNLAAEILPAELRETLLRLQLENKRLCRQE-----AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PQLSELRAQVEDLQKALQEQGGKTEDAISILLK-----RKLEEHLQKLHE---
                      allergic
                                                    disease, Parkinson's disease, neurodegenerative and
                                                                                                                                Length 1879;
                                                                                                                                                                  Indels
                    osteoporosis, severe combined immunodeficiency, eczema, rhinitis, asthma, diabetes, cancer, multiple sclerosis, Alzheimer's disease, Parkinson's disease, neurodegenerat
     thrombocytopaenia, wounds,
                                                                                                                                  ; DB 22;
4.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEERYRRYVDKARMVMQTMEPKQRPA---AGAPPELH-
                                                                                                                                8.9%; Score 322; DB
ilarity 21.1%; Pred..No. 4.1e-
Conservative 132; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRERGEELQRHLEDANRARHGLETQ - - - HRLNQ - -
                                                                                                                                                                                                                                                                                                                                                                                              -ELROSSER-AGQLEATLTSCRRRGEL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ORLAINSRR 702
     platelet disorders,
                                                                   neurological disorders
                                                                                                   1879. AA;
                                                                                                                                                                                                                                                                                                                                                              LSSOLODTOE---
                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            683 APAHAQSFLAQ-
                                                                                                                                                                  Matches 158;
                                                                                                       Sequence
                                                                                                                                       Query Match
                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208
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                                                                                                                                                                                                    126
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AAB69070 standard; Protein; 1374 AA

AAB69070

(first entry)

19-APR-2001

AAB69070

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(MEA-2). The present invention also described an antibody specific for the MEA-2 protein. The antibody can be used for the identification of egene causing diseases related to spermatogenesis. The MEA-2 nucleotide sequence is useful as a chromosome marker, and in the detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOEALAAKEAADAELGQLRAQGGSSDSSLALHERIQALEAELQAVSHSKTLLEKELQEVI 1053
Human; male enhanced antigen-2; MEA-2; identification; spermatogenesis; spermatogenesis disease; chromosome marker; pancreatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QEENFRLESGRED-----ERLRCAELEREVAELQHRNQALTSLAQEAQALKDE----- 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSLRAQLEAQRROVQELQGQRQEEAMKAEKWLFECRNLEEKYESVTKEKERLLAERDSLR 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EANEALKKOIEELOOEARKAITEOKOKMRRLGSDLTSAOKEMKTKHKAYEN-AVGILSRR 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 KLKVSNLKM"VLRSLVEYSQDVLAHPVSEEHLPDVSLIGEFSDPAELGKLLQLVLGCAIS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                   for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - OHVVMEAIQELMTKDTPDSLSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              717 LOSREQSLDALQTHYDELQARLGELQGEAASREDTICLLQNEKIILEAALQAAKSGKEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRGARRLEEGTEETSETLEKLR-EELAIKSGOVEHLQQETAALKKQMQKIKEQFLQQKVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDELROSSERAGOLEATLTSCRRRL-GELRELRROVROLEERNAGHAERTROLEDELRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --LHREVAQVRQHMADLEGHLQ----SAQK----ERDEMETHLQSLQFDKEQMVA----VT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --LIQADPSLDPTSTPVDNLAAEILPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENVSLSQQLTETQHRSMKEKGRIAAQLQGIEADMLDQEAAFMQIQEAKTMVEED--LQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---EEGDELQQRCLDLERQLMLLSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        male enhanced antigen-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --LRERMGRPEGEG-----TPGLTAKKLLLLQSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   nsefnl
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4.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                A new protein, human male-enhanced antigen-2, spermatogenesis diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 24.0%; Pred. No. 4.5e
Matches 187; Conservative 129; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.8%; Score 319; 24.0%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 12-15; 21pp; Japanese.
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Search completed: March 4, 2003, 14:58:45 Job time: 71.5679 secs

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OM protein	OM protein - protein search, using sw model
Run on:	March 4, 2003, 14:53:52; Search time 32.3446 Seconds (without alignments) 2137.006 Million cell updates/sec
 Title: Perfect score: Sequence:	US-09-763-902B-5 DIE: 3638 1 MSVDKAELCGSLLTWLQTFHSRRGPLGRLASLNLRPTDKH 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

RESULT 1 \$28589 trichohyalin - rabbit trichohyalin - rabbit trichohyalin - rabbit trichohyalin - rabbit C.Species: Oryctolagus cuniculus (domestic rabbit) C.Species: 12-Mar-1993 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999 C.Accession: \$28589 Rybfietz, M.J.; Rogers, G.E. Rybfietz, M.J.; Rogers, G.E. Rybmitted to the EMBL Data Library, December 1992 A.Bescription: Examination of the gene encoding rabbit trichohyalin. A.Reference number: \$28589 A.Accession: \$28589 A.Molecule type: DNA	A; Residues: 1-1407 <fie> A; Cross-references: EMBL:219092; NID:91746; PIDN:CAA79519.1; PID:91747 C; Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root C; Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root C; Genetics: C; Genetics: 46/3 C; Superfamily: trichohyalin; calmodulin repeat homology C; Keywords: calcium binding; citrulline; EF hand; hair; tandem repeat F; 49-81/Domain: calmodulin repeat homology <ef2></ef2></fie>	Query Match Best Local Similarity 25.5%; Pred. No. 1.9e-08; Matches 164; Conservative 110; Mismatches 262; Indels 108; Gaps 21;	129 QDHIQRIMTLEESVQHVVMRAIQELMTKDTPDSLSPETYGNFDSGSRRYYFLSEEAEE 186 	187 GDELOQRCLDLERQLMLLSEEKQSLAQENAGIRERMGRPEGEGTPGLTAKK 237	238 LLLLOSOLEGLOBENFRLESGREDERLRCAELEREVAELQHRNOAL 283 	284 TSLAQEAQALKDEMDE	331 VRQLEERNAGHAERTRQLEDELRRAGSLRA	371 ELGGGRQEEAMKAEKWLFECRNLEEKYESVTKEKERLLAERDSLREANEELRCAOLQPRG 430	431 LTQADPSLDPTSTPVDNLAAEILPAELRETLLRLQLENKRLCRQEAADRERQEELQRH 488   :     :   :   :   :
RESULT S28589 tricho C; Spec C; Date C; Atce R; Fice R; Fice Fice R; Fice Fice Fice Fice Fice Fice Fice Fice	A) Res A) Crom C) Com C) Gen C) Gen A) Int C) Sup C) Sup	Que Bes Mat	Qy Db	Qy	Qy	Oy Op	Qy Qq	OX OD	ογ
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	1741 477 1801	516 QVEDLOKALQEOGGKTEDAISILLKRKLEEHLOKLHEADLELORKREYIEELEPPTDSST	OY 5/0 AKALEELUHNLUKKDADLKAMEERYRRYUDKA	75 OORAGEERAPAHAOSFLAOORLATNS 700 	0 d 0 0 0 2 3 4 4 4	A; Molecule type: mRNA A; Residues: 1-4574 <mcl> A; Cross-references: EMBL:U53204; NID:g1 C; Genetics: A; Gene: PLEC1 C; Superfamily: plectin; alpha-actinin a F; 68-283/Domain: alpha-actinin actin-bi</mcl>	Query Match 9.4%; Score 343.5; DB 2; Length 4574; Best Local Similarity 23.2%; Pred. No. 3.6e-07; Matches 184; Conservative 126; Mismatches 263; Indels 221; Gaps 32; Qy 67 LKVSNLKMVLRSLVEYSQDVLAHPVSEEHLPDVSLIGEFSDPAELGKLLQLVL 119	QY         120 GCAISCEKKODHIQRIMTLEESVQHVVMEAIQELMTKDTPDSLSPETYGNFDSQSRRYYF         179           ::	QY         213 QENAGLERAGRPEGEGTPGLTAKKLLLLQSQLEQLQEENFRLESGREDERLRCAEL 269	OY 304 SERAGOLEATLISCRRRIGELRELRRQVRQLEERNAGHAERTROLEDELRRAGSL 358
Db 520 QTWRWQLQEEAQRRRHTLYAKPGQQEQLREEEELQREKRQEREREYREEEKLQRE 575	OY 489 LEDANRARHGLETOHRLNOQOLSELRAQVEDLOKALOEQGGKTEDAISILLKRKL 543	Db 631 REEEQLLRQEEQEIRQERE	Db 675 REEEQLLQEREEERLRRQERARKLREEEQLLRQEEQELRGERERKLREEEQL 726  Qy 664 ISAWYNWGWALQORAGEERAPAHAQSFLAQORLATNSRRQFLGR 707  Db 727 LRREEQLLRQERDRKLREEEQLLQESEEFRLRRQEREOQLRR 768	RESULT 2 A59404 A59404 Difectin [imported] - human C;Specias: Homo sapiens (man) C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002 C;Accession: C59404; A59404	Rillu, C.G.; Maercker, C.; Castanon, M.J.; Hauptmann, R.; Wiche, G. Proc. Natl. Acad. Sci. U.S.A. 93, 4278-4283, 1996 A;Title: Human plectin: organization of the gene, sequence analysis, and chromosome loca A;Reference number: C59404; MUID:96210632; PMID:8633055 A;Accession: C59404 A;Stetus: preliminary A;Molecule type: DNA A;Residues: 1-4684 <sto> A;Aross references: GB:CAA91196; NID:91296662; PIDN:CAA91196.1 C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein §</sto>	. 36;	QY         120 GCAISCEKKODHIQRIMTLEESVQHVVMEAIQELMTKDTPDSLSPETYGNFDSQSRRYF         179           III	213 QENAGLEREMGRPEGEGTPGLTAKKLLLQSQLEQLOEENFRESGREDERLRCAEL	304 304 1566 341 1626	Oy 384 EKWLPECRNLEEKYESYTEKERELLAERDSLREANEELRCAOLOPRGITOADPSL 438

DD 1867 QARRLEBELAVEGRRVQALEEVLGDLRAESREQEKALLALQQQCAEQAQEHEVE 1920  QY 390 CRNLEBEXYESYTKEKERLLAERDSLREANEELRCAQLQPRGLTQADPSLDPTSTPVDNLA 449  DAY 10:1	450 AEILPAELRETLIRIQLENKRICRQEAADRERQEELQRHLEDANRARHGLETQHRLNOQO 1945LRAESQSSRHQEEAARARAEALQEALGRAHAALQGKE-QHLLEQAE 510 LSE	Db. 1990 LSRSLEASTATLQASLDACQAHSRQLEEALRIQEGEIQDODLRYQEDVQQLQQAL 2044  Qy 555 LELQRKREYIEBLEPPTDSSTARRIEELQHNLQKKDADLRAMEBRYRRYV 604  Cy 555 LELQRKREYIEBLEPFTDSSTARRIEELQHNLQKKDADLRAMEBRYRRYV 604  Db 2045 AQRDEELRHQQEREQLLEKSLAGRVQENMIQEKQNLGLEREEBIRGLHQSVRELQLTLA 2104  Qy 605 DKARMVMQTMBERGRPAAGAPPELHSLKTQLRERDVRIRHLEMDFEKSRSQREQEBKLLI 664	Db 2105 QKBORILELRETQORNNLEALPHSHKTSPMEEQSLKLDSLEPRLGRELE 2153 Qy 665 SAWYNMGMALQQRAGEERAPAHQSFLAQORLATNS 700 Db 2154RLQAALRQTBAREIEWREKAQDLALS-LAQTKASVSS 2189	RESULT 5	A. Species: Rattus norvegicus (Norway rat) C. Species: Rattus norvegicus (Norway rat) C. Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 C. Accession: A39638; S21876 C. Accession: A39638; S21876 C. Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.; Strat J. Cell Biol. 114, 83-99, 1991 A. Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide chain wA. Reference number: A39638; MUID:91268156; PMID:2050743 A. Reference number: A39638; MUID:91268156; PMID:2050743 A. Status: preliminary A. Molecule type: mRNA A. Residues: 14687 A. Cross references: EMBL:X59601; NID:91292885; PIDN:CAA42169.1; PID:91561642 C. Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein C.; Superfamily: plectin; alpha-actinin actin-binding domain homology ACT> F: 6-103/Domain: alpha-actinin actin-binding domain homology ACT>	Query Match 9.1%; Score 332.5; DB 1; Length 4687; Best Local Similarity 22.2%; Pred. No. 1.1e-06; Matches 193; Conservative 117; Mismatches 272; Indels 287; Gaps 32;	QY 68 KVSNLKMVLRSLVEYSQDVLAHPVSEEHLPDV	QY 100SLIGEFSDPAELGKLLQLVLGCAISCEKKQDHIQRIMTLEESVQHVVMEAIQEL 153	QY 154 MT	QY 180 LSEBAEEGDELQQRC	QY 208 KQSLAQENAGLRERMGRPEGEGTPGLTAKKLLLLQSQLEQLQEENFRLESGREDERLRCA 267	Qy 268 ELEREVAELQHRNQALTSLAQEAQALKDEMD 298
1509 AEEAEAOKROAQEEAERLRROVQDESQRKRQAEVELASRVKAETEAAREKQRALQALEEL 1568 415 REANEELRCAQLQPRGLTQADPSLDPTSTPVDNLAAEILPAELRE 459 1 1 1 1 1 1::	-TLLRLQLENKRLCRQEAADRERQEELQRHLEDANRA-RHGLETQHRLNQQOLSEL 513 ::  :   :   :   :     :     :     :		ESKSISEKSKOKLEAERARKFKELMEERARLKALLKEERAR KORQLAREDAAKKARE 103/ EEKLLISAWYNMG	687 AQSFLAQQRLAINS 700 	ESULT 4  entrols  entrols  entrols  entrols  entrols  entrols  entrols  species: Homo sapiens (man)  ; Species: Homo sapiens (man)  ; Accession: T08621  ; Mack, G.J.; Rees, J.; Sandblom, O.; Balczon, R.; Fritzler, M.J.; Rattner, J.B.  ; Accession: T08621  ; Accession: T08621  ; Accession: T08621  ; Reference number: Z16462; MUID:99165428; PMID:9506584  ; Reference number: L16462; MUID:99165428; PMID:9506584  ; Residues: L2442 ~ AMAC  ; Residues: L2440 ~ AMAC  ; Residues: L2440 ~ AMAC  ; Residues: L2446 ~ AMAC  ; Residu	Query Match 9.4%; Score 342.5; DB 2; Length 2442; Best Local Similarity 23.7%; Pred. No. 2e-07; Matches 166; Conservative 114; Mismatches 224; Indels 197; Gaps 28;	70 SNLKMVLRSLVEYSQDVLAHPVSEEHLPDVSLIGEFSDPABLGKLLQLVLGCAISCEKKQ 129	130 DHIQRIMTLEESVQHVVMEAIQELMTKDTPDSLSPETYGNFDSQSRR 176 11	177 XYELSEBAEEG	219 RERMGRPEGEGTPGLTAKKLLLOSQLEQLQEENFRLESGREDERLRCAELEREVA 274  1763 HRKVGETSLLLSQREQEIVVLQQQLQEAREQGELKEQSLOSQLD 1806	275 ELQHRNQALTSLAQEAQALKDEMDELRQSSER-AGQLEATLTSCRRRLGELRELRR 329 	330 OVROLEERNAGHAERTROLEDELRRAGSLRAQLEAQRRQVGLQGQRQSEAMKAEKWLFE 389

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incoxyl end due to frameshift error is found as flocculent material in the parasitophorous vacuol lin; calmodulin repeat homology
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uence_revision 15-Oct-1999 #text_change 15-Oct-1999
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nce of C. elegans cosmid 2K546.
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anslated from GB/EMBL/DDBJ

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N'Alternate names: myosin II
N'Contains: myosin ATPase (EC 3.6.4.1)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 *sequence_revision 31-Dec-1993 *text_change 19-Apr-2002
C;Accession: S21801; PN0013; S18134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    618 QRP-----AAGAPPELHSLRTQLRERDVRIRHLEMDFEKSRSQREQEEKLLISAWYNM 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELNSLSESSGKLNGNGS----SERRSNADQI---LVDAELEJERLRTETENQRKEJERL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 TKSFETAQHDMSSNSESGDISILEKQNEELRQKRRELEEKNLELDAAVDQFKGIVFELTN 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      380 AMKAEKWLFECRNLEEKYESVTKEKERLLAERDSLREANEELRCAQLQPRGLTQADPSLD 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 NRTTHIMYFRSCTRKLWRKMFDYVNHINRTVVSSRWTDIHERIDGIYESDLPAMVNLGMA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   538 EEEKLFATKOIEELQQQIEDLQENLLKNQEHASGDVVGLKIQLEKAEVEAQQMREAKMRA 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -EEHLPDVSLIG-E 104
                                                                                                                                                                                                                                                                                                                                                           1 MSVDKAELCGSLLTWLQTFHVPS-PCASPQDLSSGLAVAYVLNQIDPSWFNEAWLQGISE 59
                                                                                                                                                                                                                                                                                                                                                                                                                     LOADLADMA----VWMEGLDATKLPLNDPQLLCNGRAFSEVLHNVDKNFFTDGWLETMPE 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GMALQQRAGEERAPAHAQSFLAQQR-----LATNSRRGPLGRLASL 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            693 VLNRSIDEVMSMRAHAGSE----EPQILLDTQKMSGALPWRSLASETRRELPTAMASI 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSDPAELGK - - - - LLQLVLGCAISCEKKQDHIORIMT - - LEESVQHVVMEAIQELMTKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 VVTLAHIGKNAKRFVDYSKALTSTHKSMMSNVAKMVTTVIDEMPENPCFHEISELHGSQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RERMGRPEGEGTPGLTAKKLLLLQSQLEQLQEENFRLESGREDERLRCAELEREVAELQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNQALTSLAQEAQALKDEMD----ELRQSSERAGQLEATLTSCRRRLGELRELRRQVRQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            440 PTSTPVDNLAAEILPAELRETLLRLQLENKRLCRQEAADRERQEELQRHLEDANRARHGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESMFEAGNLS -----EKNTLPLEIENKRL-TERIQELESLEPLKGELITLKSKNGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETQHRLNQQQLSELRAQVEDLQK-ALQEQGGKTEDAISILLK-RKLEEHLQKLHEADLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDSLSPETYGNFDSQSRRYYFLSEEAEEGDELQQRCLDLERQLMLLSEEKQSLAQENAGL
                                                                                                                                                                                                                                        DB 2; Length 772
                                                 A)Cross-references: EMBL:U29380; PIDN:AAA68733.1; CESP:2K546.1
A)Experimental source: strain Bristol N2
C;Genetics:
A;Gene CESP:2K546.1
A;Introns: 53/3; 83/2; 477/1; 496/2; 632/3; 692/3; 729/2; 745/2
                                                                                                                                                                                                                                  9.0%; Score 326.5; DB 31arity 21:1%; Pred. No. 2.9e-07; Conservative 153; Mismatches 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myosin heavy chain, neuronal (similarity) - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPGPNWKLKVSNLKMVLRSLVEYSQDVLAHPVS
                                                                                                                                                                                                                                                                 Similarity
                        1-772 <HAL>
A; Molecule type: DNA A; Residues: 1-772 < H.
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hes 164;
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Experimental source: brain
Superfamily: myosin heavy chain; myosin motor domain homology
Keywords: actin binding; ATP; coiled coll; hydrolase; methylated amino acid; nucleo
                                                                                                                                                                                                                                                     ochem. Blophys. Res. Commun. 175, 244-249, 1991
Title: A unique cellular myosin II exhibiting differential expression in the cerebr
Reference number: PN0013; MUID:91151356; PMID:1998509
                              þr
                                 mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1400 RHEEKVAAYDKLEKTKTRLQQELDDLLVDLDHQRQSACNLEKKQKKFDQLLAEEITKSAK 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           970 AKLKKLEBEQIILEDQNCKLAKEKKLLEDRIAEFTINLIEBEBEKSKSLAKLKNKHEAMIT 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLEERLRRE-----EKQRQELEKTRRKLEGDSTDLSDQIAELQAQ---IAELKMQLAKK 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRNLEEKYESVTKEKERLLAERDSLREANE-ELRCAQLQPRGLTQADPSLDPTS---TPV 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 NAGLRERMGRPEGEGT-PGLTAKKLLLLQSQLEQLQEENFRLESGREDERLRCAELEREV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 AELQHRNQALTSLAQEAQALKDEMDELRQSS----ERAGQLEATLTSCRRLGELRELRR 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             446 DNLAAEI-----LPAELRETLLRLQLENK-----RLCRQEAADRERQEELQRHLEDA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             493 NRARHGLETQHRLNQQQLSELRAQVEDLQKALQEQGGKTEDAISILLKRKLEEHLQKL-- 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 AELGKL--LQLVL---GCAISCEKK--QDHIQRIMT-----LEESVQHVVMEAIQELMTK 156
                              Title: Cloning of the cDNA encoding a neuronal myosin heavy chain from Reference number: S21801; MUID:92235856; PMID:1569576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVRQLEERNAGHAERTRQLEDELRRAGSLRAQLEAQRRQVQELQGQRQEEAMKAEKWLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1239 GRDSEHKRKKVEAQLQELQV-----KFNEGERRVTELADK-VTKLQVELDNVTGLLSQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            578 RIBELQHNLQKKDADLRAMEERYRRYVDKARMVMQTMEPKQRPAAGAPPELHSLRTQLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1277-1999/Region: light meromyosin
F;1277-1999/Region: light meromyosin
F;125/Modified site: N6,N6.N6-trimethyllysine (Lys) #status predicted
F;180/Binding site: ATP (Lys) #status predicted
F;693,703/Active site: Cys #status predicted
F;1916/Binding site: phosphate (Ser) (covalent) #status predicted
F;1943/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541-575/Region: actin binding #status predicted
553-675/Region: actin binding #status predicted
836-1999/Domain: coiled coil #status predicted <COI>
836-1276/Region: S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
8.9%; Score 322; DB 1;
Best Local Similarity 25.0%; Pred. No. 1.2e-06;
Matches 159; Conservative 118; Mismatches 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74-181/Region: nucleotide-binding motif A
1. Biol. 224, 1185-1193, 1992
le: Cloning of the cDNA encod
                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: mRNA
Residues: 1914-1998,'I' <SU2>
                                                                                                                                                                                                   Cross-references: EMBL:X62659
                                                                                                                                                                                                                                    Sun, W.; Chantler, P.D.
                                                                                                                                   Molecule type: mRNA
Residues: 1-1999 <SUN>
                                                                                                    Accession: S21801
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Db 1460 YAEERARDAEERAEKATKELSLARAELEAMEOKAEFLRKNLOE 1502  Qy 638 RDVRIRHLE	A/Cross-references: EMBL:219361; NID:9295940; PIDN:CAA79165.1; PID:9295941 A/Cross-references: EMBL:218361; NID:9295940; PIDN:CAA79165.1; PID:9295941 A/Note: sequence extracted from NCBI backbone (NCBIP:132511). B/Fietz, M.J.; Presland, R.B.; Rogers, G.E. J. Cell Biol. 110, 427-436, 1990 A/Title: The cDNA-deduced amino acid sequence for trichohyalin, a differentiation marker A/Reference number: A34209; MUID:90130632; PMID:2298812 A/Reference number: A34209 A/Reference number: A34209 A/Residues: 1016-1151,1205-1257,1281-1398,'G',1400-1549 <fi2> A/Cross-references: GBX51665; NID:941827; PIDN:CAA35992.1; PID:94828 C/Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root she covalent modifications to this protein include conversion of arginine to citrulline and A/Introns: 46/3 A/Note: single copy gene C/Superfamily: trichohyalin; calmodulin repeat homology C/Superfamily: trichohyalin; calmodulin repeat homology C/Superfamily: trichohyalin; expeat homology C/Superfamily: calmodulin repeat homology C/Superfamily: calmodulin repeat homology C/Reywords: calcium binding; citrulline; EF hand; hair; tandem repeat</fi2>	F;387-851/Region: 28-residue repeats F;387-851/Region: 23-residue repeats Guery Match  Query Match  B:84; Score 319; DB 1; Length 1549; Best Local Similarity 23:58; Pred. No. 1.3e-06; Matches 172; Conservative 104; Mismatches 241; Indels 216; Gaps 28;  Qy 126 EXCOHUGAINALLESVOHYVMEAIOELMATKOPPOSISPETYGNEDSQSR 175  :::	QY   213   QENAGIRERMGRPEGESTPGLTAKKLLILQSQLEQLQEENFRLESGREDER 263   1   1   1   1   1   1   1   1   1

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A; Residues: 1-1201 <COL>
A; Cross-references: EMBL:X53155; NID:g8219; PIDN:CAA37311.1; PID:g2546939
A; Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for resi
                                                                                                                                    A;Gene: FlyBase:Mhc
A;Cross-references: FlyBase:FBgn0002741
C;Superfamily: myosin heavy chain; myosin motor domain homology
                                                                                                                                                                                                                   C; Keywords: ATP
                                                                                                                                                                                                                                                                           Query Match
                                                                                                             Genetics
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Genes Dev. 4, 885-895, 1990
A;Yitle: Alternative myosin hinge regions are utilized in a tissue-specific fashion that A;Reference number: A35815; MUID:90346288; PMID:2116987
A;Accession: B35815
                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myosin heavy chain 2, muscle - fruit fly (Drosophila melanogaster) (fragment)
C.Species: Drosophila melanogaster
C.Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 20-Jun-2000
C.Accession: B35815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1407 AAYDKLEKTKTRLQQELDDLLVDLDHQRQSACNLEKKQKKFDQLLAEEKTISAKYAEERD 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAEAEAREKETKALSLARALEEAMEOKAELERLNKOFRTEMEDLMSSKDDVGKSVHELEK 1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 QVROLEERNAGHAERTROLEDELRRAGSLRAGLEAORROVOELOGOROEEAMKAEKWLFE 389
                                                                                                                                                                                                                                                                                                                                                                                                                                109 AELGKL--LQLVL---GCAISCEKK--QDHIQRIMT-----LEESVQHVVMEAIQELMTK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIPDSLSPETYGNFDSQSRRYYFLSEEAEEGD -- ELQORCLDLERQLMLLSEEKQSLAQE 214
                                                                                                                                                                                                                                                                                                                                                                              94; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 NAGLRERMGRPEGEGT-PGLTAKKLLLLQSQLEQLQEENFRLESGREDERLRCAELEREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |::| |:: | |:: | |:: | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | |:: | |:: | |:: | |:: | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AELQHRNQALTSLAQEAQALKDEMDELRQSS----ERAGQLEATLTSCRRRLGELRELRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRNLEEKYESVTKEKERLLAERDSLREANEEL - - RCAQLQPRGLTQADPSLDPTSTPVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAAEI -- LPAELRETLIRLOLENK -----RICROEAADREROEELORHLEDANRARHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  499 LETOHRLNOQOLSELRAQVEDLOKALQEQGGKTEDAISILLKRKLEEHLQKLHEADLELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LE-----KQIATLHAQVADMKKKMEDSVGCLETAEEV--KRKLQKDLEGLSQRHEEKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---ADLRAMEERYRRYUD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KARMVMOTMEPKORPAGA - - - - - PPELHSLRTQLRERDVRIRHLEMDFEKSRSQREQ
                                                                                                                                                        F;1278-1961/Domain: light meromyosin *status predicted <LMM>
F;1939-1961/Domain: carboxyl-terminal <CBT>
F;1955/Modified site: N6,N6,N6-trimethyllysine (Lys) *status predicted F;80/Binding site: ATP (Lys) *status predicted F;694,704/Active site: Cys *status predicted
                                                                                                                                                                                                                                                                                                                        Query Match 8.7%; Score 316; DB 1; Length 19
Best Local Similarity 24.3%; Pred. No. 2.2e-06;
Matches 153; Conservative 115; Mismatches 268; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84-764/Domain: myosin motor domain homology <MMOT>
1174-181/Region: nucleotide-binding motif A (P-loop)
552-565/Region: actin binding #status predicted
626-640/Region: actin binding #status predicted
837-1938/Domain: coiled coil #status predicted <COI>837-1277/Domain: S2 #status predicted <COI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           559 RKREYIEELEPPIDSSTARRIEELQH-----NLQKKD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1527 SKRALEQOVEEMKTQLEELEDELQATEDAK 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEKLLISAWYNMGMALQQRAGEERAPAHAQ 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1015 QTQEKLRKALEQQIKELQVRLDEAEANALKGGKKAIQKLEQRVRELENELDGEQRRHADA 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                624
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                                                                                                                       66 KLKVSNLKMVLRSLVEYS---QDVLAHPVSEEHLPDVSLIGEFSDPAELGKLLQLVLGCA 122
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    454 KAEKEKNEYYGQLNDLRAGVDHITNEKAAQEKIAKQLQHTLNEVQSKLDETNRTLNDFDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --NFRLESGREDERLRCAELEREVAELQHRNQALTSLAQEAQALKDEMDELRQSSER---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          619 ARSEELEEAKRKLQARLAEAEETIESL -- - NOKCIGLEKTKORLSTEVEDLOLEVDRANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     676 IANAAEKKOKAFDKIIGEWKLKVDDLAAELDASOKECRNYSTELFRLKGAYEEGOEOLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --NLEEKYESVTKEKERLLAERDSLREANEELRCAQLQPRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              796 VLRAQLELSQVRQEIDRRIQEKEEEFENTRKNHQRALDSMQASLEAEAKGKAEALRMKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         856 LEAD--INELEIALDH--ANKANAEAQKNIKRYQQQLKDIQTALEEEQRARDDAREQLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 - ERQ------EELQRHLEDANRARHGLETQHRLNQQQLSELRAQVEDLQKALQEQGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --EELEPPTD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SSTARRIEELQHNLQKKDAD-LRAMEERYRRYVDKARMVMQTMEPKQRPAAGA
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                                                                                                                                                                                                                                                                                                                                                                          173 OSRRYYFLSEBAEEGDELQQRCLDLERQLMLLS-----EEKQSLAQENA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               568 LGKFRNLEHDLDNLREQV-EEEAEGKAD-----LQRQLSKANAEAQVWRSKYESDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --RRLGELRELRRQVRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEERNAGHAERTRQLEDELRRAG----SLRAQLEAQRRQVQ----ELQG---QRQEE
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   Length 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --GLRERMGRPEGEGTPGLTAKKLLLLQSQLEQLQEE
8.7%; Score 315.5; DB 2;
21.3%; Pred. No. 1.4e-06;
                                                                                                                                                                                                                                               123 ISCEKKODHIORIMTLEESVQHVVME-AIQELMTKDTPDSLSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -AGQLEATLTSCR---
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                                                             Conservative 144; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380 AMKAEKWLFECR---
                      Best Local Similarity
Matches 178; Conserv
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Status: preliminary
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GRQRL-
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Matches
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                                                                                                                                                                                                                                                                       A;Cross-references: GB:L09190; NID:g292835; PIDN:AAA65582.1; PID:g292836
A;Note: authors translated the codon AGG for residue 1714 as Pro
C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root sh
Covalent modifications to this protein include conversion of arginine to citrulline and
                                        C;Accession: 445973
R;Lee, S.C.; Kim, I.G.; Marekov, L.N.; O'Keefe, E.J.; Parry, D.A.D.; Steinert, P.M.
J. Biol. Chem. 268, 12164-12176, 1993
A;Title: The structure of human trichohyalin. Potential multiple roles as a functional ed (cross-linking) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 EEPQRQRELQEE-----EEQLRKLERQELRRERQEEEQQQQR-LRREQQLRRKQEEERRE 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELRRQVRQLEERNAGHAERTRQLEDELRRAGSLRAQLEAQRRQVQELQGQRQEEAMKAEK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----WLFECRNLEEKYESVTKEKERLLAERDSLREANEELRCAQLQPRGLTQADPSLDP 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---QQEERREQQLR----REQEERREQOLRR 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVAELQHRNQALTSLAQE---AQALKDEMDELRQSSERAGQLEATLTSCRRRLGELR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1898;
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 1q21-1q21
C;Superfamily: trichohyalin; calmodulin repeat homology
C;Keywords: calcium binding; citrulline; EF hand; hair;
F;49-81/Domain: calmodulin repeat homology <EF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 EFSDPAELGK--LLQL-VLGCAISCEKKQDHIQRIMTLEESVQ---
                                                                                                                                                          ed (cross-linking) protein.
A; Reference number: A45973; MUID:93280194; PMID:7685034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

8.7%; Score 315; DB 1; 1
Best Local Similarity 24.5%; Pred. No. 2.4e-06;
Matches 168; Conservative 110; Mismatches 269;
                Species: Homo sapiens (man)
Date: 03-May-1994 #sequence_revision 01-Mar-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -KKDADLRAMEERYRRYVDKARMVMQTMEPKQRPA--
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                                                                                                                                                                                                                                                Residues: 1-1898 <LEE>
Cross-references: GB:L09190;
Note: authors translated the
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                                                                                                                                                                                                                               Molecule type: DNA
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--SARPPLREQRERQLRAEER
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AAG for resi a tissue-specific fashion 34; myosin heavy chain 4, muscle - fruit fly (Drosophila melanogaster) (fragment) C;Species: Drosophila melanogaster C;Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 13-Feb-1998 C;Accession: D35815 618 KLKVSNLKMVLRSLVEYS---QDVLAHPVSEEHLPDVSLIGEFSDPAELGKLLQLVLGCA 122 567 251 675 333 676 IANAAEKCQKAFDKIIGEWKLKVDDLAAELDASQKECRNYSTELFRLKGAYEEGQEQLEA 735 431 480 -ERG------EELORHLEDANRARHGLETQHRLNOQQLSELRAQVEDLQKALQEQGGK 530 ----ETYGNFDS 172 Lys, and 619 ARSEELEBARRKLQARLABABETIESL---NOKCIGLEKTKORLSTEVEDLOLEVDRANA SKKKL----SIENSDLLRQLEEAESQVSQLSKIKISLTTQLEDTKRLADEESRERATL LGKFRNLEHDLDNLREQV-EEEAEGKAD-----LQRQLSKANAEAQVWRSKYESDGV LEERNAGHAERTRQLEDELRRAG----SLRAQLEAQRRQVQ----ELQG---QRQEE 736 VRRENKNLADEVKDLLDQIGEGGRNIHEIEKARKRLEAEKDELQAALEEAEAALEGEENK 380 AMKAEKWLFECR-----NLEEKYESVTKEKERLLAERDSLREANEELRCAQLQPRGL --- ELQRKREYI----- EELEPPID-------GLRERMGRPEGEGTPGLTAKKLLLLQSQLEQLQEE------241; Length 1175; as A.Cross references: FlyBase:FBgn0002741 C;Superfamily: myosin heavy chain; myosin motor domain homology C;Keywords: ATP for residue 649 Ricollier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, Genes Dev. 4, 885-895, 1990 Griss Dev. 4, 885-895, 1990 A;Title: Alternative myosin hinge regions are utilized in A;Reference number: A35815; MUID:90346288; PMID:2116987 A;Accession: D35815 123 ISCEKKODHIORIMILEESVOHVVME-AIOELMTKDTPDSLSP---Local Similarity 21.3%; Pred. No. 1.5e-06; nes 176; Conservative 144; Mismatches 267; DB 2; TQADPSLDPTSTPVDNLAAEILPAELRETLLRLQ-----8.6%; Score 314.5; 21.3%; Pred. No. 1.5 IGC OSRRYYFLSEEAEEGDELQQRCLDLERQLMLLS-531 TEDAISILLKRKLEEHLQKLHEADL-----Note: the authors translated the codon Residues: 1-1175 <COL>
Cross-references: EMBL:X53155

Db 1476 LSLLNEVDIMKEHLEESDRVRRSLQOELQDSISNKDDFGKNVHELEKAKRSLEAELNDMR 1535  Qy 515 AQVEDLQKALQEGGGKTEDAISILLKRKLEEHLQKLHEADLELQRKREYIEEL 567	SSULT 15 101997	omain: myosin mo Region: nucleoti Region: actin bii Region: actin bii Abomain: colled ARegion: 31 8/Region: 11ght iing site: AFP (L. Active site: Cys	8) CONSELVATIVE 153; Mismat. SSGLAVAYVLNOIDPSWFNEAWLQGIS.	104 LSEEKOSLAQENAGLRERMGRPEGEGTPGLTARKLLLLGSQLEQ	Db 1110ARIEELEEELEAERNARAKVEKORAELNRELEEL-GERLDEAGGATSAQIELNKKR 1164
OY 573SSTARRIEELCHNLOKKDAD-LRAMEERYRRYVDKARMYMQTMEPKQRPAAGA 624	RESULT 14 T16416 T16416 T16416 T16416 T16416 T16416 T16416 C. Pate: 20. Sep-1999 #text_change 21-Jan-2000 C. Pate: 20. Sep-1999 #sequence_revision 20. Sep-1999 #text_change 21-Jan-2000 C. Pate: 20. Sep-1999 #sequence_revision 20. Sep-1999 #text_change 21-Jan-2000 C. Pate: 20. Sep-1999 #sequence_revision 20. Sep-1999 #text_change 21-Jan-2000 C. Pate: 20. Sep-1999 #sequence_revision 20. Sep-1999 #text_change 21-Jan-2000 C. Pate: 20. Sep-1999 #sequence_revision 20. Sep-1999 #text_change 21-Jan-2000 C. Pate: 20. Sep-1999 #sequence_revision 20. Sep-1999 #text_change 21-Jan-2000 A. Pate: 20. Sep-1999 #sequence_revision 20. Sep-1999 #text_change 21-Jan-2000 A. Pate: 20. Sep-1999 #sequence_revision 20. Sep-1999 #text_change 21-Jan-2000 A. Pate: 20. Sep-1999 #sequence_revision 20. Sep-1999 #text_change 21-Jan-2000 A. Pate: 20. Sep-1999 #sequence_revision 20. Sep-1999 #text_change 21-Jan-2000 A. Sep-1999 #text_change 21-Jan-2000 A. Sep-19	C; Superfamily: myosin heavy chain; myosin motor domain homology F;81-763/Domain: myosin motor domain homology <a href="https://www.chain.com/motor-domain-nomology-chi/o/">https://ww.chain.com/motor-domain-nomology-chi/o/</a> Query Match  8.6%; Score 314.5; DB 2; Length 1956; Best Local Similarity 21.6%; Pred. No. 2.6e-06; Matches 151; Conservative 136; Mismatches 247; Indels 165; Gaps 26; Oy 70 SNLKMVLRSLVEX'SQDVLAHPVSELHEPDVSLIGEFSDPAELGKLLQLVLGCAISCEKKO 129 OY 130 DHIORIWRILABLEDSKDHLAE	1082 EELQHQLTRYDEESANVTLMQKQMRDMQTTIDELREDMETERNARNAEMTRREVVAQ 1082 EELQHQLTRYDEESANVTLMQKQMRDMQTTIDELREDMETERNARNAEMTRREVVAQ 1082 EELQHQLTRYDEESANVTLMQCLMSRKDEEVNATKRAIEQIQHTMEGKIEEQKAKFEVVAQ 1084 III	Db 1258 ANLAESDEHKRTLIDQLERSRDELDHLNRVREEEEHAFANMQRRLATAEGQIGELNEQIQ 1317  933 QLEERNAGHAERTROLEDELRRAGSLRAQLEAQRRQVQELQG 374  1318 EETRLKKANINRARQLEDEKNALLDEKEEAGGRAHLEKEIHAARQGAGBARKAEESVN 1377  97 375 QRQEEAMKAEKWIFECRNLEEKYESVTKEKERLLAEKEIHAARQGAGBARKAEESVN 1377  98 375 QRQEEAMKAEKWIFECRNLEEKYESVTKEKERLLAEKBIHARQGAGBARKAEESVN 1377  99 435 DPSLDPTSTPVDNLAABILDAELRETLLRLQLENKRLCRQEAADRERQ-482  90 435 DPSLDPTSTPVDNLAABILPAELRETLLRLQLENKRLCRQEAADRERQ-482  91 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	

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73 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40, Last sequence update)
40, Last annotation update)
(PCN) (Hemidesmosomal protein 1) (HDI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 360; DB 1;
Pred. No. 8.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 VRQLEERNAGHAERTRQLEDELRRAGSLRA-----
                                                                                                                                                                                                                                                                                                                                                                    Keratinization; Repeat; Calcium-binding
DOMAIN 5-100 LIKE
                              HSSP; P02633, 4ICB.
InterPro; IPR001751; CaBP_S100.
Interpro; IPR002048; EF-hand.
Pfam; PF00036; efhand; 1.
Pfam; PF01023; S_100; 1.
                                                                                                                                                                                                     Pfam, PF01023, S_100, 1
Probom, PD003407, cabe_5100, 1
PROSITE, PS00018, EF_HAND, 1
PROSITE, PS00303, S100_CABP, 1.
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Q15149; Q16
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SEQUENCE
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between the Swiss Institute of Bloinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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"A compound heterozygous one amino-acid insertion/nonsense mutation in the plectin gene causes epidermolysis bullosa simplex with plectin deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Loss of plectin causes epidermolysis bullosa with muscular dystrophy: cDNA cloning and genomic organization.";
Genes Dev. 10:1724-1735(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: INTERLINKS INTERMEDIATE FILAMENTS WITH MICROTUBULES AND MICROFILAMENTS AND ANCHORS INTERMEDIATE FILAMENTS TO DESMOSOMES OR HEMIDESMOSOMES. COULD ALSO BIND MUSCLE PROTEINS SUCH AS ACTIN TO MEMBRANE COMPLEXES IN MUSCLE. MAY BE INVOLVED NOT ONLY IN THE FORSELINKING AND STABILIZATION OF CYTOSKELETAL INTERMEDIATE FILAMENTS INTERMEDIATE FILAMENTS ON DEFENDANCS.
-!- SUBUNIT: HOWODIMER OR HOMOTERAMER.
-!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE PRODUCTS OF ALTERNATIVE PRODUCTS. SUBURITY FILENCE OF A ALTERNATIVE PRODUCTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McDean W.H.I., Pulkkinen L., Smith F.J.D., Rugg E.L., Lane E.B.,
Bullrich F., Burgeson R.E., Amano S., Hudson D.L., Owaribe K.,
McGrath J.A., McMillan J.R., Eady R.A.J., Leigh I.M., Christiano A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN MUSCLE, HEART, PLACENTA AND SPIRAL CORD.
-!- DOMAIN: THE N-TERMINGS INTERACTS WITH ACTIN, THE C-TERMINUS WITH VIMENTIN, DESMIN, GFEPP, CYTOKERATINS, LAMIN B: WHEREAS BOTH THE N-PIM: PHOSSHORY CAN BIND INTEGRIN BETA-4.
-!- PIM: PHOSSHORY LATED BY CDC2; REGULATES DISSOCIATION FROM INTERNEDIATE FILAMENTS DURING MITOSIS (BY SMILARITY).
-!- DISEASE: DEFECTS IN PLECI ARE THE CAUSE OF EPIDERMOLYSIS BULLOSA
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                         MEDLINE-96210632; PubMed-8633055;
Liu C.-G., Maercker C., Castanon M.J., Hauptmann R., Wiche G.;
"Human plectin: organization of the gene, sequence analysis, and
chromosome localization (8q24).";
Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT MD-EBS LEU-429 INS.
MEDLINE-21090821; PubMed-11159198;
Bauer J.W., Rouan F., Kofler B., Rezniczek G.A., Kornacker I.,
Muss W., Hametner R., Klausegger A., Huber A., Pohla-Gubo G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pulkkinen L., Smith F.J.D., Shimizu H., Murata S., Yaoita H., Hachisuka H., Nishikawa T., McCean W.H.I., Ultto J., Helmorzygous deletion mutations in the plectin gene (Pleci) in with epidermolysis bullosa simplex associated with late-onset
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SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
SIMILARITY: CONTAINS 33 PLECTIN REPEATS.
SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WARIANT MD-EBS 1003-GLN--ALA-1005 DEL.
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                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
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G-S-R-X. BY RKDRRPRS. HFWYLTN ARRTPHVQ. ETDVVORGSGI PAERAVIR	•	115 254; G ABLGKLLDLVL 1           1           1         1
S OF G: 22) (BY 3VMVAKKI SVMVARKI MYWPAR EEVSDET SSVLDPAI )).		; Length 4684; 7; 50; Indels 254; G -LIGEFSDPAELGKLLQLVL
REPEATS OI (BY CDC2) EVLFREGVAN RRUKREYAMYN RRYRREVAMYN RRYRREVAMYN ROGAGASNGSVI SCOPORM 3). OOFORM 3). BSS). BSS). 2). 2). 2). 2). 2). 2). 2). 2). 2). 2		DB 1; Length 4684; hes 250; Indels 254; G hes 250; Indels 254; G DVSLIGEFSDPAELGKLLLUVL :                 QLGRQLRYYRESADP-'LGAWLO MTKDTPDSLSPETXGNEDSOSRRXYF               ILSEE
AA TANDEM F PRITY). RITY). WRRAMGIRALY WRRAMGIRALY WRRAMGIRALY SPETYASION SPETYASIO	REDITOR AND THE SECOND TO THE SECOND THE SEC	344; DB 1; Length 4684;  NO. 1.4e-07;  SMALCHES 250; Indels 254; Gi EHLPDVSLIGEFSDPAELGKLLULVL
SIMILARITY).  4 X 4 AA TANDEM REPEATS OF G-S-R-X. PHOSPHORYLATION (BY CDC2) (BY STMILARITY) WVAGMLMPRDOLIAIYEVLFREGWVAKKDRRPRSLHPHVP GVTNLLOVMRAMASLARGLVRETFANCHFFWYLTURGTLAHL ROYTHLPPEIVAASLORVRRELEEVSPETPVVPATTORTLA ROYTHLPPEIVAASLORVRRELEEVSPETPVVPATTORTLA ROYTHLPPEIVAASLORVRRELEEVSPETPVVPATTORTLA ROYTHLANT - MGGEDARVRAVSEDVSGSGSPSGD TLPWNLGKTQRSRRSGGGAGSNGSVLDPAERAVIRIA (IN ISSOFORM 2 AND ISOFORM 3). L -> LL (IN MD-EBS). /FTIG=VAR_011337. S -> F (IN REF. 2). H -> N (IN REF. 2). H -> N (IN REF. 2). N -> Y (IN REF. 2). V -> A (IN REF. 2).		core 344; DB red.No. 1.4e- Mismatches PVSEELLPDVS
S IM S IM	> H < B O J R R N W N K W F F N D W K M Z >  , \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	9.5%: Score 24.2%: Pred. 1ve 109; Mi EYSODVLAH-PVS EYSODVLAOTDVR MTLEESVOHVWE
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DOMAIN MOD_RES VARSPLIC VARSPLIC VARIANT CONFLICT	CONFLICT CON	Query Match Best Local Similarity Matches 196; Conser 65 WKLKVSNLKMVLR 1314 WRERVA 120 GCAISCEKKODHI 1362DARRRQEQI 1362DARRRQEQI 1361 LLEBIERHGEKVE 213 QENAGLRERMGRP 213 QENAGLRERMGRP 11451 QELVDLRTHYSE- 270
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license@isb-sib.ch) 96.1; 96.1; 28.1; 28.1; 96.1; 65.1; 65.1; 65.1; 10ctnn.like. Plectin_repeat. Slo_plectin. Spectrin. in; 19. iectin; 1. iectin; 1. if 33. if 5. if if if if if if if if if if if if if i	liciry Noboliza Oboliza 11 E 11 E 11 E 11 E 11.	PLECTIN PLECTIN PLECTIN PLECTIN PLECTIN PLECTIN PLECTIN PLECTIN PLECTIN PLECTIN PLECTIN PLECTIN PLECTIN PLECTIN PLECTIN PLECTIN PLECTIN PLECTIN PLECTIN
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or send a cor send a cor send a cor send; 254 EMBL; U53 EMBL; U63 EMBL; W97	Phospod Diseasy Domain Domain Domain Domain REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT	REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT

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EMBL;
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1626 KRQAQEEAERLKRQVQDESQRKRQAEVELASRVKARAEAAREKQRALQALEELRLQAEEA 1685
                                                                                                                               1861 QGEQQRQLLEEELAR-----LQREAAAATQKRQELEAELAKVRAEMEVLL---ASK 1908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain with a three-domain structure based on a central alpha-helical coil "; three-domain structure based on a central alpha-helical J. Cell Biol. 114:83-99(1991).
             1566 SEAEIQAKARQAEAAERSRLRIEEEIRVVRLQLEATERQRGGAEGELQALRARAEEAEAQ 1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2; 3; 4), AND TISSUE SPECIFICITY
                                              -----HAER-TRQLEDELRR------AGSLRAQLEAQRRQVQELQG--QRQEEAMKA 383
                                                                                                             EKWLFE-----CRNLEEKYESVTKEKERLLAERDSLREANEELRCAQLOPRGLTQADPSL 438
                                                                                                                                                                                                                                                ----ADRE------ROEEL-ORHLEDANRARHGLETOHRLNQQQLSELRA--- 515
                                                                                                                                                                                                                                                                                                             QVEDLOKALQEQGGKTEDAISILLKRKLEEHLQKLHEADLELQRKREYIEELEPPTDSST 575
                                                                                                                                                                                                                                                                                                                                                                            576 ARRIEELQHNLQKKDADLRAMEERYRRYVDKA------RWVMQTMEPKQRPAA 622
                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GAPPELHSLRIQLRERDVRIRHLEMDFEKSRSQREQEEKLLISAWYNWGMAL 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                             Liu C.-G., Maercker C., Castanon M.J., Hauptmann R., Wiche G.: "Human plectin: organization of the gene, sequence analysis, and chromosome localization (8924):"; Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
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Wiche G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wiche G., Becker B., Luber K., Weitzer G., Castanon M.J.,
Hauptmann R., Stratowa C., Stewart M.;
"Cloning and sequencing of rat plectin indicates a 466-kD
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MEDLINE-91268156; PubMed-2050743;
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"Plectin transcript diversity: identification and tissue distribution of variants with distinct first coding exons and rodless isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; Structural protein; Cytoskeleton; Actin-binding;
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CH 2.
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nterPro; IPR005326; S10_plectin.
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fam; PF00307; CH; 2.
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SM00150; SPEC; 4.
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PIR; S21876; S21876.
HSSP; Q01082; 1BKR.
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								E FILAMENTS. S OF G-S-R-X.	SIMILARITY). WAGMIMPLDOLRIYEVLFREGVMVAKKDRRPRSLHPHVP GYTNIQVMRAMISLKARGLYRETFAMCHFYWLLTNEGIDHL RQYLHLPPEIVPASLQRVRRPVAMVMPARRRSPHVQTMQGP	LGCPPKRGPLPAEDPAREERQYYRKKEREGAPETPVVSAT VOTLARPOEPFTPAT -> MSQQRLRVPEPEGLGSKRTSS EDNLYLAVLRASEGKK (IN ISOFORM 2): MVAGMLMPLDQLRAIYEVLFREGVMVAKKDRRPRSLHPHVP	GVINLAVMRAMISLRAKGLYKETFAWCHYWY LYNBGLDHL VYLHLPPETVPASLGRYRRPVAMVMPARRREPHVGTWY LGCPPKRGPLPAEDPAREEROYYRKREREEGAAPETPVVSAT IVGTLARPGPEPTPAT -> MEPSGSLFPSLVVVGHVVSLA	AVWHWKKGHKQAQDEQ (IN ISOFORM 3).  WACKGHALPLOGLRAIYEVLEREGVMVAKKDRRERSLHPHVP GVTNLQVWRAMTSLRARGLYRETEARGHEYWYLTURGIDHL RQYLHLPPEIVPASLQRVRREVAMVMPARRRSPHVQTMQGP LGCPPRRGFLPAEDPAREERQVYRREREEGAPETPVVSAT TYGTLARPOBEDFPAP> DVSAGSGSSPSPGDTLPWNLG WANGSGGSPEGDFAPA.		Lengin 4007; Indels 287; Gaps	PVSEEHLPDV99	VMEAIQEL ::   : TQLLERWQAV	DTPDSLSPETYGNFDSQSRRYYF	180LSEEAEEGDELQQRC
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update)
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f a single phosphorylation site.";
Chem. 271:8203-8208(1996).
ION: INTERLINKS INTERMEDIATE FILAMENTS WITH MICROTUBULES AND
                                 MICROFILAMENTS AND ANCHORS INTERMEDIATE FILAMENTS TO DESMOSOMES OF HEMIDESMOSOMES. MAY BE INVOLVED NOT ONLY IN THE CROSSLINKING AND STABILIZATION OF CYTOSKELETAL INTERMEDIATE FILAMENTS NETWORK, BUT ALSO IN THE REGULATION OF THEIR DYNAMICS.
SUBGUNIT: HOMODIMER OR HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structural protein; Cytoskeleton; Actin-binding;
                                                                                          DOMAIN: THE N-TERMINUS INTERACTS WITH ACTIN, THE C-TERMINUS WITH VIMENTIN, DESMIN, GRAP, CYTOKERATINS, LAMIN B; WHEREAS BOTH THE NAND THE C-TERMINUS CAN BIND INTEGRIN BETA-4.
                                                                                                                            REGULATES DISSOCIATION FROM
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                                                                                                                                                 -i- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
-i- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
-i- SIMILARITY: CONTAINS 3 PLECTIN REPEATS.
-i- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
-i- SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
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CENTRAL FIBROUS ROD DOMAIN
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SPECTRIN 2.
SPECTRIN 3.
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ATP-binding; Calmodulin-binding; Actin-binding;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

DOMAIN: THE RODIKE PALL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last ennotation update)
Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Bos taurus nonmuscle myosin heavy chain B mRNA, complete cds.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 10 DOMAIN.
                                                                                                                                                                                                                                                                           1976 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hara M., Ishiguro N., Shinagawa M.;
Bos taurus nonmuscle myosin heavy cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FISSUE-Brain cortex;
MEDLINE-95301542; PubMed-7782316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pro; IPR002017; Spectrin.
Pro; IPR001609; myosin_head.
PF000603; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002928; Myosin_tail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterPro; IPR000048; IQ_region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB022023; BAA36494.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 204-302 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fam; PF02736; Myosin_N; 1.
RINTS; PR00193; MYOSINHEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U15716; AAA87715.1;
                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PDUVUCC.
SMART; SM0015; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      toh K., Adelstein R.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                   1824 LRKASES 1830
                                                                               694 QRLATNS 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CBI_TaxID-9913;
                                                                                                                                                                                                                                                                           MYHA_BOVIN
Q27991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nterPro;
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1178 ELKKALEEETKSHEAQIQDMRQRHATALEELSEQLEQAKRFKANLEKNKQGLETDNKELA 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1298 EAEKKGIKFAKDAAGLESQLQDTQELLQEETRQKLNLSSRIRQLEEERSSLQEQQEE-EE 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1534
                                                                                                                                                                                                                                                                                                                                                                                    1120 IAELQEDFESEKASRNKAEKQKR--DLSBELEALKTELEDTLDTTAAQQELRTKREQEVA 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1633 IEAANKARDEVIK---QLRKLQAQMKDYQRELEEARASRDEIFAQSKESEKKLKSLEAEI 1689
                                                                                                                                                                                                                                                                        101 LIGEFSD-PAELGKLLQLVLGCAISCEKKQDHIQRIM-----TLEESVQHVVMEAIQEL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            617
                                                                                                                                                                                                                                                                                                                                                     154 MIKDIPDSLSPETYGNFDSQSRRYYFLSEEAEE-GDELQQRCLDLERQLMLLSEEKQSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                 213 QENAGLRERMGRPEG--EGTPGLTAKKLLLLQSQLEQLQEENFRLESGR-----EDERLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 C--AELEREVAELQHRNQALTSLAQEAQALKDEMDELR-QSSERAGQLEATLTSCRRRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1357 EARRSLEKQLQALQAQLTDTKKKVDDDLGTIENLEEAKK--KLLKDVEVLSQRLEEKALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain,
type A) (Nonmuscle myosin heavy chain,
MYH9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 ELRRA----GSLRAQLEAQRRQVQELQG--QRQEEAMKAEKWLFE----CRNLEEK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1475 EAEAREKETKALSLARALEEALEAREEAERONKOLRADMEDLMSSKDDVGKNVHELEKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1586 QNEEKK----RLLIKQVRELEAELE------DERKQRALAVASKKKMEIDLKDLEAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 618 ORPAAGAPPELHSLRTQLRERDVRIRHLEMDFEKSRSORE-----QEEKLLISAWYNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LRELRRQ-----VRQLEERNAGHAERTRQLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 YESVTKEKERLLAERDSL-----REANEELRCAQLQPRGLTQADPSLDPT-STPVDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAEILPAELRETLLRLQLENKRLCRQEAADRERQ-----EELQRHLEDANRARHGLETQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504 RLNQQQLSELRAQVEDLQKALQEQGGKTEDAISILLKRKLEEHLQKLH-EADLELQRKRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      563 YIEELEPPTDSSTARRIÈELQHNLQKKDADLRAMEERYRRYV-----DKARMVMQTMEPK
                                                                                                                                                                                           Query Match

8.8%; Score 321; DB 1; Length 1976;
Best Local Similarity 24.8%; Pred. No. 5.6e-07;
Matches 174; Conservative 120; Mismatches 286; Indels 122;
                                                                         COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL)
ALKYLATION (SH-2) (POTENTIAL)
                                                                                                                                                          MW; 6144354451C0F790 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1690 LOLOEELASSERARRHAEQ -- ERDELADEIANSASGKSALLD 1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             671 GMALQORAGEERAPAHAQSFLAQORLAŢNSRRGPLGRLASLN 712
                  Alkylation; Multigene family.
1 785 MYOSIN. HEAD-LIKE
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                                                        815
1976
185
701
711
                                                      786 8
845 19
178 1
701 7
711 7
1976 AA;
                                                                                                                                  MOD_RES
SEQUENCE
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Q62812;
Myosin; A
Coiled co
DOMAIN
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MYH9_RAT
KKW
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LQHRNQALTSLAQEAQALKDEMDELRQSSERAGQLEATLTSCRRRGELRELRRQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1991 (Rel. 19,
01-OCT-1994 (Rel. 30,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                 1278 LOVELDSVIGL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   richohyalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRHY_SHEEP.
P22793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRHY_SHEEP
                                                                                                                                                                                                                                                                                                         217
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                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modelide and prospective as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1228 ELANEVKALLQCKGDSEHKRKK---VEAQLQELQVK-----FSEGERVR-TELADKVSK 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1053 LEGDSTDLSDQIAELQAQIAELKMQLAKKEEELQAALARVEEEAAQKNMALKKIRELETQ 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1171 ILKKT---LEDEAKTHEAQIQEMRQKHSQAVEELAEQLEQTKRVKATLEKAKQTLENERG 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSPETYGNFDSQSRRYYFLSEE----AEEGDELQQRCLDLERQLMLLSEEKQSLAQENA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GL-RERMGRPEGEGTPGLTAKKLLLLQSQLEQLQEENFRLESGREDERLRCAELEREVAE 275
                                                                                                                                                     SUBDUIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, SIMILARITY: CONTAINS I MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS I 10 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 PAELGKLLQLVLGCAISCEKKQ----DHIQRIMT-LEESVQHVVMEALQELMTKDTPD-S 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 LQGISEDPG---PNWKLKVSNLKMVLRSLVEYSQDVLAHPVSEEHLPDVSL--IGEF-SD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                              Choi O.H., Park C., Itoh K., Adelstein R.S., Beaven M.A.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS,
CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALKYLATION (SH-1) (POTENTIAL)
ALKYLATION (SH-2) (POTENTIAL)
W; 9B9876D9681FB19E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50096; IQ; 1.
Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL). ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

8.8%, Score 320.5; DB 1;
Best Local Similarity 23.7%; Pred. No. 5.8e-07;
Matches 179; Conservative 133; Mismatches 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL).
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYOSIN HEAD-LIKE
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InterPro; IPR0000048; IQ_region.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01576; Myosin_tall; 1.
Pfam; PF02736; Myosin_N; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00063; myosin_head; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               704 70
1961 AA;
                                                                      SEQUENCE FROM N.A.
                                           NCBI_TaxID=10116
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MOD_RES
SEQUENCE
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DOMAIN
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repeat.";
J. Cell Biol. 110:427-436(1990).
J. Cell Biol. 10:427-436(1990).
J. Cell Biol. INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES
IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE
INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR
LAYER OF THE BPIDERMIS: IT LATER BECOMES CROSS-LINKED TO KIF BY
ISODIPEPTIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1589 VROVREMEABLE------DERKQRSIAMAARKKLEMDLKDLEAHIDTANKNREEAIK 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLRKLOAOMKDCMRDVDDTRASREEILAOAKENEKKLKSMEAEMIOLOEELAAAERAKRO 1699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1325 ISLSTKIKQMEDEKNSFREQLEBEEEBAKRNLEKQIATLHAQVTDMKKKMEDGVGCLETA 1384
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-1- SUBUNIT: HOMODIMER (PROBABLE).
-1- ALTERNATIVE PRODUCTS: AT LEAST TWO FORMS MAY BE PRODUCED BY
ALTERNATIVE SPLICING OF THE SAME GENE.
-1- TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES SUCH AS
THE INNER ROOT SHEATH (IRS) OF HAIR FOLLICLES AND MEDULLA, AND IN
THE EPITHELIA OF THE TONGUE, HOOF AND ROMEN.
-1- DOWAIN: CONSISTS OF NINE DOMAINS. DOMAIN I CONTAINS TWO EF HAND
CALCIUM-BINDING DOMAINS. DOMAINS 2-4. 6, AND 8 ARE ALMOST
ENTIRELY ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REPEATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: MONOMER (PROBABLE).
TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES SUCH AS TISSUE RPECIFICITY: FOUND IN THE HARD MEDULLA, AND IN THE FILIFORM PAPILLAE OF DORSAL TONGIE EPITHELIUM (PROBABLE).
DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND CACLUM-BINDING DOMAINS. 2-4, 6, AND 8 ARE ALMOST ENACIGURED AS A SERIES OF PEPTIDE REPEATS OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRANDED ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS OF DOMAINS 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The structure of human trichohyalin. Potential multiple roles as a functional EF-hand-like calcium-binding protein, a cornified cell envelope precursor, and an intermediate filament-associated (cross-
                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93280194; Pubmed-7685034; Lee S.-C., Kim I.-G., Marekov L.N., O'Keefe E.J., Parry D.A.D., Steinert P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'Keefe B.J., Hamilton B.H., Lee S.-C., Steinert P.M.; "Trichohyalin: a structural protein of hair, tongue, nail, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1731-1898 FROM N.A., AND CHARACTERIZATION MEDLINE-93315897; Pubmed-7686953;
                                                                                                                                                                                                                    01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                         1898 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epidermis.";
J. Invest. Dermatol. 101:65S-71S(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linking) protein.";
J. Biol. Chem. 268:12164-12176(1993)
                                                                                                                                                                         STANDARD;
           683 APAHAOSFLAQOR 695
                                                      986 DRKFREELSROER 998
                                                                                                                                                                                                                                            01-OCT-1994 (Rel. 30, 15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIFFERENTIATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                          CBI_TaxID=9606;
                                                                                                                                                                                                                                                                                           richohyalin.
                                                                                                                                                                         PRHY_HUMAN
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                                                                                                                                                    TRHY_HUMAN
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                                                                                                                               RESULT 8
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EQEE-ERREQOLRREQEERREQOLRREQEERREQOLRREQOLRREQOLRREQOLRREQO 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVAELQHRNQALTSLAQE----AQALKDEMDELRQSSERAGQLEATLTSCRRLGELR--- 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFSDPAELGK - - LLQL - VLGCAISCEKKQDHIQRIMTLEESVQ - - - - HVVMEAIQELMTK 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X 26 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 AQENAGLRERMGRPEGEGTPGLTAKKLLLLQSQLEQLQEENFRLESGREDERLRCAELER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 AA APPROXIMATE TANDEM REPEATS.
30 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                     EF-HAND 1 (LOW AFFINITY) (POTENTIAL)
EF-HAND 2 (HIGH AFFINITY) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 24.5%; Pred. No. 9.7e-07;
Matches 168; Conservative 110; Mismatches 269; Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRDROYR -> RSETGSTG (IN REF. -> K (IN REF. 2).
-> G (IN REF. 2).
-> G (IN REF. 2).
-> A74B5947FB62E31D CRC64;
                                                                                                                                                                                                                                                                EF-HAND 2 (HIGH AFFINITY) (1
6 X 13 AA TANDEM REPEATS OF
                                                                                                                                                                                                                                                                                                                                                                      (APPROXIMATE)
                                                                                                                                                                                                         Repeat; Calcium-binding
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                                          InterPro; IPR001751; CaBP_S100
                                                         InterPro; IPR002048; EF-hand.
InterPro; IPR002017; Spectrin.
Pfam; PF00036; efhand; 1.
Pfam; PF01023; S_100; 1.
                                                                                                                    Fram, PF01023; S.100; 1. ProDom; PP003407; CaBP_S100; PROSITE; PS00018; EF_HAND; 1. PROSITE; PS00303; S100_CABP_F.
                                                                                                                                                                                                                                                  33
73
390
Senew; HGNC:11791; THH
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                   MIM; 190370;
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CONFLICT
SEQUENCE
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Dunham I., Hunt A.R., Collins J.E., Brusklewich R., Beare D.M.,
A Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
Baggulley C., Balley J., Barlow K.R.,
Baggulley C., Balley J., Bridgeman A.M., Buck D., Burgess J.,
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Burtill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
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Aclare S., McMurray A.A., Milne S.A., Mortimore B.J.,
Aclare S., McMurray A.A., Milne S.A., Mortimore B.J.,
Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
Scott C.E., Spragon L., Steward C.A., Sulscon J.F., Syann R.M.,
Scott C.S., Spragon L., Steward C.A., Sulscon J.E., Syann R.M.,
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P35579; 060805;
01-JUN-1994 (Rel. 29, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain,
MYH9.
                                      386 ----WLFECRNLEEKYESVTKEKERLLAERDSLREANEELRCAQLQPRGLTQADPSLDP
                                                      441 TSTPVDNLAAEILPAELRETLLRLQLENKRLCRQEAADRERQEELQRHLEDANRARHGLE
                                                                                                                                             TQHRLNQ -- QQLSELRAQVEDLQKALQEQGGKTEDAISILLKRKLEEHLQKL---HEADL
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                               798 GRORL---SARPPLREQREROLRAEER 821
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                                                                                                                                                                                               ELQRKREYIEELEP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
A Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H.; Lao H.I.,
A Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nquyen T., Pan H.,
A Phan S., Ol S., Olan Y., Ray L., Ren O., Shaull S., Sloan D., Song L.,
A Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
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A Scroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
A Wilkinson P., Bodentelch A., Hartman K., Hu X., Khan A.S., Lane L.,
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Gdula D., Adelstein R.S., Weir L.;
"Human nonmuscle myosin heavy chains are encoded by two genes located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  May-Hegglin anomaly.",
Nat. Genet. 26:1.06-108(2000).
-I- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS,
CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seri M., Cusano M., Gangarossa S., Caridi G., Bordo D., Lo Nigro C.. Ghiggeri G.M., Ravazzolo R., Savino M., Del Vecchio M., d'Apolito M Iolascon A., Zelante L.L., Savoia A., Balduini C.L., Noris P., Magrini U., Belletti S., Heath K.E., Babcock M., Glucksman M.J., Aliprandis E., Bizzaro N., Desnick R.J., Martignetti J.A., "Mutations in MXH9 result in the May-Hegglin anomaly, and Fechtner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cochaker L.E., Gonzalez D.A., Tung N., Lemons R.S., le Beau M.M. Kraout M.A., Clayton L.K., Tenen D.G., 'Cellular myosin heavy chain in human leukocytes: isolation of 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA clones, characterization of the protein, chromosomal localization, and upregulation during myeloid differentiation."; Blood 78:1826-1833(1991).
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MEDLINE-20428193; PubMed-10973260;
Kelley M.J., Jawien W., Ortel T.L., Korczak J.F.;
"Mutation of MYH9, encoding non-muscle myosin heavy chain A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /ARIANTS MHA/FINS/SBS K-93; C-702; C-1165; H-1424 AND K-1841
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"Human nonmuscle myosin heavy chain mRNA: generation
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Proc. Natl. Acad. Sci. U.S.A. 87:1164-1168(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'The DNA sequence of human chromosome 22.";
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MEDLINE-90138958; PubMed-1967836;
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Nat. Genet. 26:103-105(2000).
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Tilahun Y., Wright H.;
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1240 KGDSEHKRKKVEAQLQELQVKFNEGERVRTELADKVTKLQVE-LDNVTGLLSQSDSKSSK 1298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 AELQHRNQALTSLAQEAQALKDEMDELRQSS----ERAGQLEATLTSCRRLGELRELRR 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390 CRNLEEKYESVTKEKERLLAERDSLREANEEL--RCAOLOPRGLTQADPSLDPTSTPVDN 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448 LAAEI -- LPAELRETLIRILQI, ENKRICRQEAADRERQEE---LQRHILEDANRARHGLETQ 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 NAGLRERMGRPEGEGT-PGLTAKKLLLLQSQLEQLQBENFRLESGREDERLRCAELEREV 273
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Last annotation update
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FTIG=VAR_010797
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-> EE (
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                       DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTEN COMPOSED OF 4 HEPTAPETIDES. CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILS.

DISEASE: DEPECTS IN MYH9 ARE THE CAUSE OF MAY-HEGGLIN ANOMALY (MAA), AN AUTOSONAL DOMINANT MACROTHROMBOCYTOPENIA CHARACTERIZED BY THROMBOCYTOPENIA, GLANT PLATELETS AND LEUKOCYTE INCLUSIONS. DISEASE: DEPECTS IN MYH9 ARE THE CAUSE OF FECHTNER SYNDROME
                                                                                                                                                                                             FEDUS AND THE STATE THE CONTROL OF THE STATE THE CHARACTERIZED BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUKOCYTE INCLUSIONS.
BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUKOCYTE INCLUSIONS.
WITH ADDITIONAL ALPORT-LIKE CLINICAL FEATURES OF SENSORINEURAL DEAFUSES, CATARACTS AND NEPRITIS.
DISEASE: DEFECTS IN WHY ARE THE CAUSE OF SEBASTIAN SYNDROME (SBS), AN AUTOSOMAL DOMINANT MACROTHROMBOCYTOPENIA CHARACTERIZED BY THROMBOCYTOPENIA, GIANT PLATELETS AND LECKOCYTE INCLUSIONS.
DISEASE: DEFECTS IN WHY ARE THE CAUSE OF AN AUTOSOMAL DOMINANT FORM OF NONSYNDROMIC SENSORINEURAL DEAFUSES (DENALT) WHICH IS CHARACTERIZED BY PROGRESSIVE HEARING IMPAIRMENT AND
LIGHT CHAIN SUBUNITS (MLC) AND 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
Coiled coil; Alkylation; Multigene family; Disease mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS I MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 1 IQ DOMAIN.
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ALKYLATION (SH-2) (POTENTIAL)
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ATP (POTENTIAL).
ACTIN-BINDING.
ACTIN-BINDING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nterPro; IPR004009; Myosin_N.
nterPro; IPR002018; Myosin_tail.
nterPro; IPR002017; Spectrin.
nterPro; IPR001609; myosin_head.
fam; PF00063; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1
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EMBL; M69180; AAA61765.1
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Genew; H
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Myosin; Muscle
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                                                                                                                                       TISSUE-Adductor muscle, MEDLINE-92011595; PubMed-1917970; MEDLINE-92011595; PubMed-1917970; MINITERY L., Goodwin E.B., Szent-Gyoergyi A.G., Complete primary structure of a scallop striated muscle myosin heavy chain. Sequence comparison with other heavy chains reveals regions that might be critical for regulation."; J. Biol. Chem. 266:18469-18476(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHOOLING WINDSCLE CONTRACTION.

-1- FUNCTION: MUSCLE CONTRACTION.

-1- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ATPASE
ACTIVITY THAT IS ACTIVATED BY F-ACTIN.

-1- SUBDUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

-1- SUBCELLULAR LOCATION: Thick filaments of the myolibrils.

-1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.
Aequipecten irradians (Bay scallop).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (*RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 777-836.

REDLINE-94173332; PubMed-8127365;

Ale X., Harrison D.H., Schlichting I., Sweet R.M., Kalabokis V.N.

Szent-Gyorgyi A.G., Cohen C.;

Structure of the regulatory domain of scallop myosin at 2.8-A

esolution.",
                                                                                                                                                                                                                                                                                                                                                TISSUE-Adductor muscle;
MEDLINE-910881919; Pubmed-2263488;
MYLLray L., Goodwin B.B., Szent-Gyorgyi A.G.;
"Nucleotide sequence of full length cDNA for a scallop striated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structure of the regulatory domain of scallop myosin at resolution: implications for regulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 777-836 MEDLINE-96419133; Pubmed-8805510;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       muscle myosin heavy chain.";
Nucleic Acids Res. 18:7158-7158(1990).
                                                  Pectinoidea; Pectinidae; Argopecten.
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InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_Lail.
InterPro; IPR002017; Spectrin.
InterPro; IPR001609; myosin_head.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00193; MYOSINHEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X55714; CAA39247.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ture 368:306-312(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00015; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB; 1SCM; 30-APR-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; S13557; S13557
                                                                                                                                                                                                                                                                                                                             SOUENCE FROM N.A.
                                                                                                                      SEQUENCE FROM N.A.
                                                                      WCBI_TaxID=31199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02736:
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993 KKALEEANKKTSDSLQAEEDKCNHLNKLKAKLEQALDELEDNLEREKKVRGDVEKAKRKV 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1280 ENSDLTRQLEDAEHRVSVLSKEKSQLSSQLEDARRSLEEETRARSKLQNEVRNMHADMDA 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1460 LQSELENSQKESRGYSAELYRIKASIEEYQDSIGALRRENKNLADEIHDLTDQLSEGGRS 1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 ODVLAHPVSEEHLPDVSLIGEFSDPAELGKLLQLVLGCAISCEKKODHIQRIMTLEESVQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1165 EAELLKIRRDLEEASLQHEAQISALRKKHQDAANEMADQVDQLQKVKSKLEKDKKDLKRE 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1400 ITEAANAKCSALEKAKSRLQQELEDMSIEVDRANASVNQMEKKQRAFDKTTAEWQAKVNS 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 ---LOBENFRLESGREDERLRC-----AELEREVAELQHR------NQALTSL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQEAQALKDEMDEL----RQSSERAGQLEATLTSCRRRLGE----LRELRRQVRQLEERN 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- CAQLOPRGLTQADPSLDPTSTPVDNLAAEILPAELRETLLRLQL 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENKRICRQ -- EAADR ------ERQEELQRHLEDANRARHGLETQHRLNQQQLSE 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              570 PIDSSTAR------RIEELQHNLQKKDADLRAMEERYR-----RYVDKARM 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            802 QDQRIGLS---VIQRNIRKWLVLRNWQW-------WKLYSKVKPLLSIARQEEEMK 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            848 EQLKOMDKMKEDLAKTERIKKELEEQNVTLL------EQKNDLFLQLQTLEDSMG 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 HVVMEAIQELMIKDIPDSLSPETYGNFDSQSRRYYFLSEEAEEGDELQQRCLDLERQLML 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                897 D-QEERVEKLIMQK-----ADFESQIK------ELEERLLDEEDAAAD 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             933 LEGIKKKMEADNANLKKDIGDLENTLOKAEQDKAHKDNQISTLOGEISQQDEHIGKLNKE 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339 AGHAERTRQLEDELRRAGSLRAQLEAQR----RQVQELQGQRQEEA------MKA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 QDLSSGLAVAYVLNQIDPSWF---NEAWLQGISEDPGPNWKL--KVSNLKMYLRSLVEYS 83
protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1225 MDDLESOMTHNMKNKGCSE---KVMKQFESOMSDLNARLEDSORSI--NELQSOKSRLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 513 LRAQVEDLOKA----LOEGGGKTEDAISILLKRKLEEHLOKLHEADLELORKREYIEELEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --DFEKSRSQREQEEKLLISAWYNMGMALQQRAGEERAPAHAQSFLAQQRLATNSR 701
                                                                                                                                                                                                                                                                                                                                                                                                                         8.6%; Score 312; DB 1; Length 1938;
llarity 20.1%; Pred. No. 1.3e-06;
Conservative 153; Mismatches 287; Indels 228;
                                                                                                          RODLIKE TAIL (S2 AND LMM DOMAINS)
COILED COIL (POTENTIAL)
TAP (BY SIMILARITY)
ALKYLATION (SH-1) (BY SIMILARITY)
ALKYLATION (SH-2) (BY SIMILARITY)
                                Calmodulin-binding; 3D-structure. MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                      222821 MW; A5CCE4127D1A4896 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 LSEEKQSLAQENAGLRERMGRPE----GEGTPGLTAKKLLLLQSQLEQ-
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                                                                                     805
1938
1938
                                                                                                                                                                                                                                                                                                                                                                   1938 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418, NEELR-----
                       ATP-binding; Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 168;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                     DOMAIN
NP_BIND
MOD_RES
MOD_RES
                                                                                  DOMAIN
                                                                                                                DOMAIN
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DOMAIN
DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBGNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNIT: (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MHC) AND 2 CHAIN SUBUNITS (MHC-2).
-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CRARACTERISTIC FOR ALPHA-HELICAL COILES COILS.
-1- SIMILARIYY: CONTAINS 1 NYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                chain-B and
                                                                                                                                                                                                                                                                                                                                                                                                                                      two genes located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: CELLULAR MYGSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS, CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
1520 THELDKARRRLEMEKEELQAALEEAEGALEQ----EEAKVMRAQLEIATVRNEIDKR 1572
                                                                                                                    01-FEB-1996 (Rel. 33, Last sequence update).
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain,
type B) (Nonmuscle myosin heavy chain-B) (NMMRC-B).
MYH10.
                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                  Phillips C.L., Yamakawa K., Adelstein R.S.; aCloning of the cDNA encoding human nonmuscle myosin heavy analysis of human tissues with isoform-specific antibodies. J. Muscle Res. Cell Motil. 16:379-389(1995).
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 63-722 FROM N.A.
MEDLINE-91316803; PubMed-1860190;
Simons M., Wang M., McBride O.W., Kawamoto S., Yamakawa K.,
Gdula D., Adelstein R.S., Weir L.;
*Human nonmuscle myosin heavy chains are encoded by two gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50096; IQ; 1.
Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
Coiled coil; Alkylation; Multigene family.
                                                                             Ā
                                                                             1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMR001609; myosin_head
                                                                                                                                                                                                                                                                                         MEDLINE-96025307; PubMed-7499478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02736; Myosin_N; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nterPro; IPR000048; IQ_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00063; myosin_head; 1.
                                                                                                              (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          on different chromosomes.";
Circ. Res. 69:530-539(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M69181; AAA99177.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P10587; 1BR2.
Genew; HGNC:7568; MYH10.
                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B61231; B61231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00015; IQ;
                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR004009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; IPR002017
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 160776;
                                                                                                            01-JUN-1994
                                                                             MYHA_HUMAN
P35580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nterPro;
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                                                                 MY HA_HUMAN
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28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1298 EAEKKGIKFAKDAASLESQLQDTQELLQEETRQKLNLSSRIRQLEEE---KNSLQEQQEE 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1355 EEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEAKKKLLKDAEALSQRLEEKALA 1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1475 EAEAREKETKALSLARALEEALEAKEEFERONKOLRADMEDLMSSKDDVGKNVHELEKSK 1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           618 ORPAAGAPPELHSLRTQLRERDVRIRHLEMDFEKSRSQRE-----QEEKLLISAWYNM 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1178 ELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKRFKANLEKNKGGLETDNKELA 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364
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                                                                                                                                                                                                                                                   101 LIGEFSD-PAELGKLLQLVLGCAISCEKKQDHIQRIM-----TLEESVQHVVMEAIQEL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 YESVTKEKERLLAERDSL-----REANEELRCAQLQPRGLTQADPSLDPT-STPVDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 AAEILPAELRETLLRLQLENKRLCRQEAADRERQ-----EELQRHLEDANRARHGLETQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLNQQQLSELRAQVEDLQKALQEQGGKTEDAISILLKRKLEEHLQKLH-EADLELQRKRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         563 YIBELEPPTDSSTARRIEELQHNLQKKDADLRAMEERYRRV-----DKARMVMQTMEPK
                                                                                                                                                                                                                                                                                154 MIKDIPDSLSPETYGNFDSQSRRYYFLSBEAEE-GDELQQRCLDLERQLMLLSBEKQSLA
                                                                                                                                                                                                                                                                                                                                                                           1120 IAELQEDFESEKASRNKAEKQKR--DLSEELEALKTELEDTLDTTAAQQELRTKREQEVA
                                                                                                                                                                                                                                                                                                                                                                                                                       QENAGLRERMGRPEG--EGTPGLTAKKLLLLQSQLEQLQEENFRLESGR-----EDERLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C--AELEREVAELQHRNQALTSLAQEAQALKDEMDELR-QSSERAGQLEATLTSCRRRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --LRRQVRQLEE-----RNAGHAERTRQLEDELRRAGSLRAQLEA
                                                                                                                                                                                                             Indels 125;
                                                                                                                                                               Length 1976;
                                                         35 ATP (POTENTIAL).
31 ALKYLATION (SH-1) (POTENTIAL).
328938 MW. B2BB87FF35EA124F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Buryarchãeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                      IQ.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                         Conservative 117; Mismatches 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1690 LOLOEELASSERARRHAEO--ERDELADEITNSASG 1723
                                                                                                                                                                 8.4%; Score 306.5; DB 1
24.3%; Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) DNA double-strand break repair rad50 ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 671 GMALQQRAGEERAPAHAQSFLAQQRLA---TNSRRG 703
MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      886 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40, Created)
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Archaeoglobus fulgidus.
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1976
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701
711
                      786 83
845 197
178 18
701 70
711 77
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POWERSON STREET, SPECIAL SPECI

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390 DLLSKAKEEEKEITEKLKKLIAKKSSLKTRGAQLKKAVEELKSAE----RTCPVCGRELDE 446
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Structural differences in the
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NCBI_TaxID=7962;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rad50/mre11 complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mre11 by unwinding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----AIQELMTKDTPDSLSPETYGNFDS 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The complete genome sequence of the hyperthermophilic, sulphate educing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                    Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and/or repositioning DNA ends into the mrell active site (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Forms a complex with mrell (By similarity).
SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the Swiss Institute of Bioinformatics and the
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                                                                                                    / ATCC 49558;
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InterPro; IPR003395; SMC_N.
InterPro; IPR002017; Spectrin.
Pfam; PF02463; SMC_N; I.
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                                                                                                                                 TEDLINE-98049343; PubMed-9389475;
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SUBBNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBGNITS (MIC), 2 ALKALI LIGHT CHAIN SUBGNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBDNITS (MLC-2), SUBCELLULAR DOCATION: Thick filaments of the myofibrils. DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97176447; PubMed-9023993;
Imal J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.;
TeDNA cloning of myosin heavy chain isoforms from carp fast skeletal
muscle and their gene expression associated with temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY. MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
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                                                                                                                                                                              EHRKNIMAEYTREMKRIAEELAKADEIEKKLKERLEKVEKALEKOETVLKYROMVDELKA
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T-----STPVDNLAAEILPAELRETLLRLQLE--NKRLCRQEAADRERQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watabe S., Imal J., Nakaya M., Hirayama Y., Okamoto Y., Masaki H. Uozumi T., Hirono I., Aoki T.; "Temperature accilimation induces light meromyosin isoforms with different primary structures in carp fast skeletal muscle."; Blochem. Blophys. Res. Commun. 208:118-125(1995).
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                                                                                                   CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS
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16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, fast skeletal muscle.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                            HLEDANR---
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                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1059 DLKLAQESIMDLENE---KQQSDEKIKKKDFEISOLLSKIEDEQSLGAQLQ----- 1106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RQSSERAGQLEATLTS-CRRRLGELRELR----RQVRQLEERNAGHA-----ERTRQL 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 NEKMVERSEVEYSODVLAHPVSEEHLP----DVS-LIGEFSDPAELGKLLQLVLGCAISC 125
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MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HAM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myosin; Muscle protein; Colled coll; Thick filament; Actin-binding; ATP-binding; Methylation; Alkylation; Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1935;
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ALKYLATION (SH-1).
ALKYLATION (SH-2).
                                                              SUBFRACMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW; 9A1244B67D63C83B CRC64;
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HINGE.
COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 180; Conservative 114; Mismatches 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.4%; Score 305,5; DB 1
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ACTIN-BINDING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probam: PF02736; Myosin_N; 1.
PRINTS; PR00193; MYOSINHEAVY.
Probom; PD000355; Myosin_head; 1.
SWART; SMO015; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO04009; Myosin_N.
PR002928; Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myosin_tail; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00063; myosin_head; 1
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1935 AA;
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SEQUENCE
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      THILITITIES AND BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH 
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numen periplakin: genomic organization in a clonally unstable region of chromosome 16p with an abundance of repetitive sequence elements."; Genomics 56:160-168(1999).
                                                                                                                                            1467 ELEGAQKEARSLSTELFKMKNSYEEALDHLETLKRENKNLQQEISDLTEQLGETGKSIHE 1526
                                                                                                                                                                                                                                                                                                                                                                       1527 LEKAKKTVESEKSEIQTALEEAEGTLEHEESKILRVQLELN-QVKSEIDRKLAEKDEEME 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1586 QIK----RNSQRVIDSMQSTL---DSEVRSRNDALRVKKKMEGDLNEMEIQ-LSHANRQA 1637
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                                                  1352 QEAKAEL---ORGMSKANSEV--AOWRTKYETDAIORTEELEEAKKKLAORLODAEESIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                          --- ROEAAD-----REROEELOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Keratinocytes;
MDDLINE-98075094; PubMed-9412476;
RUhrberg C., Hajlbaker M.A.N., Parry D.A.D., Watt F.M.;
Ruhrberg C., novel component of cornified envelopes and d
"Periplakin, a novel component of cornified envelopes and d
that belongs to the plakin family and forms complexes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Rothenberger K., Tan E.M.L., Ryoo Y.W., Cho B.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aho S., McLean W.H.I., Li K., Uitto J.;
Ano S., McLean W.H.I., Li K., Uitto J.;
CDNA cloning, mRNA expression, and chromosomal mapping
mouse periplakin genes.";
Genomics 48:242-247(1998).
                                                                                                                                                                                                                     --ARHGLETQHRLN---QQQLSELRAQV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      682 RAPAHAQS----FLAQQRLATNSRRGPLGRLASLN 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99162402; PubMed-10051401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell Biol. 139:1835-1849(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IISSUE-Keratinocytes;
MEDLINE-98190524; PubMed-9521878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IISSUE-Brain;
MEDLINE-98290545; PubMed-9628581;
                                                                                                             -----LRETLLRLQLENKRLC----
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1602 ADSGINHDSRLWSLERELDDLKRLSKDKDLEIDELQKRLGSVAVKREQRENHLRRSI--- 1658
    960 EQHKNQLLQEELEALQLQLRALEQETRDGGQEYVVKEVLRIEPDRAQADEVLQLREELEA 1019
                                                                    1250 RLREEIVDKTRLIERCDLEIYQLKKEIQALKDTKPQVQTKEVVQEILQFQEDPQTKEEVA 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1485 RKLAALEKAEVKEKVVLSESVQVEKGDTEQEIQ-RLKSSLEEESRSKRELDVEVSRLEAR 1543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 LESGRE------DERLRCAELEREVAELQHRNQALTSLAQEAQALKDEMDELRQSSE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---SLDPTSTPVDNLAAEILPAELRETLLRLQLENKRLCRQEAADRERQEELQR-- 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --PPELHSLRTQLRERDVRIRHLEMDFEKSRSQREQEEKLLISAWYNM 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aquifex aeolicus.
Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             515 AQVEDLQKA------LQEQGGKTEDAISILLKRKLEEHLQKLHEADLELQRKREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --HL-----EDANRAR-HGL-----ETQHR--LNQQQLSELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              564 IEELEPPTDSSTARR--IEELQHNLQKKDADLRAMEERYRRYVDKARMVMQTMEPKQRPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                ----EEKYESVTKEKERLLAERDSLREANEELRCAQLQPRGLTQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Probable DNA double-strand break repair rad50 ATPase.
RAD50 OR AQ_1006.
                                                                                                                                                                                                         306 RAGOLEATLTSCRRLGELRELRRQVRQLEERNAGHA--ERTRQL--
                                                                                                                                                                                                                                                                                                                                                                     --EDELRRAGSLRAQLEAORR---OVQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             978 AA.
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                                             218 LRERMGRPEGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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067124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not removed. Usage by and for commercial reement (See http://www.lsb-slb.ch/announce/
                                                                                                                                                                                                                                             SSUE SPECIFICITY: EXPRESSED IN STRATIFIED SQUAMOUS EPITHELIA AND
                                                                                                                                                                                SUBCULT: HOMODIMER OR A HETERODIMER WITH EVPL (POTENTIAL).
SUBCELLULAR LOCATION: ASSOCIATED WITH DESMOSOMES AND INTERMEDIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytoskeleton; Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 KQDHIQRIMTLEESVQHVVMEAIQELMT-----KDTPDSLSPETYGNFDSQSRRYYFLSE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 906 RROLENEVKSTQEEIWTLRNQGPQESVVRKEVLKKVPDPVLEESF----QQLQR--TLAE 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SLAQENAG 217
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                                           X
            Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. IX "Prediction of the coding sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA Res. 5:31-39(1998).
-!- FUNCTION: COMPONENT OF THE CORNIFIED ENVELOPE OF KERATINOCYTES.
MAY LINK THE CORNIFIED ENVELOPE TO DESMOSOMES AND INTERMEDIATE
                                                                                                                                                                                                                                                             IN SOME OTHER EPITHELIA. INDUCTION: DURING DIFFERENTIATION OF EPIDERMAL KERATINOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

8.4%; Score 304.5; DB 1; Length 1756;
Best Local Similarity 21.4%; Pred. No. 2.5e-06;
Matches 183; ¿conservative 129; Mismatches 270; Indels 275;
Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 2 PLECTIN REPEATS.
SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
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BAA25494.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 448 LAAEILPAELRETLLRIQ------LOOKRICROEAADRERQEELOR 487
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the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 PGLTAKKLLLLQSQLEQLQEENFRLESGREDER------LRCAELEREVAELQHRNQ 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DELRQSSERAGQLEATLTSCRRLGELREL 327
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                              rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding and/or repositioning DNA ends into the mrell active site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.3%; Score 302; DB 1; Length 978;
22.1%; Pred. No. 1.8e-06;
Lve 122; Mismatches 220; Indels 176; Gaps
           involved in DNA double-strand break repair (DSBR). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.

NP BIND 32 39 ATP (BX SINTARITY).

DOMAIN 160 826 COILED COIL (POTENTAL).

SEQUENCE 978 AA; 115897 WW; 9B0F2BF51ADD1151 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 KEILKELSQLSSSLKEKEREYEQAKQEFEDLSERVEKGKKLVAE----TEEKLEKIKEL

    SUBUNIT: Forms a complex with mrell (By similarity).
    SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.

                                                                                                                                                                                                                                                                                                           Usage by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115897 MW;
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673 KSKLE 677

Search completed: March Job time: 36.2109 secs

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EFSDPAELGK--LLQL-VLGCAISCEKKQDHIQRIMTLEESVQ----HVVMEAIQELMTK 156
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                                                                                                      March 4, 2003, 14:55:07; Search time 24 9261 Seconds (without alignments) 848.711 Million cell updates/sec
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3638
1 MSYDKAELCGSLLTWLQTFH......SRRGPLGRLASLNLRPTDKH 719
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/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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                                                                                                                                                                                                                                                                                                     262574 seqs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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798 GRORL---SARPPLREOREROLRAEER 821
                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 30-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Feditick, Michael F.
REGISTRATION NUMBER: 36,75
                                                                                                                                                                                                                                                                                                                                  1898 amino acids
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: (714) 760-9502
FOR SEQ ID NO: 9
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203 EPPDEBQLRRRELLELRRKGREEKQQQRRERQDRVFQEEEEKEWRKRETVLRKEEEKLQE 262
                                        DIPD---SLSPETYGNFDSQSRRY--YFLSEEAEEGDELQQRCLDLERQLMLLSEEKQSL.211
                                                                                                                                                                          ---QQEERREQQLR----REQEERREQQLRR 353
                                                                                                                                                                                                        272 · EVAELQHRNQALISLAQE---AQALKDEMDELRQSSERAGQLEATLISCRRRLGELR--- 325
                                                                                                                                                                                                                                                                                         326 ELRRQVRQLEERNAGHAERTRQLEDELRRAGSLRAQLEAQRRQVQELQGQRQEEAMKAEK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----ERREQOLRREQEERR--EORLKROEEEERLOORLRSEQOLRR--E 560
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                                                                              EEPORORELOEE-----EEOLRKLERQELRRERQEEEOQOOR-LRREQQLRRKQEEERRE
                                                                                                                       212 AQENAGLRERMGRPEGEGTPGLTAKKLLLLQSQLEQLQEENFRLESGREDERLRCAELER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
URRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          692 AQQRLATNSRRGPLGRLASLNLRPTDK 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 94, Application US/08800644 Patent No. 5958752 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
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Lee, Seung-Chul
Kim, In-Gyu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chung, Soo-Il
                                                                                                                                                                  317 QQEER--REQQERRE---
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APPLICANT:
APPLICANT:
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EFSDPAELGK -- LLQL - VLGCAISCEKKQDHIQRIMTLEESVQ --- - HVVMEAIQELMTK 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVAELOHRNQALISLAQE---AQALKDEMDELRQSSERAGOLEATLISCRRRLGELR--- 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELRROVRQLEERNAGHAERTRQLEDELRRAGSLRAQLEAQRRQVQELQGQRQEAMKAEK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIPD---SLSPETYGNFDSQSRRY--YFLSEEAEEGDELQQRCLDLERQLMLLSEEKQSL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263. EEPQRQRELQEE-----EEQLRKLERQELRRERQEEEQQQQR-LRREQQLRRKQEEERRE 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQENAGLRERMGRPEGEGTPGLTAKKLLLLQSQLEQLQEENFRLESGREDERLRCAELER
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                                                                                                                                                                                                                                                                                                                                                                  Length 1898;
                                                                                                                                                                                                                                                                                                                                                            8.7%; Score 315; DB 2; 24.5%; Pred. No. 1.3e-15;
                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 24.5%; Pred. No. 1.3e
Matches 168; Conservative 110; Mismatches
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          692 AQQRLAINSRRGPLGRLASLNLRPIDK 718
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOSTON
                                                                                                                                                                                                                                                                                                                 525 QE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 GISEDPGPNWKLKVSNLKMVLRSLVEYSQDVLAHPVSEEHLPDVSLIGEFSDPAELGKLL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----MGDILQTPQFQMRRLKKQLADERSNRDELE--L 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 QLVLGCAISCEK-----KQDHIQRIMTLEESVQHVVME--AIQELMTKDTPDSLSPETY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 ETLKQCQDLKTEKSOMDRKINQLSE--ENGDLSFKLREFASHLQQLQDALNELTEEHSKA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 TQE---WLEKQAQLEKELSAALQDKKCLEEKNEILQGKLSQLEEHLSQLQDNPPQEKGEV 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------QALTSLA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 GNF-----DSQSRRYYFLSEEAEEGD-----ELQQRCLDLERQLMLLSEEKQSL 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294; Indels 233;
                                                    APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: "NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
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Best Local Similarity 23.2%; Pred. No. 2.8e
Matches 198; Conservative 130; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 DKAELCGSLLTWLQTFHVPSPCAS - - PQDLSSGLAVA
                                                                                                                                                                                                2: TESTA, HURWITZ & THIBEAULT
125 HIGH STREET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US/08/466,390
06-JUN-1995
Sequence 4, Application US/08466390
Patent No. 5686562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEY/AGENT INFORMATION:
3: PITCHER ESQ, EDMUND R
ISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 ---- LRCAELEREVAELQHRN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  URRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                          OMPUTER READABLE FORM:
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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----GAPPELHS----LRTQLRERDVRIRHLEMDF----EKSRSQREQEEKLLISAWYNM 670
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                                        340 GHAERTROLEDELRRAGSLRAQLEAQ---RROVQELQG--QRQEEAMK--AEKWLFECRN 392
                                                                                                                                                                                                                                                               698 DOLOEOLOALKESLKVTKGSLEEEKRRAADALEEQORCISELKAETRSLVEOHKRERKEL 757
                                                                                                                                                                                                                                                                                                                                           182 ---QEELQRHLEDANRARHGLETQHR----LNQQQ--LSELRAQVEDL-----QKAL 524
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                                                                                                                    393 LEEKYESVTKEKERLLAERDSL---REANEELRCAQLQ
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Patent No. 5698439
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                           COUNTRY:
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                                                                                                                                               CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 LGDVLQLETLKQEAATLAANNTQLQARVEMLETERGQQEAKLLAERGHFEEEKQQLSSLI 468
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                                                                                                                                                                                                                                                                                                                                                                                                                294 ETLKOCODLKTEKSOMDRKINQLSE--ENGDLSFKLREFASHLOQLODALNELTEEHSKA 351
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                                                                                                                     4 DKAELCGSLLTWLQTFHVPSPCAS---PQDLSSGLAVA-----YVLNQIDPSWFNEAWLQ 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---QEELQRHLEDANRARHGLETQHR-----LNQQQ--LSELRAQVEDL-----QKAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434 ADPSLDPTSTPVDNLAA-----EILPAELRETLLRLQLENKRLCRQEAADRER----
                                                                                  Indels 233;
                                         Length 2101;
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llarity 23.2%; Pred. No. 2.8e-15;
Conservative 130; Mismatches 294;
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Patent No. 5780596
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LRCAELEREVAELQHRN---
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                                                        Similarity
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                                                                            Matches 198;
JS-08-470-950-4
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139 DGLNLNEDLENFLOKAPVPSTCSSTFPEELSPPSHQAKREIRFLELQKVASSSSGNNFLS 198
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                                    OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2101,
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                                 NOVEL MALIGNANT CELL TYPE MARKERS INTERIOR NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.25
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Matches 198; Conservative 130; Mismatches
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CEL
TITLE OF INVENTION: INTERIOR NUCLEAR MA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 125 HIGH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/467,781
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: PITCHER ESO, EDMUND R REGISTRATION NUMBER: 27,829 REFERENCE/DOCKET NUMBER: MTE TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                      : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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36;

tches 198; Conservative 130; Mismatches 294; Indels 233; Gaps

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. HAQQLATAAEEREASLRERDAALKQLEALEKEKAAKLETLQQQLQVANEARDSAQTSVTQ	EILPAELRETLLRLOLENKRLCROEAADRER		QEELQRHLEDANRARHGLETQHRLNQQQLSELRAQVEDLOKAL   :	QGGKTEDAISILLKRKLEEHLQKLHEADLELQRKREYIEELEPPT	EEERAGRKGLEARLLQLGEAHQAETEVLRRELAEAMAAQHTAESECEQLVKEVAAWR	DSSTARRIEELGHNLQKKDADLRAMEERYRRYVDKARMYMQIMEPKQRPAA-	-CEKARQELQ-	EKS	SROONKLAELHANLARALOOVQEKEVRAOKLADDLSTLOEKMAATSKEVARL							ÞΕ	4						#1.		-									5
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ASLRE	NLAA -	 ELQAC	ANRARE	06GF	LLQLGE	NLQKKI ::	GAMFOE	<b>LR</b> I	LARALC		TA 933			i	Ľ,	٠	6	ESTA HURWITZ			FORM:	ğ, ο	tIn Re	N DATA	435	Ä.	ORMATI	BER:	INFORM 7248-7(	8-7100 ID NO	tisrice	ear protein		0
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AQQLAT	DPSLDP	QREKAE	OEEL   :      CEOL	OE	SERAGR	SSTARR	SYEDSO	GAP	ROONKL	MALOOR - ::	STLVRK		187-4 4. App	5783	ANT:	2.5	OF SE	ADDRESSEE:	. M.	E: MA FRY: USA	UZIO ER REA	MEDIUM TYPE: COMPUTER: I	OPERATING SOFTWARE:	r APPL ICATIO	FILING DATE: CLASSIFICATION:	APPLIC ICATIO	FILING DATE: TORNEY/AGENT	STRATI	MMUNIC PHONE:	FAX: ION FO	CE CHA	LOGY:	87-4	
581.H	434 A	641 A	482 - 698 DQ	525 01	758 EI	572 DS	815 DC				920 -	۰ د	195-4	Patent No. 5783403	APPLICANT:	TITLE OF IN	NUMBER OF SEQUENCES	ADDRES	CITY	COUNTRY	COMPUTER	COMPUT	SOFT	CURRENT APPLICATION DATA: APPLICATION NUMBER: US		PRIOR A	FILING DATE: ATTORNEY/AGENT INFORMATION: MAME: PIECUED DEC. EDUIN	REGI	TELECOMMUNICATION INFORMATION TELEPHONE: & 617/248-7000	TELEFAX: 617/248-7100 INFORMATION FOR SEQ ID NO:	SEQUENCE CHARACTERISTICS LENGTH: 2101 amino ac myDE: amino acid	TOPOLOGY: 1	-08-195-487	+ c/1
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8.6%; Score 311.5; DB 1; Length 2101; 23.2%; Pred. No. 2.8e-15;

Query Match Best Local Similarity

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352 TQE---WLEKQAQLEKELSAALQDKKCLEEKNEILQGKLSQLEEHLSQLQDNPPQEKGEV 408
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                                                                                             GISEDPGPNWKLKVSNLKMVLRSLVEYSQDVLAHPVSEEHLPDVSLIGEFSDPAELGKLL 115
                                                                                                                                           199 GSPASP----- 235---- 235
                                                                                                                                                                                       116 QLVLGCAISCEK-----KQDHIQRIMTLEESVQHVVME--AIQELMTKDTPDSLSPETY 167
                                                                                                                                                                                                                                                                                                                  294 ETLKQCQDLKTEKSQMDRKINQLSE--ENGDLSFKLREFASHLQQLQDALNELTEEHSKA 351
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                                                                                                                                                                                                                                                                               168 GNF------DSQSRRYYFLSEEAEEGD-----ELQQRCLDLERQLMLLSEEKQSL 211
                                                                                                                                                                                                                                                                                                                                                                          AQENAGLRERMGRPEGEGTPGLTAKKLL----LLQSQLEQLQEENFRLESGREDER--- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434 ADPSLDPTSTPVDNLAA-----EILPAELRETLLRLQLENKRLCRQEAADRER---- 481
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4 DKAELCGSLLTWLQTFHVPSPCAS--PQDLSSGLAVA----YVLNQIDPSWFNEAWLQ 55
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atent No. 5882876
GENERAL INFORMATION:
APPLICANT: TOURATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: UNVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
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                                                                                                                                                       116 QLVLGCAISCEK-----KQDHIQRIMTLEESVQHVVME--AIQELMTKDTPDSLSPETY 167
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                                           ---QEELQRHLEDANRARHGLETQHR----LNQQQ--LSELRAQVEDL-----QKAL 524
                                                                                 698 DOLÓEGLGALKESLKVTKGSLEEEKRRAADALEEGGRCISELKAETRSLVEGHKRERKEL 757
                                                                                                                              -- QGGKTEDAISILLKRKLEEHLQKLHEADLELQRKREYIEELEPPT 571
                                                                                                                                                                                                                       DSSTARRIEELQHNLQKKDADLRAMEERYRRYVDKARMVMQTMEPKQRPAA------ 622
641 AQREKAELSRKVEELQACVETARQEQHEAQAQVAELELQLRSE---QQKATEKERVAQEK 697
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CURRENT FILING DATE: 1999-11-30
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Patent No. 6287790
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Best Local Similarity 23.2%; Pr
Matches 198; Conservative 130;
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SOFTWARE: PatentIn V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHAERTRQLEDELRRAGSLRAQLEAQ --- RRQVQELQG -- QRQEEAMK -- AEKWLFECRN 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.6%; Score 311.5; DB 2; Best Local Similarity 23.2%; Pred. No. 2.8e-15; Matches 198; Conservative 130; Mismatches 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 LEEKYESVTKEKERLLAERDSL---REANEELRCAQLQ----
                        TESTA, HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                         07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 248-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACIERTS...
EBNGTH:
                                                                                                                                                                                                                                                                                                                                                                             NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                          TIORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---- LRCAELEREVAELOHRN-
                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                           125 HIGH STREET
                                                                                                                                                                                                                                                                      APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                          OMPUTER READABLE FORM:
    ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 GSPASP---
                                                                                                                              02110
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293

5 08:37:50 2003

Wed Mar

; TYPE: amino acid	, MOLECULE TYPE: protein PCT-US93-06160-4	Query Match Best Local Similarity 23.2 Matches 198; Conservative	OV A DKABLISSCIED	139	Oy 56 GISEDPGPNWKLKVSNLKMV	116	236 ELAENRKLLTEKDAQIA	168	294	QY 212 AQENAGLRERMGRPEGEGTP 	Ov 264 LRCAELEREVAELOHR	409 LG	QY 288 QEAQALKDEMDELRQSSERA	Db 469 TDLOSSISNLSQAKEELEQA	Qy 340 GHAERTROLEDELRRAGSLR	Db 523 GLKQQAKEKQAQLAQTLQ	Qy 393 LEEKYESVTKEKERLLAERD	Db 581 HAQQLATAAEEREASLRERD	OY 434 ADPSEDPTSTPVDNLAA	Db 641 AQREKAELSRKVEELQACVE	OY 482OEELORHLEDANRARHG	Db 698 DQLQEQLQALKESLKVTKGS	Oy 525 OEOGGKT	DD 758 EEERAGRKGLEARLLQLGEA	QY 572 DSSTARRIEELQHNLQKKDA	DD 815 DGYEDSQQEEAQYGAMFQEQ	QY 623GAPPELHSLRTQ	DD 868 SROONKLAELHANLARALOO	OY 671 GMALOORAGEERAPA 685	DD 920 -ETLVRKAGEQQETA 933	RESULT 10	Seqúenc
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etlkoeaatlaanntoloarvemletergogeakllaerghfeeekoolssli 468	ATLISCRRRIGELRELRRQVRQLEERNA 339  -	GQRQEEAMKAEKWLFECRN	7EQLSSSLKQKEQQLKEVAEKQEATRQD 580	VTKEKERLLAERDSLREANEELRCAQLQ	LCROEAADRER	AELELQLRSEQOKATEKERVAQEK 697	DRHLEDANRARHGLETQHRLNOQOLSELRAQVEDLQKAL 524		:    :   : :: :   ABAMAQHTAESECEQLVKEVAAWR 814		-CEKARQELQEAKEKVAGIESHSELQI 867	DFEKSRSQREQEEKLLISAWYNM 670.       : : :    DLSTLQEKMAATSKEVARL 919						TELL TYPE MARKERS OF THE		Ę				,	;	Version #1.25						
LGDVLQL	QEAQALKDEMDELRQSSERAGQLE :  :	GHAERTRQLEDEL	GLKQQAKEKQAQL	LEÉKYES :: HAQQLATI	ADPSLDPTSTPVDNLAA	1 AOREKAELSRKVEELQACVETARQEQHEAQAQVAELELQLRSE-	QEELA   :  DOLOEOLA	OE	:  EEERAGRKGLEARLL	DSSTARRIEELQHNLOKKDADLRAMEERYRR	DGYEDSQOEEAOYGAMFQEOLMTLKEE	3GAPPELHSLRTQLRERDVRIRHLEMDFEKSRSGREGEEKI 	GMALQORA	- ETLVRK		-06160-4	Sequence 4, Application PC/TUS9306160 GENERAL INFORMATION:			CORRESPONDENCE ADDRESS: ADDRESSEE: TESTA HURWITZ & THIBEAULA	STREET	DUNTRY: USA	ZIP: 02109	E E	G SYSTEM: PC-DOS/MS-DOS	ICATION DATA:		ION: I INFORM	REGISTRATION NUMBER: 27,829 REFERENCE CHOCKET NIMBER: MTD-013	TION INFORMATION: 617/248-7000	TELEFAX: 617/248-7100 INFORMATION FOR SEO ID NO: 4: SEQUENCE CHARACTERISTICS:	LENGTH: 2101 amino acids
DD 409	Oy 288 Db 469		00 523	Oy 393 Db 581		Db 641	Oy 482 Db 698		Db 758		DD 815	Oy 623 Db 868	0у 671	Db 920		RESULT 9 PCT-US93-06160-4	; Sequent ; GENER		TIT :	ŭ										TEL .	INF	

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36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GISEDPGPNWKLKVSNLKMVLRSLVEYSQDVLAHPVSEEHLPDVSLIGEFSDPAELGKLL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIVLGCAISCEK-----KQDHIQRIMTLEESVQHVVME--AIQELMTKDTPDSLSPETY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :) : | | : | | | | | | | | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNF------DSQSRRYYFLSEEAEEGD-----ELQQRCLDLERQLMLLSEEKQSL 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GAPPELHS----LRTQLRERDVRIRHLEMDF----EKSRSQREQEEKLLISAWYNM 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------QALTSLA 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---OEBLORHLEDANRARHGLETQHR----LNQQQ--LSELRAQVEDL-----QKAL 524
                                                                                                                        Gaps
                                                                                                                                                                                                              DKAELCGSLLIWLQTFHVPSPCAS--PQDLSSGLAVA----YVLNQIDPSWFNEAWLQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|
EEBRAGRKGLEARLLQLGEAHQAETEVLRRELAEAMAAQHTAESECE---QLVKEVAAWR
                                                                                                            233;
           Length 2101;
8.6%; Score 311.5; DB 5; Length ;
llarity 23.2%; Pred. No. 2.8e-15;
Conservative 130; Mismatches 294; Indels
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4, Application US/08685576
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                                                   al Similarity
198; Conserv
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1011
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                                                                                                                                                                                                          LKIEGETOKRCLTONDLKMOTOQVNTLKMSEKQLKOEN--NHLMEMKNNLEKON-AELRK 850
                                                                                                                                    EERTLKOKVENLLLEAEKRCSLL-----DCDLKQSQQKINELLKQKDVLNEDVRNLT 793
                                                                                                                                                                                                                                                                              QVEDL --- QKALQEQGGKTEDAISILLK -- - RKLEEHLQKLHEADLELQRKREYIEELEP 569
--LOGOROEEA-MKAEKWLFECRN-----LEEKYESVTKEKERLLA 409
                                        582 EKSNMEIDMTYQLKVIQQSLEQEEAEHKATKARLADKNKIYESIEEAKSEAMKEMEKKLL 741
                                                                                           ERDSLREANEEL-----RCAQLQPRGLTQADPSLDPTSTPVDNL--AAEILPAELRETL 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---MDFEKSRSQREQEEKLLI
                                                                                                                                                                               LRLQLENKRLCRQEADDRERQEEL-----QRHLEDANRARHGLETQHRLNQQQLSELRA
                                                                                                                                                                                                                                                                                                                                                                                                 1012 SAAAIKAQFEKQLLTERTLKTQAVNKLAE----IMNRKEPVKRGNDTDVRRKEK 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         665 SAWYNMGMALQQRAGEERAPAHAQSFLAQQRLATNSRRGPLGRLASLNLRPTDK 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: YEN, TIMOTHY J.
APPLICANT: RATINER, JEROME B.
TITLE OF INVENTION: NUCLBIC ACID ENCODING A
TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: DANN, DORFMAN, HERRELL AND SKILLMAN 1601 MARKET STREET, SUITE 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, JANET E.
REGISTRATION NUMBER: 36.257
TELECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08353700 Patent No. 5599919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     629 HSLRTQLRERDVRIRHLE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (215) 563-410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3248 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHEICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 QELMTKDTPDSLSPETYGNFDSQSRRYYFLSEEAEEGDELQQRCLDLERQLMLLSEEKQS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 ENLLLSD-----SPSCRENDSIQSRK-----NEESQEIQKKLYTLEEHLSNEMQAKEE 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 LAGENAGLRERMGRPEGEGTPGLTAKKLLLLOSOLEOLOBENFRLESGREDERLRCAELE 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 8.3%; Score 301; DB 2; Length 1388; Best Local Similarity 23.1%; Pred. No. 1e-14; Matches 165; Conservative 113; Mismatches 220; Indels 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LEDELRRAGSLRAQLEAQRRQVQE
                                                                                                                          APPLICANT: Takahashi, No. 5906819uaki
TTLE OF INVENTION: RHO TARGET PROTEIN RHO-KINASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -TSCRRRLGELRELRRQVROLEERN-
                                                                                                                                                                                                                                            3000 K Street, N.W., Suite 500
                                                                                                     Ito, Masaaki
Takahashi, No. 5906819uaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,576
FILING DATE: 24-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: JP 8-131206
26-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 7-325129
FILING DATE: 20-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 8-17150
FILING DATE: 05-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bent, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 16 ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                      Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 1388 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-685-576-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           OMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 ----AGHAERTRQ-
                                                                                                                                                                                                                                                                      Washington
                                                                                    Nakano
                                                                                                                                                                                                                                                                                                                  Y: USA
20007-5109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FICATION:
                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 TL---
                                                                                                                                                                                                                                                                                                                    COUNTRY:
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1905 SKLHLQEVQLMTKIEACIELEKIVG------ELKKEN----SDLSEKLEYFSCDHQE 1951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2218 EKLRVRIEADEKKOLHIAEKLKERERENDSLKDKVENLERELOMSEENQELVILDAEN-- 2275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 SEEHLPDVSLIGEFSDPAELGKLLQLVLGCAISCEKKQDHIQRIMTLEESVQHVVMEAIQ 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -QKKDAD-----LRAMEERYRR 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 ELMTKDTPDSLSPETYGNFDSQSRRYYFLSEE----AEEGDELQQRCLDLERQLMLLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2006 EKASIEHE---------ALYLEADLEVVQTEKLCLEKDNENKQKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 RCAELEREV-----AELQHRNQALTSLAQEAQALKDEMDELR-QSSERAGQLEATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EELRC-----AQLQ-PRGLTQADPSLDPTSTPVDNLAAEILPAELRETLLRLQLENKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2158 NKEKELLVKESESLQARLSESDYEKLNVSKALEAALVEKGEFALRLSSTQEEVHQLRRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2103 AEVKEKTELLQTLSSDVSELLKDKTHLQEKLQSLEKDSQALSLTKCELENQIAQL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375 QRQEEAMKAEKWLFECRNLEEKYE--SVTKEKERLLAER------
                                                                                                                                                                                         PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 8.2%; Score 297; DB 5; I
Best Local Similarity 21.9%; Pred. No. 6.6e-14;
Matches 160; Conservative 128; Mismatches 260;
                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTONEX/AGENI INFORMATION:
RAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SKAEVETLKTQIEEMARSL----
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                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
SUFFATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
IFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    531 TED-----AISILLKRK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3248 amino acids
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                                                                                    READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                         19103-2307
                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                    OMPUTER
        STATE:
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GENERAL INFORMATION:
APPLICANT: Yen, Timothy J.
APPLICANT: Rattner, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1905 SKLHLOEVQLMTKIEACIELEKIVG------ELKKEN----SDLSEKLEYFSCDHQE 1951
                                                                                                                                                                                                                                                                                                                                              1952 LLORVETSEGLNSDLEMHADKSSR-----EDIGDNVAKVNDSWKERFLDVENELSRIRS 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ALYLEADLEVVQTEKLCLEKDNENKQKVI 2042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2158 NKEKELLVKESESLOARLSESDYEKLNVSKALEAALVEKGEFALRLSSTQEEVHOLRRGI 2217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2218 EKLRVRIEADEKKOLHIAEKLKERERENDSLKDKVENLERELOMSEENOELVILDAEN-- 2275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2276 -----SKAEVETLKTQIEEMARSL-----KIFELDLVTLRSEKENLTKQIQEKQGQ 2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2322 LSELDKLLSSFKSLLEEKEQAEIQIKEESKTAVEMLONQLKELNEAVAALCGDQEIMKAT 2381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 TSCRRRLGELRELRRQVRQLEERNAGHAERTRQLEDELRRAGSLRAQLEAQRRQVQELQG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -DSLREAN 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EELRC-----AQLQ-PRGLTQADPSLDPTSTPVDNLAAEILPAELRETLLRLQLENKR 470
                                                                                                                                                                                   92 SEBHLPDVSLIGEFSDPAELGKLLQLVLĞCAISCEKKQDHİQRIMTLEESVQHVVMEAIQ 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LEEHLQKLHEA-----DLELQRKR 561
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                           152 ELMTKDTPDSLSPETYGNFDSQSRRYYFLSEE----AEEGDELQQRCLDLERQLMLLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----AELOHRNOALTSLAQEAQALKDEMDELR-OSSERAGQLEATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 EKOSLAQENAGLRERMGRPEGEGTPGLTAKKLLLLQSQLEQLQEENFRLESGREDER--L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  471 LCRQEAADRERQEELQRHLEDANRARHGLETQHRLNQQQLSELRAQVEDLQKALQEQGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          655 -QREQEE----KLLISAWYNMGMALQQRAGEERAPAHAQSFLAQQRLATNSRRGPLGRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2103 AEVKEKTELLOTLSSDVSELLKDKTHLQEKLQSLEKDSQALSLTKCELENQIAQL----
                                                                                                                                     Indels 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      603 YVDKARMVMQTMEPKQRPAAGAPPELHSLRTQLRERDVRIRHLEMDFEKSRS----
                                                                                 Length 3248;
                                                                                                                                  Conservative 128; Mismatches 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Dann, Dorfman, Herrell and Skillman
1601 Market Street Suite 720
                                                                              8.2%; Score 297; DB 1; 21.9%; Pred. No. 6.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   375 ORQEEAMKAEKWLFECRNLEEKYE--SVTKEKERLLAER-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EYIEELEPPTDSSTARR--IEELQHNL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2554
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                                                                                                          Similarity
     HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1006 EKASIEHE-
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STREET: 10
; ORGANISM:
US-08-353-700-1
                                                                                                                                  Matches 160;
                                                                              Query Match
                                                                                                            Local
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562 2382

RESULT 12

28;

Indels

418

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712 ELEIAR---TNOEHAALEAENSKGEVETLKAKIEGMTQSLRGLELDVVTIRSEKENLTNE 1768
                                                                                                                                                                                                                                                                      1430 NKEKELLVKESESLOARLSESDYEKLNVSKALEAALVEKGEFALRLSSTOEEVHOLRRGI 1489
                                                                                                                                                                                                                                                                                                                                                  E--QSLDPPIEEEHQLRNSIEKLRARLEADEKKQLCVLQQLKESEHHADLLKGRVENLER 1711
                                                                                                                                                                               1375 AEVKEKTELLOTLSSDVSELLKDKTHLQEKLOSLEKDSQALSLTKCELENQIAQL---- 1429
                                                                                  1315 VCLEBELSVVTSERNQLRGELDTMSKKTTALDQLSEKMKEKTQELESHQSECLHCIQVAE 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----KVFELDLVTLRSEKENLTKQIQEKQGQ 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             655 -OREQEE----KLLISAWINMGMALQQRAGEERAPAHAQSFLAQQRLAINSRRGPLGRLA 709
---ALYLEADLEVVQTEKLCLEKDNENKQKVI 1314
                                                                                                                                  315 TSCRRRLGELRELRRQVRQLEERNAGHAERTRQLEDELRRAGSLRAQLEAQRRQVQELQG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LEEHLOKLHEA------DLELORKR 561
                                            --AELQHRNQALTSLAQEAQALKDEMDELR-QSSERAGQLEATL 314
                                                                                                                                                                                                                                                                                                                     --AQLQ-PRGLTQADPSLDPTSTPVDNLAAEILPAELRETLLRLQLENKR
                                                                                                                                                                                                                                                                                                                                                                                                                  471 LCRQEAADRERQEELQRHLEDANRARHGLETQHRLNQQQLSELRAQVEDLQKALQEQGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            603 YVDKARMYMOTMEPKORPAAGAPPELHSLRTQLRERDVRIRHLEMDFEKSRS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN RHO-KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                375 ORQEEAMKAEKWLFECRNLEEKYE--SVTKEKERLLAER-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP 7-325129
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SKAEVETLKTQIEEMARSL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08685576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYIEELEPPTDSSTARR--IEELQHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHO TARGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eloppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakano, Takeshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              531 TED-----AISILLKRK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rakahashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1817 ELNERVAALH 1826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              710 SLNLRPTDKH 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3000 K
                                                      265 RCAELEREV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ELKKEN----SDLSEKLEYFSCDHQE 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 ELMTKDTPDSLSPETYGNFDSQSRRYYFLSEE-----AEEGDELQQRCLDLERQLMLLSE 206
                  2440 ELEIAR----INQEHAALEAENSKGEVETLKAKIEGMTQSLRGLELDVVTIRSEKENLINE 2496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEEHLPDVSLIGEFSDPAELGKLLQLVLGCAISCEKKQDHIQRIMTLEESVQHVVMEAIQ 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKQSLAQENAGLRERMGRPEGEGTPGLTAKKLLLLLQSQLEQLQEENFRLESGREDER--L 264
                                                                                                                                                                       655 -QREQEE----KLLISAWYNMGMALQQRAGEERAPAHAQSFLAQQRLATNSRRGPLGRLA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 182; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCES: 8
                                                                                603 YVDKARMVMQTMEPKQRPAAGAPPELHSLRTQLRERDVRIRHLEMDFEKSRS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2482;
                                                                                                                                                                                                    2497 LQKEQERISELBIINSSFENI---LQEKE-QEKVQMKEKSSTAMEMLQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 296;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ICATION NUMBER: US/08/328,254 NG DATE: 24-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1177 SKLHLOEVOLMTKIEACIELEKIVG---
                                                                                                                                                                                                                                                                                                                                                                                                                             pplication US/08328254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 21.9%; Pr
Matches 160; Conservative 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campbell, Cathryn A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhu, Xuellang
APPLICANT: Lee, Wen-Hwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                              2545 ELNERVAALH 2554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                    710 SLNLRPTDKH 719
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1032 TQAVNKLAEIMNRKEPVKRGNDTDVRRKEK 1061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 466 LEQRCKSVNTRLEKVAKELEEEITLRK--NVESTLRQLEREKALLQHKNAEYQRKADHEA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 QELMTKOTPDSLSPETYGNFDSQSRRYYFLSEEAEEGDELQQRCLDLERQLMLLSEEKQS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          418 ENLLLSD-----SPSCKENDSIQSRK-----NEESQEIQKKLYTLEEHLSTEIQAKEE 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 ERLRCAE-----LEREVAELQHRNQALTSLAQEAQALKDEMDE----LRQSSERAGQLEA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- RQVRQLEERNAGHAE---- 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---RCAQ 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426 LOPRGLTQADPSLDPTSTPVDNL--AAEILPAELRETLLRLQLENKRLCRQEAADRERQE 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484 EL-----QRHLEDANRARHGLETQHRLNQQQLSELRAQVEDL---QKALQEQGGKTEDA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          925 EQLARSIAEEQYSDLEKEKIMKELEIKEMMAR-----H--KQELTEKDATIASLEETNR 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    647 ---MDFEKSRSQREQEEKLLISAWYNMGMALQQRAGEERAPAHA-----QSFLAQQRLA 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------ 10GORQ 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 535 ISILLK---RKLEEHLQKLHEADLELQRKREYIEELEPPTDSSTARRIEELQHNLQKKDA 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :: :| | :| | 584 TQAESSKQIQQLESHNRDLQDKNCLLETAKLKLEKEFINLQSVLESERRDRTHGSEIIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           592 DLRAMEERYRRYVD-KARMVMQTMEPKQRPAAGAPPELHSLRTQLRERDVRIRHLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 126; Mismatches 241; Indels 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 1388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEA-MKAEKWLFECRN----LEEKYESVTKEKERLLAERDSLREANEEL---
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                                                                                                                                                                                                                                 16887/843
                                          APPLICATION NUMBER: JP 8-17150
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA: JP 8-131206
APPLICATION NUMBER: JP 8-131206
FILING DATE: 26-APR-1996
(TTORNEY/AGENT INFORMATION:
                                                                                                                                                                             NAME: Bent, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 1(
20-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 TLTSCRRLGEL----RELR---
                                                                                                                                                                                                                                                                            (202)672-5300
(202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                          1388 amino acids
                                                                                                                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1388 amino aci
                       RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Matches 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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119 LGCAISCEKKQDHIQRIMTLEESVQHVVMEAIQELMTKDTPDSLSPETYGNFDSQSRRYY 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370 QELQGQRQEEAMKAEKWLFECRNLEEKY------ESVTKEKE------RLLAE----R 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 225; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 ONEVESVTGMINEAEGKAIK--LAKDVASLSSQLQDTQE--------LLQE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 MGC---LEFDEERAQQEDALAQQAFEEARRTREFEDRDRSHREEMEAKANLDKNKQ--- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ELQQRCLDLERQLMLLSEEKQSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 EVAELQHRNQALISLAQEAQALKDEMD---ELRQSSER-AGQLEATLISCRRRLGEL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---RELRROVROLEERNAGH--AERTR-QLEDELRRAGSLRAQLEAGRRQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 885
                                                                                                                                                                    APPLICANT: Claxton, David
TITLE OF INVENTION: Markers for Detection of Chromosome 16
TITLE OF INVENTION: Rearrangements
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.8%; Score 284.5; DB 2; Best Local Similarity 20.8%; Pred. No. 1e-13; Matches 160; Conservative 127; Mismatches 257;
                                                                                                                                                                                                                                                                                     SEE: Harness, Dickey & Pierce, P.L.C.: P.O. Box 828
Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAME: Smith, Deann F.
REGISCREATION NUMBER: 31683
REFERENCE/DOCKET NUMBER: 2115-00869COB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 641-1600
TELEPHONE: (810) 641-1600
TELEPHONE: (810) 641-1600
TELEPHONE: (810) 641-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       September 25, 1995
                       Sequence 4, Application US/08533306A
Patent No. 5837457
                                                                                                                                               APPLICANT: Siciliano, Michael J. APPLICANT: clastico, David TITLE OF INVENTION: Markers for IITLE OF INVENTION: Rearrangement TITLE OF INVENTION:
                                                                                                                        Francis S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       885 amino acids
amino acid
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                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 FLSEEAEEGD-----
                                                                                                                      Collins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                             ADDRESSEE:
US-08-533-306A-4
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455	493 563	539 623	576 680	629 740	662	
412 DSLREANEELRCAQLQPRGLTQADPSLDPTSTPVDNLAAEILPA 455 :	456 ELRETLLRLQLENKRLCRQEAADRERQEELQRHLED:	494 RARHGLETQHR-LNQQQLSELRAQVEDLQKALQEQGGKTEDAISILL 539 1:	540 KRKLEEHLOKLHE	577RRIEELOHNLOKKDADLRAMEERYRRYDKARMYMOTMEPKORPAAGAPPELH	630SLRTQLRERSPORIRHLEMDFEKSRSQREGEEKLSRSQREGEEKL	663 -LISAWYNMGMALQORAGEERAPAHAOSFLAQORLATNSRR 702 
412	456	494, 564	540	577	630	663
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Search completed: March 4, 2003, 15:06:22 Job time: 38,9261 secs

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                                                                                                                                     (without alignments)
1761.695 Million cell updates/sec
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Sequence 120,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                               3638
1 MSVDKAELCGSLLTWLOTFH.....SRRGPLGRLASLNLRPTDKH 719
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Sequence 21
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Sequence 2,
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Sequence 4,
Sequence 19
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Sequence 4
                                                                                                                 March 4, 2003, 14:58:57; Search time 17.2109 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:
/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ptodata/2/pubpaa/US10_NEW_PUB.pep
ptodata/2/pubpaa/US10_PUBCOMB.pep
                                                                                                                                                                                                                                                                                                                                                                     188354
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                               188354 segs, 42170167 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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Gapop.10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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. 4	0 26	5.5	7.3	1033	6	-843A-7	Seguence 75, Appl
. 7	11 262	2.5	7.2	888	თ	o	Sequence 73, Appl
(1		0.5	7.2	1286	σ	US-10-017-216-7	Sequence 7, Appli
(4	 Ε	259	7.1	830	6	US-10-033-245-7	7,
. 1	24	259	7.1	830	6	US-10-033-223-7	Sequence 7, Appli
. *			7.1	830	σ	US-10-033-167-7	7,
(4		259	7.1	830	თ	US-10-033-244-7	۲,
			7.1	830	σ	US-10-033-435-7	7
		259	7.1	830	о О	US-10-032-990-7	۲,
. 4			7.1	830	12	US-10-033-246-7	Sequence 7, Appl1
11)		259	7.1	830	12	US-10-033-301-7	7,
(*)			7.1	830	12	US-10-033-326-7	~
(*1		251	٠.	611	10	US-09-216-393-81	81
,		250	6.0	1242	σ	US-09-925-299-911	911
,		250	6.9	1242	2	US-09-925-299-911	Sequence 911, App
	5 24	9.5	٠	2568	10	US-09-866-108-3	Sequence 3, Appli
(.)		5.5	6.7	.099	10	US-09-864-761-47959	Sequence 47959, A
(-)		3.5	6.7	1711	10	US-09-771-161A-219	Sequence 219, App
	18 . 243	3.5	6.7	1711	10	US-09-771-161A-220	22
(.)		3.5	6.7	1805	σ	US-09-820-843A-73	73, A
4		9.5	9.9	606	<u>ه</u>	US-09-925-299-988	988
4		9.5	•	606	10	US-09-925-299-988	e 98
4		227		945	10	US-09-745-763-191	Seguence 191, App
4		5.5	6.2	1155	σ	US-09-738-626-5764	5764,
	4 . 22	m		1045	10	9-815-242-10	Sequence 10617, A
4	22	223	•	923	6	US-,09-820-843A-112	Sequence 112, App
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------ELRQSSE 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 RERMGRPEGEGTPGLTAKKLLLLQSQLEQLQEENFRLESGREDERLRCAELEREVAEL-Q 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --- RLDTATQQR----AELEARVARLAA 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 2310;
                                                                                                                                                                                                                                                                                                                                                               OF LEISHMANIASIS
                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE ITTLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMAN' FILE REFERENCE: 210121.420C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 AEEGDELQQRC-----LDLERQLMLLS----EEKQSLA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 5e-10;
96; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.7%; Score 315; DB 9
25.5%; Pred. No. 5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/991,496
CURRENT FILLING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 137
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , TYPE: PRT
, ORGANISM: Leishmania major and chagasi
US-09-991-496-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   760 EARVARLAADGDEARQO----LAANAEELQO
                  Sequence 120, Application US/09991496
Patent No. US20020169285A1
                                                                                                                               Campos-Neto, Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 HRNQALTSLAQEAQALKDEMD---
                                                                                                                                                                            illon, Davin C.
keiky, Yasir A.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 25.5
Matches 176; Conservative
                                                                                                     Steven G.
-09-991-496-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 120
LENGTH: 2310
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QY         278 HRNQALTSLAQEAQALKDEMD	09   395 EKYESVTKEKERLLAERDSLREANEELRCAQLQPRGLTQADPSLDPTSTP 444   1   1   1   1   1   1   1   1   1	OY 526 -EGGGKTEDAISIL	100 100 100 20, 108 108		; SEQ ID NO 120 ; SEQ ID NO 120 ; TYPE: PRT ; ORGANTSM: Leishmania major and chagasi ; ORGANTSM: Leishmania major and chagasi US-09-874-923-120  Query Match  Bost Local Similarity 25.5%; Pred: No. 5e-10;  Matches 176; Conservative 96; Mismatches 205; Indels 214; Gaps
RAGOLEATLTSCRREIGELRELROYVROLEERNAGHAERTROLEDELRR 354	VDNIAAEILPAELRETLLELQLENKRLCROEAADRERQEELQRH 488	568 EPPTDSSTARRIEELQHNLQKKDADLRAMEERYRRYUDKARWWQTWEPK-OR 619	SULT 2	118 rrsion 3.0 cro5893_12 L6202.3 cre 116899664 8.7%; Score 315;	Best Local Similarity 25.5%; Pred. No. 5e-10; Matches 176; Conservative 96; Mismatches 205; Indels 214; Gaps 32;  184 AEEGDELQORCLDLERQLMLLSEEKQSLA

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Query Match 8.7%; Score 315; DB 9; Length 2354; Best Local Similarity 26.1%; Pred. No. 5.1e-10; Matches 184; Conservative 99; Mismatches 251; Indels 170; Gaps 34;	QY 139 EESVQHVVMEAIQELMTKDTPDSLSPETYGNFDSQSRRYYFLSEEAEEGDELQQR 193 1:	QY 194 CLDLERQLMLLSERKQSLAQENAGLRERMG-:RPEGEGTPGLTAKK 237 11   1   1   1   1   1   1   1   1   1	QY 238 LLLLQSQLEQLQEBNFRLESGREDERLRCAELEREVAELQHRNQALTSLAQEA 290	OY 291 QALKDEMDELRQS-SERAGQLEATLTSCRRRLGELR-ELRRQVRQLEERNAGHAER 344 :	OY 345 TROLEDELRRAGSLRAQLEAQ-RRQVQELQGQRQEEAMKAEKWLFECRNLEEKYESVTKE 403	QY 404 KERLLABRDSLREANEELRCAQLQPRGLTQADPSLDPTSTPVDNLAA 450	QY 451EILPAELRETLIRLQLENKRLCRQEAADRERQEELQRHLEDAN 493	OY 494 RARHGLET	QY 525 QEQGGKTEDAISILLKRKLEBHLQKLHEADLELQRKREYIEELEPPTDS 573	QY 574 STARRIEELQHNLQKKDADLRAMEERYRRYVDKARMVMQTMEPKQRPA 621	QY 622 AGAPPELHSLRTGLRERDVRIRHLEMDFEKSRSQREQEEKLLISAWYNMGMA 673  1353 ANAEELQGRLDTATQQRAELEARVARLAADRDEARQQLAANAEELQGRLDTA 1404	QY 674 LQQRAGEERAPAHAQSFLAQQRLATNSRGPLGRLASL 711 	RESULT 5 US-09-927-597-2 ; Sequence 2, Application US/09927597 ; Publication No. US20030032018A1	ĞΣ	; APPLICANT: Freedman, Kichard ; APPLICANT: Craven, Andrew ; APPLICANT: Sakowicz, Roman , APPLICANT: Jarman Tampo	INVENTION: FRENCE: CYTOF	RRENT FILING DATE: 2001-( MBER OF SEQ ID NOS: 17 FTWARE: FastSEQ for Windov	; SEQ ID NO 2 ; LENGTH: 1945 ; TYPE: PRT
OY 184 AEEGDELQORCLDLERQLMLLSEEKQSLAQENAGL 218   1	QY 219 RERMGRPEGEGTPGLTAKKLLILOSOLEGICGENFRLESGREDERLRCAELEREVAEL-Q 277  1	QY 278 HRNQALTSLAQEAQALKDEMD	OY 306 RAGQLEATLISCRRIGELRELRRQVRQLEERNAGHAERTRQLEDELRR 354	OY 355AGSLRAQLEAQRRQVQELQGQRQEEAMKAEKWLFECRNLE 394	QY 395 EKYESVTKEKERLIAERDSILREANBELRCAQLOPRGITQADPSIDPTSTP 444 :::  ::  ::	OY 445 VDNIAAEIIPAELRETILRIQLENKRICROEAADRERQEELORH 488   1882   1883   1884   1885	Qy 489 LEDANRARHGLET	QY 526 -EQGGKTEDAISILKRKLEEHLQKLHEADLELQRKREYIEEL 567	QY 568 EPPTDSSTARRIEELQHNLQKKDADLRAMEERYRRYVDKARWYMQTMEPK-OR 619 :	OY 620 PAAGAPPELHSLRTOLRERDVRIRHLEMDFEKSRSQREGEEKLLISAWYNMG 671	OY 672 MALQORAGEERAPAHAOSFLAOORLAINS 700  DD 1320 TAIQORAELEARVARLAADGDEARQQLAANA 1350	RESULT 4 US-09-820-843A-113 Sequence 113, Application US/09820843A Publication No. US20030039965A1	GENERAL INFORMATION:  APPLICANT: Council of Scientific and Industrial Research  TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI  TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES	; FILE REFERENCE: Q53415; CURRENT APPLICATION NUMBER: US/09/820,843A; CURRENT FILING DATE: 2001-03-30; NIMBER OF SEC IN NOG. 118	NOMBER OF SEM ID NOS: 110 ; SEO ID NO 113 : TENIOFH: 2364	; TYPE: PRT ; ORGANISM: L. major ; FRATURE:	NAME/KEY: misc_feature CTHER INFORMATION: AC005802_5 L6202.3 NAME/KEX: misc_feature	; OTHER INFORMATION: g1 6899670 US-09-820-843A-113

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGKAIKLAKDVASLSSQLQDTQELLQEETROKLNVSTKLRQLEEERNSLQDQLDEEMEAK 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --EAQVQEMRQKHAQAVEELTEQLEQFKRAKANLDKNKQTLEKENADLAGEL-RVLGQAK 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                             1084 QIAELKMOLAKKEEELQAALARLDDEIAQKNNALKKIRELEGHISD---LQEDLDSERAA 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1141 RNKAEKOKRDLGEELEALKTELEDTLDSTATO--QELRAKREQEVTVLKKALDEETRSH- 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1367 ONLE---RHISTLNIQLSDSKKKLØDFAS--TVEALEEGKKRFQKEIENLTQOYEEKAAA 1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            488 HLEDANRARHGLETQHRLNQQQLSELRAQVEDLQKALQEQGGKTEDAISIL-----LKR 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------KLHEADLELQRKREY------IEELEPPTD 572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSQSRRYYFLSEEAEEGDELQQRCLDLERQLMLLSEEKQSLAQENAGLRERMGRPEGEGT 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 AISCEKKQ----DHJQRIMT-LEESVQHVVMEAIQELMTKDTPD-----SLSPETYGNF 170
                                                                                                                                                                                                                                                                                                                                               68 KVSNLKMYLRSLVEYSQDVLAHPVSE-----EHLPDV-SLIGEFSDPAELGKLLQLVLGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     573 SSTARRIEELQHNLQKKDADLRAMEERYRRYVDKARM----VMQTMEPKQRPAAGAPPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q - - ALKDEMDELRQSSERAGQLEATLTSCRRRLG - - - ELRELRRQVRQLEERNAGHAERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YESVTKEKERLLAERDSLREANEELRCAQLQPRGLTQADPSLDPTSTPVDNLAAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGLTAKKLLLLQSQLEQLQEENFRLESGREDERLRCAELEREVAELQHRNQALTSLAQEA
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                                                                                                                                                                                                                                                Indels 158;
                                                                                                                                        Length 1945;
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APPLICANT: Hartman, James
TITLE OF INVENTION: Human smooth muscle myosin heavy chain
FILE REFERENCE: CYTOPO18
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                                                                                                                                                                                                                                                      Mismatches 277;
                                                                                                                                        .8.2%; Score 299; DB 9;. 24.5%; Pred. No. 3.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :09-94/-59/-4 K:
Sequence 4, Application US/09927597
Publication No. US20030032018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                Conservative 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Malik, Fady
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
APPLICANT: Craven, Andrew
                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEQGNMEAMS 1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EERAPAHAQS 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLEEHLQ----
; ORGANISM: Human
US-09-927-597-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-09-927-597-4
                                                                                                                                                                                                      Best Local Sir
Matches 179;
                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1754
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1641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1307 EGKAIKLAKDVASLSSQLODTQELLQEETRQKLNVSTKLRQLEEERNSLQDQLDEEMEAK 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     472 SKYADERDRAEAEAREK-----ETKALSLARALEEALEAKEELERTNKMLKAEMEDLVS 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CEVEHKK-KKLEAQVQELQSK-----CSDGERAR-AELNDKVHKLQNEVESVTGMLNEA 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1697 MOLOEDLAAAERARKQADLEKEELAEELASSLSGRNALODEKRLEARI---AQLEEELE 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                           .084 QIAELKMQLAKKEEELQAALARLDDEIAQKNNALKKIRELEGHISD---LQEDLDSERAA 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---OLVSNLEKKQRKFDQLLAEEKNIS 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1141 RNKAEKOKROLGEELEALKTELEDTLDSTATO--OELRAKREOEVTVLKKALDEETRSH- 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --EAQVQEMRQKHAQAVEELTEQLEQFKRAKANLDKNKQTLEKENADLAGEL-RVLGQAK 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SLSPETYGNF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RQLEDELRRAGSLRAQLEAQRRQVQELQGQRQEEAMKAEKWLF--ECRNL----EEK--- 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSQSRRYYFLSEEAEEGDELQQRCLDLERQLMLLSEEKQSLAQENAGLRERMGRPEGEGT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q--ALKDEMDELRQSSERAGQLEATLTSCRRLG---ELRELRRQVRQLEERNAGHAERT 345
                                                                                                                                                                                                                                                                                                                                                                                                    68 KVSNLKMVLRSLVEYSQDVLAHPVSE----EHLPDV-SLIGEFSDPAELGKLLQLVLGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1582 QFERDLQARDEQNEEKRRQLQRQLHEYETELEDERKQRALAAAAKKKLEGGLKDLELQAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   488 HLEDANRARHGLETQHRLNQQQLSELRAQVEDLQKALQEQGGKTEDAISIL-----LKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KLHEADLELQRKREY------IEELEPPTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 PGLTAKKLLLIQSQLEQLQEENFRLESGREDERLRCAELEREVAELQHRNQALTSLAQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397 YESVTKEKERLLAERDSLREANEELRCAQLQPRGLTQADPSLDPTSTPVDNLAAE-
                                                                                                                                                                                                                                                                                  Length 1979;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AISCEKKQ----DHIQRIMT-LEESVQHVVMEAIQELMTKDTPD--
                                                                                                                                                                                                                                                                                                                                            Conservative 116; Mismatches 277;
                                                                                                                                                                                                                                                                                        8.2%; Score 299; DB 9; 24.5%; Pred. No. 3.3e-09;
CURRENT APPLICATION NUMBER: US/09/927,597
CURRENT FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yu, Xuanchuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1754 EEQGNMEAMS 1763
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                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 179; Conserv
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                                                                                       SEQ ID NO 4
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                                                                                                                                                                                                                                US-09-927-597-4
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966 RNSCTVITDLEEQLNQLTEDNAELNNQNFY---LSKQLDEASGANDEIVQ
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                                                                                                                    10-017-216-2
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APPLICANT: Miranda, Maricar
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: No. US20020123622Alel Human Kinases and Polynucleotides Encoding
FILE REFERENCE: LEX-0289-USA
                                                                                                                                                                                                                                                                                                                                                                                                                      28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SRKLQEIKEQE 556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 TSCRRRLGELRELRRQVRQLEERNAGHAERTRQLEDELRRAGSLRAGLEAGRRQVQEL-- 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 SGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKME 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 DHIQRIMTLEESVQHVVMEAIQELMTKDTPDSLSPETYGNFDSQSRRYYFLSEEAEEGDE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- LRQSSERAGQLEATL 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESVTKEKERLLAERDSLREANE-----ELRCAQLQPRGLTQADPSLDPTSTPVDNLAAE 451
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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EMISELRQOKFYLETQAGKL---EAQNRKLEEQLEKISHQDHSDKNRL-LELETRLREVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- MLLSEEKQSLAQENAGLRERMGRPEGEGTPGLTAKKLLLLQSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         617 GKPEVGEYAKLEKINAEQOLKIQELQEKLEKAVKASTEATELLQNIRQAKERA---EREL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         577 RRIEELQHNLQKKDADLRAMEERYRRYVDKARMVM----QTMEPKQRPAAGAPP---ELH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- LRSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQVMDLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452 ILPAELRETLLRLQLENKRLCRQEAADRERQEELQR--HLEDANRARHGLETQHRL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ESGREDERLRCAELEREVAELQH-----RNQ
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels. 260;
                                                                                                                                                                                                                                                                                                                                                                        Length 1958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 QEMTRLHRRVSEVEAVLSQKEVELKASETQRSLLEQDLATYITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SLIGEFSDPAELGKLLQLVL
                                                                                                                                                                                                                                                                                                                                                                           DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----CSSLKRSLEQARMEVSQEDDKALQLLHDIREQ-----
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                                                                                                                                                                                                                                                                                                                                                                      8.0%; Score 290; DB
llarity 19.8%; Pred. No. 1.1e
Conservative 137; Mismatches
                                                                                                                                                                                NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                    CURRENT APPLICATION NUMBER: US/10/028,946
CURRENT FILING DATE: 2001-12-20
                                                                                                                                       60/258,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    506 --NQQQLSELRAQVEDLQKALQEQ-
                                                                                                                                  PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2000-12-27
                                                                                                                                                                                                                                                                                                ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 162; Conserv
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                                                                                                                                                                                                                                 SEQ ID NO 4
LENGTH: 1958
                                                                                                                                                                                                                                                                                                                          JS-10-028-946-4
                                                                                                                                                                                                                                                                               TYPE: PRT
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APPLICANT: KAPELLER-LIBERMANN, Rosana
TITLE OF INVENTION: 13245, A No. US20020160483Alel Human Myotonic Dystrophy Type
TITLE OF INVENTION: Minase and Uses Therefor
FILE REFERENCE: 10147-5701
CURRENT APPLICATION NUMBER: US/10/017,216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415 REANE-----ELRCAQLQPRGLTQADPSLDPTSTPVDNLAAEILPAELRETLLRLQLEN 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| || :| :| || :| :| | : :| || || :| || 850 'GKL---EAQNRKLEEQLEKISHQDHSDKNRL-LELETRLREVSLEHEEQKLELKRQLTEL 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -LEBHLOKLHEADLELORKREYIEELEPPTDSSTARRIEELQHNLOKKDADL 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SRKLQEIKEQE 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 ALTSLAQEA------QALKDEMDELRQSSERAG--QLEATLTSCRRRLGELRELRRQV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469 KRLCRQEAADRERQEELQR--HLEDANRARHGLETQHRL-----NQQQLSELRAQVEDL 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 SGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKME 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 DHIQRIMTLEESVQHVVMEAIQELMTKDTPDSLSPETYGNFDSQSRRYYFLSEEAEEGDE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --ESGREDERLRCAELEREVAELQH-----RNQ 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470 QEMTRIHRRVSEVEAVLSQKEVELKASETQRSLLEQDLATYITE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 20.2%; Pred. No. 1.1e-Us; Matches 162; Conservative 134; Mismatches 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SLIGEFSDPAELGKLLQLVL
ROLEERNAGHAERTROLEDELRRAGSLRAQLEAQRROVOEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 290; DB 9;
Pred. No. 1.1e-08
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                                                                                                                                                                                                 Sequence 2, Application US/10017216
Patent No. US20020160483A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60 PRIOR FLING DATE: 2000-10-23 NUMBER OF CE OF THE PRIOR PRIOR PRIOR OF THE PRIOR PRIOR OF THE PRIOR PRIOR OF THE PRIOR OF THE PRIOR OF THE PRIOR OF THE PRIOR OF THE PRIOR OF THE PRIOR OF T
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-10-017-216-2
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KAMEEKKKKYUKAKMVMQIMEPKQRPAAGAPPELHSLKTQLREK	849 EMISELROOKFYLETOAGKLEAONRKLEEOLEKISHODHSDRNKL-LELETKLKEVS
1014 RSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQVMDLEALNDELLEKERQWEAWR 1073	Oy 506NQQQLSELRAQVEDLQKALQEQ
639DVRIRHLEMDFEKSRSQREGEEKLLISAWYNMGWALQQRAGEERAPAHAQ 688	DD 905 LEHEEGKLELKROLTELOLSLOERESOLTALOAARAALESQLROAKTELEETTAEAEEEI 964
ELORMLDTEKOSRARADORITESROVVE	OY 536 SILLKRKLEEHLOKLHEADLELORKREYIEBLEPPTDSSTA 576
689 SFLAQORLAINSRRGPLGRL 708	DD 965 QALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEASG 1021
1131 QALKEQKLKAESLSDKLNDL 1150	Qy 577 RRIEELQHNLOKKDADLRAMEERYRRYUDKARMVMQTMEPKQRPAAGAPPELH 629
6 INC	Db 1022 ANDEIVQLRSEVDHLRREITEREMQLISQKQTMEALKTTCTMLEEQVMDLE 1072
10-028-946-2 Sequence 2, Application US/10028946	OY 630 SLRIQLRERDVRIRHLEMDFEKSRSQREQEEKLLISAWYNMG 671
Patent No. US20020123622A1	Db 1073 ALNDELLEKERQWEAWRSVLGDEKSQFECRVRELQRMLDTEKQSRARADQRITESRQVVE 1132
APPLICANT: Yu, Xuanchuan APPLICANT: Miranda, Maricar	OY 672 MALQORAGEERAPAHAOSFLAQORLATNSRRGPLGRL 708
APPLICANT: Friddle, Carl Johan TITLE OF INVENTION: No. US20020123622A1el Human Kinases and Polynucleotides Encoding	DD 1133 LAVKEHKAEILALQQALKEQKLKAESLSDKLNDL 1166
FILE REFERENCE: LEX-0289-USA CURRENT APPLICATION NOMBER: US/10/028, 946	RESULT 10
28	03-10'01/ 210-4   Sequence 4, Application US/10017216   13-4
	GENERAL INFORMATION:
SOFTWARE: FastSEQ for Windows Version 4:0 SEQ ID NO 2	; APPLICANT: KAPELLER-LIBERMANN, Rosana ; TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myotonic Dystrophy Typ
LENGTH: 2054 TYPE: PRT	e and Uses Therefor
ORGANISM: homo sapiens	CURRENT APPLICATION NUMBER: US/10/017,216
-10-058-340-2	; CURRENT FILING DATE: 2001-10-23 ; PRIOR APPLICATION NUMBER: US 60/242,429
1) arity 19 8%; Dre	: 2000-10-23 NOS: 7
atches 162; Conservative 137; Mismatc	; SOFTWARE: Patentin Ver. 2.1
92 SEEHLPDVSLIGEFSDPAELGKLLQLVLGCAISCEKKQ 129	
410 SGEELPFVGFSYSKALGILGRSESVYSGLDSPAKTSSWEKKLLIKSKELQDSQDXCHKME 469	
130 DHIORIMTLEESVOHVVMEAIOELMTKDTPDSLSPETYGNFDSQSRRYYFLSEEAEEGDE 189	
	atch 8.0%; Score 290; DB 9; Length 2055; cal Similarity 20.0%; Pred. No. 1.1e-08;
190 LOORCIDIEROLMLISEEKOSLAOENAGLRERMGRPEGEGTPGLTAKKLILLOSOL 245	Matches 165; Conservative 132; Mismatches 266; Indels 262; Gaps 28;
:     :     :          :	86 VLAHPVSEBHLPDVGC
246 EQLOEENFRLROGREDERLRCAELEREVAELOHRNG 281	401 VPAEFLAFSGEELPFVGFSYSKALGYLGKSESVVSSLDSPAKVSSMEKKLLIKSKELUDS
557 YQAQVEEMRLAMNQLEEDLVSARRRSDLYESELRESRLAAREFRRKATECQHKLLKAKDQ 616	122 AISCERKODHIOKIMILEESVOHVOMEAIQELMIKDIPUSLSPEITGNFUSQSKRITELS 18
282 ALTSLAGEA	UD 401 UDACHAMEQEMIKLHRRVSEVEAVLSQNEVELAGASETQRSLEEQULAIIIIE 312 OV 182 EEAREGDELOORCLDLEROLMLLSEEKOSLAOENAGIRERMGRPEGEGTPGLTAKK 237
617 GRPEVGEYAKLEKINAEQOLKIQELØEKLEKAVKASTEATELLQNIRQAKERAEREL 673	513SSLKRSLEOARMEVSOEDDRALOLLHDIREDSRK
315 TSCRRRGELRELRROVRQLEERNAGHAERTRQLEDELRRAGSLRAQLEAGRRQVGEL 372	238 LLLQSQLEQLQEENPRL
ENLEGANDE STED TRAN EVERERARIO DENNA VARIE I MEANEMANDULLA LASQUIGNED TOTAL	DD 548 LOEIKEGEYGAQVEEMRLAMNQLEEDLVSARRRSDLYESELRESRLAAEEFKRKANECQH 607
3/3	279 RNQALTSLAQEAQALKDEMDE
398 ESVTKEKERLLAERDSLREANEELRCAQLOPRGLTQADPSLDPTSTPVDNLAAE 451	DD 608 KLMKAKDOGKPEVGEYSKLEKINAEQOLKIQELQEKLEKAVKASTEATELLQNIRQAKER 667
<u> - 띨</u>	307
TLLRLQLENKRLCRQEAADRERQEELQRHLEI	008 AEKELEKLHNKEDSSEGIKKKLVEAEEKKHSLENKVKKLEIMEKKENKLKDUIQIKS
	OY 367 ROVOELAEKWLFE 389

326 197	Qy 270EREVAELOHRNQALTSLAGEAQALKDEMDELRQSSERAGQLEATLTSCRRRLGELRE
269 154	Qy 227 GEGTPGLTAKKLLLLQSQLEQLQEENFRLESGREDERLRCAEL-
226 95	Qy 180 LSEEAEEGG;ELQGRCLDLERQLMLLSEEKQSLAQENAGLRERMGRPE
ps 24;	Query Match 7.8%; Score 284.5; DB 9; Length 868; Best Local Similarity 23.8%; Pred. No. 8.9e-09; Matches 139; Conservative 106; Mismatches 189; Indels 151; Ga
	GRANISM: Homo sapiens US-09-884-001-19
•	SEQ ID NO 19 LENGTH: 868
	E: 1998-12 NOS: 19
	T APPLICATION NUMBER: US/09 TFILING DATE: 2001-06-18
	ON: Methods ON: Contain Immunex GNK/
	CANT: Virca, G. Duke CANT: Willis, Cynthia R.
	ublication No. US20020182656A1 ENERAL INFORMATION:
	RESULT 11 US-09-884-001-19 :-Sequence 19, Application US/09884001
	Db 1124 TESROVVELAVKEHKAEILALQQALKEQKLKAESLSDKLNDL 1165
	QY 664 ISAWYNMGMALQQRAGEERAPAHAQSFLAQQRLATNSRRGPLGRL 708
1123	Db 1064 EEQVLDLEALNDELLEKERQWEAWRSVLGDEKSQFECRVRELQRMLDTEKQSRARADQRI
663	Qy 625 PPELHSLRTQLRERDVRIRHLEMDFEKSRSQREQEEKLL
1063	
K 24 K	COTTON OF THE PROPERTY OF THE
568	
955 .	Db 896 ETRLREVSLEHEEOKLELKROLTELOLSLOERESOLTALQAARAALESOLRQAKTELEET
527	AQVEDLOKALOEQ
501 · · · · · · · · · · · · · · · · · · ·	QY 444 PVDNLAAEILPAELRETLLRIQLENKRICRQEAADRERQEELQRHLEDANRARHGLET
839	Db 785 NMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSEANKLAANSSLFT
443	ELRCAQLQPRGLTQADPSLDPTST
784	Db 725 EQIQOMADKILELEEKHREAQVSAQHLEVHLKQKEQHYEEKIKYLDNQIKKDLADKESLE

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; ORGANISM: Mus musculus
US-10-017-216-5
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US-10-017-216-5
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Best Local Similarity 20.9
Matches 162; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/017,216
CURRENT FILING DATE: 2001-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/242,429 PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION: 13245, A NO. US20020160483A1el Human Myotonic Dystrophy Type P ITLE OF INVENTION: Kinase and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 1641
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244 GKPEVGEYSKLEKINAEQQLKIQELQEKLEKAVKAST----EATELLQNIRQAKERAERE 299
                                                                                                             184
                                                                                                                                                                                                                   141
                                                                                                                                                                                                                                                                                                                                                                        130 DHIQRIMTLEESVQHVVMEAIQELMTKDTPDSLSPETYGNFDSQSRRYYFLSEEAEEGDE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          600 YRRYVDKARMVMQTMEPKQRPAAGAPPELHSLRTQLRERDVRIRHLEMDFEKSRSQREQE 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             544 EEHLQKLHEAD----LELQRKREYIEELEPPTDSSTARRIEELQHNLQKKDADLRAMEER 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350 KQVEDLKSQLVAQDDSQRLVEQEVQEKLRETQEYNRIQKELERE--KASLTLSLMEK---
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                                                    282 ALTSLAQEAQALKDEMDELRQSSERAGQLEATLTSCRRRLGELRELRRQVRQLEERNAGH 341
                                                                                                                                                            246 EQLOEENFRL----
                                                                                                                                                                                                                                                                  190 LOORCLDLEROL----MLLSEEKOSLAQENAGLRERMGRPEGEGTPGLTAKKLLLLQSQL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 RLRQDMKVQKLKEQETTGILQTQLQEAQRELKEAARQHRDDLAALQEESSSLLQDKMDLQ 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 LCQMQLETEK------ERVSLLET-----
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                                                                                                                                                                                                                ----CSSLKRSLEQARMEVSQEDDKALQLLHDIREQ-----SRKLQEIKEQE 183
                                                                                                                                                                                                                                                                                                                      QEMTRLHRRVSEVEAVLSQKEVELKASETQRSLLEQDLATYITE-----
                                                                                                                                                                                                                                                                                                                                                                                                                               SGEELPFVGFSYSKALGYLGRSESVVSSLDSPAKVSSMEKKLLIKSKELQDSQDKCHKME 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LREKWE--KERSWHQQELAKALESLEREKMELEMRIKEQQTEMEAIQAQREEERTQAESA 255
                                                                                                        YQAQVEEMRLMMNQLEEDLVSARRRSDLYESELRESRLAAEEFKRKANECQHKLMKAKDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQRLLVLQEADSIRQQELSALRQDMQEAQGEQKELSA-QMELLRQEVKEKEADFLAQEAQ 463
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                                                                                                                                                            -ESGREDERLRCAELEREVAELQH----RNQ 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -QLRASLWAQEAKAAQLQLRLRSTESQLE--
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                                                                                                                                                                                                                                                                                                                         ---- 140
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2y 342 AERTROLEDELRRAGSLRAQLEAQRRQVQ-ELQGGRQEEAMK 382 	2y 383ELRCAQLOPRGLT 432 	2y 433 QADPSLDPTSTPVDNLAAEILPAELRETLLRLQLENKRLCRQEAADRERQEELQRHLE 490  :          :       :       :	3y 491 DANRARHGLETQHRLNQQQLSELRAQVEDLQKALQEQ527 :::     :     :     :	QY 528GGKTEDAISILLKRKLEEHLQKLHEADLEL 557 :	QY 558 QRKREYIEELEPPTDSSTARRIEELQHNLQKKDADLRAMEERYRRYVDKARMVM·-·-OT 613 :	P. P.	653	RESULT 13 IIS-04-815-242-11828	Sequenc	; PERENL INCOMPLIEN.; APPLICANT: HASSIDEN.; APPLICANT: Oblsen, Karl L.	 ; APFLICANT: TITWILLY, JOHN D. ; APPLICANT: Yamamoto, Robert T. ; APPLICANT: Yamamoto, Robert T.	; APPLICANT: Xu, H. Howard ; TITLE OF INVENTION: Identification of Essential Genes in : TITLE OF INVENTION: Prokarvotes	REFERENCE: ELITE NT APPLICATION N	NT FILING DATE: 2001-	; PRIOR FILING DATE: ZOUG-U3-ZI ; PRIOR APPLICATION NUMBER: 60/206,848 ; PRIOR FILING DATE: 2000-05-32	APPLICATION N	APPLICATION N	APPLICATION N	APPLICATION N	APPLICATION N FILING DATE:	; NUMBER OF SEQ ID NOS: 14110 ; SOFTWARE: PeatSEQ for Windows Version 4.0 . erg in No 11828	P24,	ORGANISM: Pseudomonas aeruginosa US-09-815-242-11828	

GENERAL INFORMATION:
APPLICANT: KAPELLER-LIBERMANN, ROSANA
TITLE OF INVENTION: 13145, A No. US20020160483A1el Human Myotonic Dystrophy Type
TITLE OF INVENTION: Kinase and Uses Therefor
FILE REFERENCE: 10147-57U1
CURRENT APPLICATION NUMBER: US/10/017,216

CURRENT FILING DATE: 2001-10-23 PRIOR APPLICATION NUMBER: US 60/2 PRIOR FILING DATE: 2000-10-23 NUMBER OF SEQ ID NOS: 7 SOFTWARE: Patentin Ver. 2.1

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520 -----LQKALQEQGGKTEDAISI-----550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGELRELRROVROLEERNAGHAERTROLEDELRRAGSLRAQLEAQRROVQELQGQR---- 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462 LRLOLENKRLCROEAADRERGEELGRHLEDANRARHGLETGHRLNGQQLSELRAQVED-- 519
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                                                                                                     353 APEQELSAAAAEEAGIALEQAEQGM--QAWQQQWDAFNQQSAEPRRQAEVQQSRIQHLEQ 410
                                                                                                                                          SLVEYSQDVLAHPVSEEHL-----PDVSLIGEFSDPAELGKL----LQLVLGCAI 123
                                                                                                                                                                    SCEKKQDHIQRIMTLEESVQHVV--------MEAIQELMTKDTPDSLSP 164
                                                                                                                                                                                                                                              ::| :|: | : | : | 48 --- SEGGGAERLEQLEQELORINGRIASLEALQQAERLEPEW 514
                                                                                                                                                                                                                                                                                                             AE---LEREVAELQHRNQA---LISLAQEAQALKDEMDELRQSSERAGQLEATLISCRRR 320
                                     Gaps
                                                                    26 ASPQDLSSGLA--VAYVLNQIDPSWFNEAWLQ-----GISEDPGPNWKLKVSNLKMVLR 77
                                     Indels 196;
7.6%; Score 277; DB 10; Length 1162; 23.8%; Pred. No. 3.2e-08;
                                      Matches 174; Conservative 113; Mismatches 248;
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Patent No. US20020160483A1
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1016 INAGLQALFPK 1026
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                        Similarity
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Best Local 3
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09/761,142

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ORGANISM: Drosophila melanogaster US-10-108-605-217
                   PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 0200-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver 2.1
LENGTH: 879
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                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STPVDNLAAEILPAELRETLLRLQLENKRLCRQEAADRERQEELQR--HLEDANRARHGL 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 KQD----HIQRIMTLEESVQHVVMEAIQELMTKDTPDSLSPETYGNFDSQSRRYYFLSEEA 184
                                                                                                                                                                                                                                                                                                                                            YOAQVEEMRLMMNOLEEDLVSARRRSDLYESELRESRLAAEEFKRKANECOHKLMKAKDO 157
                                                                                                                                                                                                                                                                                                                                                                                        LEQLQEENFRLESGREDERLRCAELEREVAELQHRNQALTSLAQEAQALKDEMDELRQSS 304
                                                                                                                                                                                                                                                                                                                                                                                                                                GKPEVGEYSKLEKINAEQQLK-----IQELQEKLEKAVKASTEATEL---LQNIRQAK 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 KSEQIQQMADKILELEEKHREAQVSAQHLEVHLKQKEQHYEEKIKVLDNQIKKDLADKES 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEPPTDSSTARRIEELQHNLQKKDADLRAMEERYRRYVDKARMVM----QTMEPKQRPAA 622
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                                                                                                                                                                                                                                                      EQDLATYITECSSLKRSLEQARMEVSQE-----DDKALQLLHDIREQSRKLQEIKEQE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : | | :::| | | ::| | | ELETRIREVSLEHEEQKLELKRQLTELQLERESQLTALQAARAALESQLRQAKTELE
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                                                                                                                                                                        Indels 170;
                                                                                                                            Length 1597;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETQHRL-----NQQQLSELRAQVEDLQKALQEQ------
                                                                                                                                                                    Matches 145; Conservative 134; Mismatches 258;
                                                                                                                            Score 276; DB 9;
Pred. No. 5.2e-08;
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Sequence 217, Application US/10108605; Patent No. US20020160934A1
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APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
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; SEQ ID NO 6
; LENGTH: 1597
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-017-216-6
                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 LMTKDTPDSLSPE---TYGNFDSQSRRYYFLSEEAEEGDELQQRCLDLERQLMLLSEEKQ
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                                                                                                                                                                                                                                                                                                                                                    40 VLNQIDPSWFNEAWLQGISEDPGPNWKLKVSNLKMVLRSLVEYSQDVLAH--PVSEEHL-
Length 879;
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                 DB 9;
                                                                                                                                                                      Matches 150; Conservative 136; Mismatches 258;
                                                                                                        . 5e-08;
        Score 270.5;
Pred. No. 5.5
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Job time : 31.2109 secs
                                                                                                Similarity
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870         92.9         399         22         AAE04208         Human           870         92.9         399         22         AAE04230         Human           870         92.9         399         23         ABG64487         Human           807         86.2         386         24         ABG64487         Human           807         86.2         386         24         ABG64487         Human           33.5         78.4         184         22         AAE04290         Human           492         23         AAM9358         Human         Human           30.5         13.9         360         22         AAM129037         Human           30.5         13.9         360         22         AAM38965         Human           30.5         13.9         360         22         AAM38965         Human           10.0         13.9         172         22         AAM38965         Human           10.1         434         22         AAX93212         A human           10.9         11.6         737         22         AAE02019         Human           10.9         11.6         53         AAU09628	102.5 11.0 319 18 102.5 11.0 319 20 102.5 11.0 319 22 102.5 11.0 339 21 102 10.9 426 23 102 10.9 437 23 102 10.9 510 23 102 10.9 510 23	39 102 10.9 542 23 AAE22281 Human deleted nect 40 102 10.9 549 23 AAE22282 Human deleted nect 41 102 10.9 549 23 AAE22282 Human nectin-3-hum 42 102 10.9 549 23 AAE22282 Human nectin-3-hum 43 102 10.9 555 22 AAM30143 Human nectin-3-lum 44 102 10.9 555 22 AAM30143 Human nectin-3-lum 45 102 10.9 555 23 AAE23287 Human nectin-3-lin AAY82322  ID AAY82328  ID AAY82322  ID AAY82328  ID AAY82328  ID AAY82328  ID AAY82328  ID AAY82328  ID AAY82328  ID AAY82328  ID AAY82328  ID AAY82328  ID AAY82328  ID AAY82328  ID AAY82328  ID AAY82328  ID AAY82328  ID AAY82328  ID A	
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GenCore ve Copyright (c) 1993 - in - protein search, using sw m March 4, 2003, 14:50:4 US-09-763-902B-6 score: 936 I MGILLGHLLGHLTVDTYGR. table: BLOSUM62	Searched: 9084/0 seqs, 133230620 resigues  Total number of hits satisfying chosen parameters: 908470  Minimum DB seq length: 0  Maximum DB seq length: 2000000000  Post-processing: Minimum Match 0%  Maximum Match 10%  Listing first 45 summaries	Database : A_Geneseq_101002:*    SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*   SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*   SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*   SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*   SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*   SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*   SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*   SIDS2/gcgdata/geneseqfyeneseqp-embl/AA1980.DAT:*   SIDS2/gcgdata/geneseqfyeneseqp-embl/AA1980.DAT:*   SIDS2/gcgdata/geneseqg-embl/AA1980.DAT:*   SIDS2/gcgdata/geneseqfyeneseqp-embl/AA1990.DAT:*   SIDS2/gcgdata/geneseqfyeneseqp-embl/AA1991.DAT:*   SIDS2/gcgdata/geneseqfyeneseqp-embl/AA1991.TATIDATIDAT:*   SIDS2/gcgdata/geneseqfyeneseqp-embl/AA1991.DAT:*   SIDS2/gcgdata/geneseqfyeneseqp-embl/AA2001.DAT:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.    SUMMARIES   SUMMARIES

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molecules (PTAMS) given in ANY 82117 to ANY 8224. The PTAMS have cytostatic, antiarthritic, antiasthmatic, immunosuppressant, antiarthritic, antialiabetic, antilipaemic, antialiapemic, antiarthrematic, antialiapemic, antipositic, antiposit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trafficking, such as allergies, asthma, urticaria and autoimmune haemolytic anaemia. Anti-PTAM antibodies may be used as antagonists, as a targeting or delivery mechanism for bringing pharmaceutical agents into cells or tissues expressing PTAM and for diagnosis of PTAM-related disorders. PTAM, its catalytic or immunogenic fragments are useful for drug screening using libraries of compounds. PTAM polynucleotides are useful itor generating hybridisation probes useful in mapping the
                                                                                                                                                                              New human protein transport-associated polypeptide and polynucleotide useful for diagnosis, prevention and treatment of cell proliferative and secretory disorders such as leukemia, cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA08035 to AAA08042 encode the human protein transport-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      naturally occurring genomic sequences
                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 67; 75pp; English
                                           WPI; 2000-256642/22.
                                                                                           N-PSDB; AAA08040
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175 AA; Sequence

GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120 Gaps 1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60 121 DGNQVVRDKITELRVQKHSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDG 175 Length 175; Indels 100.0%; Score 936; DB 21; 100.0%; Pred. No. 6.3e-83; 1ve 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 175; Conservative 61 61 合 ò

121

AAY30814 standard; Protein; 306 AA 12-OCT-1999 AAY30814; 

(first entry)

Human secreted protein encoded from gene 4.

Secreted protein; prevention; treatment; protein therapy; gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; blood disorder; developmental abnormality; fetal deficiency; leukemia; autoimmune; acne; hepatic disease; renal disease; lymphoma; inflammation; allergy; achima; Alzheimer's disease; cognitive disorder; schizophrenia; obesity; sepsis; osteoporosis; arthritis; infection; AIDS; connective tissue disorder; transplant rejection; diabetes; psorlasis; cardiovascular disorder; reproductive disorder; food addiliue; food preservative; human; primer; early promoter; GAS; gamma activation element

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This invention describes novel isolated human genes and the secreted proteins they encode. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions eg. by protein for preventing, the properties and asample or by determining the presence of mutations in polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for the polynucleotides of the invention based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and fetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, Alzheimer's and cognitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma, sepsis, acne, psoriasis, cardiovascular disorders, and reproductive disorders. The polypeptides or polynucleotides can also be used as food additives or preservatives: The polypeptide are also useful for identifying their binding partners. This sequence represents a secreted protein described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders, schizophrenia, obesity, osteoporosis, arthritis, infections, AIDS, connective tissue disorders, transplant rejection, diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated human genes potentially useful for, e.g. developmental abnormalities and fetal deficiencies
                                                                                                                                                                                                                                                                                                           Rosen CA, Ruben SM;
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                                                                                                                                                                                                                                                                                                           Moore PA,
                                                                                                                                      98US-0074341.
98US-0074037.
98US-0074118.
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N-PSDB; AAZ00805.
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                 WO9940100-A1
                                                                                                04-FEB-1999;
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GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
                                                                                                                              Gaps
                                                          MGILLGLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
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Length 306;
                              Indels
 100.0%; Score 936; DB 20;
100.0%; Pred. No. 1.4e-82;
iive 0; Mismatches 0;
  Ouery Match 100.
Best Local Similarity 100.
Matches 175; Conservative
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AAY41691 standard; Protein; 321 AA AAY41691 ID AAY XX AC AAY XX DT 07-

AAY41691;

07-DEC-1999

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98US-0084643
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N-PSDB; AAZ33935.
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                                                                                  07-MAY-1998
                                                                                                                                                    5-MAY-1998
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                         Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.
Human PRO 362 protein sequence
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9805-0082767
9805-0082336
9805-0083332
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                                                                                                           WO9946281-A2
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Chen J;

Yuan J, Baker KP,

Gurney A,

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polypeptides
                                                                                                                                                                                                                                                                                      The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation
New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGNQVVRDKITELRVQ------136
|||||||||||||||||
DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                         of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies, AA233891 to AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR
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Length 321;

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Query Match
Best Local Similarity 64.7
Matches 174; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferrara 1
Goddard 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -DEC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DEC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shelton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - NON-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -DEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -JAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kljavin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -APR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -APR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    systemic lupus erythematosis, rheumatoid arthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, scleroderma, falopathics inflammatory mypathies, dermacmyositis, polymyosthis, soloroderma, sjogren's syntemic sclerosis, scleroderma, sjogren's syntemic vaculitis, sarcoidosis, autoimmune hemolytic antoimmune hemolytic paroxysmal nocturnal hemoglobinuria, antoimmune thrombocytopenia, idopathic thrombocytopenia purpura, immune-mediated thrombocytopenia, thrombocytopenia, clarae's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic glomerulonephitis, diabetes mellitus, immune-mediated renal disease, glomerulonephitis, debetes mellitus, immune-mediated renal disease, glomerulonephitis, dependent nervous systems such as multiple sclerosis, of the central and peripheral nervous systems such as multiple sclerosis, and indipathic polymerucopathy, hepatobiliary diseases, infectious hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, B, C, D, E, nonhepatotropic viruses, autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory and fibrotic lung diseases, gluten-sensitive enteropathy, Whipple's disease, autoimmune or immune mediated skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The specification describes A33 related antigens PRO301, PRO362 and PRO245. The methods and compositions of the invention are useful for the treatment and diagnosis of inflammatory disease and tumours in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seases allergic diseases of the lung such as eosinophilic pneumonias, sopathic pulmonary fibrosis and hypersensitivity pneumonitis
                            -----KHSSKLLKTK 146
                                                                               181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A33 related antigen; PRO301; PRO362; PRO245; inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             such inflammatory diseases include of inflammatory bowel disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transplantation associated diseases disease. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Napier MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigens PRO301, PRO362 and PRO245 related to A33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of the PRO362 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gurney AL,
                                                                                                                                     147 TEAPTIMIYPLKAISTVKQSWDWTTDMDG 175
                                                                                                                                                                    241 TEAPTIMIYPLKAISTVKQSWDWITDMDG 269
                                                                                                                                                                                                                                                                                                                  AAY23322 standard; protein; 321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represents the PRO362 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 47; Fig 3; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US19437.
97US-0066364.
98US-0078936.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      32-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashkenazi A, Fong S,
Tumas D, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GETH. ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPI; 1999-404743/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409927098-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JUN-1999
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                            137
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181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
                                                                                                                                                                                                                       61 GSDPVTIFLENDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
                                                                                                                                                                                                                                                                                                                                        121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
                                                                                                                                                                                             61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, secreted protein; transmembrane protein; PRO; EST; cytostatic; expressed sequence tag; detection; cancer.
                                           94; Gaps
                                                                                             1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Desnoyers L, Eaton L, W, Gerber H, Gerritsen ME; Gurney AL, Hillan KJ; Roy MA;
                                                                                                                           1 MGILLGLLLLGHLITVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR
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                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO362 (UNQ317) protein sequence SEQ ID NO:52.
Score 870; DB 20;
Pred. No. 3.7e-76;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E; Fong S, Gao W, Gerber
PJ, Grimaldi CJ, Gurney Al
Napler MA, Pan J, Paoni N
TA, Tumas D, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 TEAPTIMIYPLKAISTVKQSWDWTTDMDG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 TEAPTIMIYPLKAISTVKQSWDWTTDMDG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Botstein D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB44247 standard; Protein; 321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-US00219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0162506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000WO-US00277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-US00376
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Godowski PJ,
Kuo SS, Napi
Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US3127
                                                                                                                                                                                                                                                                                             121 DGNQVVRDKITELRVQ----
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sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bloactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bloactive molecules to cells. AAC788600 to AAC7887 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumourigenesis; defection; neoplastic cell growth; proliferation; cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
                                                                                  Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour; diagnosis; neoplastic disease; identification; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGILLGLLLCHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR
                                                                                                                                                                                                                                                            to AAC78599 represent polynucleotide and EST (expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 870; DB 21; Length 321;
Pred. No. 3.7e-76;
0; Mismatches 1; Indels 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PR0362 protein sequence SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 TEAPTTMTYPLKATSTVKQSWDWTTDMDG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEAPTIMIYPLKAISTVKQSWDWTTDMDG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB24047 standard; Protein; 321 AA
                                                                                                                                                                                                    Claim 12; Fig 22; 636pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 64.7%;
Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JAN-2000; 2000WO-US00277
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99US-0123957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGNQVVRDKITELRVQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1mmunological disorder
WPI; 2000-611443/58.
N-PSDB; AAC78472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 AA;
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12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-SEP-2000
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                                                                                                                                                                                                                                                            AAC78458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
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inflammatory disorders and immunological disorders can be treated.
AAC58123 to AAC58224 represent hybridisation probes and PCR primers used in the isolation of the human PRO sequences. AAC58225 to AAC58241 and AAB24054 to AAB24056 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes an isolated antibody (Ab) that binds to one of the human proteins (P) designated PR0213, PR01330, PR01449, PR0237, PR03124, PR0352, PR03644, PR05131, PR03139, PR03130, PR03130, PR03130, PR03130, PR03130, PR03130, PR03130, PR03130, PR03130, PR03132, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, PR03131, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          can be identified and used as antagonists. Benign or malignant tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGOVGSEQHSDIVKFVVKDSSKLLKTK 240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GSDPVITFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----KHSSKLLKTK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated antibody for use in compositions and methods for the diagnosis and treatment of neoplastic cell growth and proliferation mammals, including humans, and in monitoring tumor treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                           ΜA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGILLGLLLIGHLIYDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurney AL, Klein RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score, 870; DB 21;
Pred. No. 3.7e-76;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 TEAPTIMIYPLKATSTVKQSWDWTTDMDG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                       Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TEAPTIMIYPLKATSTVKQSWDWTTDMDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 61; Fig 14; 195pp; English.
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64.78;
99US-0126773.
99US-0130232.
99US-0131445.
                                                                                                                  99WO-US23089
                                                                                                                                                                                                                                                              99WO-US31243
                                                                                                                                                   99WO-US28313
                                                                                                                                                                                                                     99WO-US28564
                                                                                                                                                                                                                                                                                           99WO-US31274
                                                                                                                                                                                        99WO-US2855
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Desauvage FJ,
                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-572269/53.
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Matches 174; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAC58231
                                                                                                                                            30-NOV-1999;
02-DEC-1999;
                                                                                                                  05-OCT-1999
                                                                                                                                                                                                                  02-DEC-1999
                                                                             28-APR-1999
                                                                                                                                                                                                                                                                                           30-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                           Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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ID AAB3
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AC AAB3
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AAB33429 standard; Protein; 321 AA

AAB33429;

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Henzel W;
                                                                                                                                                antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spendyloarthropathy; systemic sclerosis; sarcoidosis; didopathic inflammatory myopathy; systemic sclerosis; byroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune haemolytic anaemia; diseases;
                                                                              Human, immune related disease, diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyrold; antidiabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
                                                                                                                                                                                                                                   demyellnating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; immunological disease; transplantation associated disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gurney AL, Hebert C,
), Shelton DL, Smith
Rood WI, Yan M;
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                                                                                                                                                                                                                                                                                                            graft rejection; graft-versus-host-disease
                                                Human PRO362 protein UNQ317 SEQ ID NO:80.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan J, Pennic, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9WO-US12252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-013237
                (first entry)
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990S-01456
990S-01467
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Tumas D,
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Kabakoff RC, I
Stewart TA, Tu
                                                                                                                                                                                                                                                                                                                                                                              WO200053758-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                14-SEP-2000.
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proteins, anti-TRO antibodies, agonists and antagonists are useful for treating and diagonisting immune related diseases. The human PRO proteins, anti-TRO antibodies, agonists and antagonists are useful for treating and diagonisting immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathes, systemic scalerosis, diopathic inflammatory myopathies, 5) ogren's systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases, inflammatory bowel disease, gluten-sensitive enteropathy and whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, inflammatory contimunue or immune-mediated skin diseases, allergic diseases.

Immunological diseases of the lung and transplantation associated diseases including graft rejection and graft-versus-host-disease.

AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58678 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                           Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
                                                                                                                                                                                                                                                           The present invention describes sixty four human PRO proteins which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGNOVVRDKITELRVOKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
181 QINNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP. 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGILLGLLLGHLIYDTYGRPILEVPESVTGPWKGDVNLPCTYDFLQGYTQVLVKWLVQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels: 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO362; human; antitumour; tumour; therapy; cytostatic;
breast cancer; ovarian cancer; renal cancer; colorectal cancer.
uterine cancer; prostate cancer; lung cancer; bladder cancer;
central nervous system cancer; melanoma; leukaemia; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
92.9%; Score 870; DB 21; Length 321;
Best Local Similarity 64.7%; Pred. No. 3.7e-76;
Matches 174; Conservative 0; Mismatches 1; Indels 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGNQVVRDKITELRVQ--------
                                                                                                                                                                                                       Claim 33; Fig 32; 309pp; English.
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                        WPI; 2000-572271/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 AA;
                                                N-PSDB; AAC58594
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AAY95346
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Homo sapiens

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renal, colorectal, uterine, prostate, lung, bladder and central nervous
system cancer, melanoma and leukaemia. Methods for the recombinant
expression of the antitumour proteins are also provided.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of human antitumour protein PR0362, as deduced from a foetal brain cDNA clone (see AAA49725). PR0362 has a mol.wt. of 35,544 and a piof 8.51. It has homology to A33 antigen protein and to the HCAR protein as well as to Dayoff sequences. A claimed method for inhibiting the growth of a tumour cell comprises exposing the tumor cell to PR0739, PR0320, PR0312, PR0321, PR0324, PR0312, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0313, PR0
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                                                                                                                                                                                                                                                                                                           'note- "protein kinase phosphorylation site"
                                                                                                                                                                                                                                                   "glycosaminoglycan attachment site"
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                                                                                                                                                                                        "transmembrane domain"
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Napier MA, Pitti RM, Wood WI;
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                                                           label- Signal_peptide
Location/Qualifiers
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label- PRO362
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N-PSDB; AAA49725.
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AAB19393-B19407 represent secreted human proteins. The secreted proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ostecarthritis; burn; incision; stem cell disorder; osteoporosis; osteoarthritis; burn; incision; ulcer; periodontal disease; neuropathy; nervous system disease; bone growth; cosmetic plastic surgery; gut protection; gut regeneration; fibrosis; cancer; bone marrow transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  burns, incisions, ulcers, periodontal diseases, central and peripheral nervous system diseases and neuropathies, for healing fractured bones and to induce cartilage and/or bone growth in cosmetic plastic surgery
                                                                                                                                                                                                                 181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
                                                                                           GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
                         1 MGILLGLELLGHLIYDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR
                                                                                                                         61 GSDPVIIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP
MGILLGLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            generation in patients receiving cancer chemotherapy, treating b
marrow transplantation patients and for healing fractured bones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted human proteins useful for stimulating blood cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of a human secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                 147 TEAPTIMIYPLKATSTVKQSWDWTTDMDG 175
                                                                                                                                                                                                                                                                                                                                                                                                            241 TEAPTTMTYPLKATSTVKQSWDWTTDMDG 269
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N-PSDB; AAC61882.
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20-AUG-1999;
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Score 870; DB 21; Pred. No. 3.7e-76; 0; Mismatches 1;

Query Match Best Local Similarity 64.7%; Matches 174; Conservative

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Length 321;

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    regeneration, for the
The proteins are also useful for gut protection or regeneration, for th treatment of lung or liver fibrosis, for stimulating blood cell generation in patients receiving cancer chemotherapy and for treatment of bone marrow transplantation patients.
                                                                                                                                                             181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use in genetic manipulation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to primers for synthesising full length cDNA
                                                                                          94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; SEQ ID NO 3986; 1380pp + sequence listing; English.
                                                                      DB 21; Length 399,
                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Human; full length cDNA; cDNA synthesis; oligo-capping
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                                                                    Score 870; DB 21
Pred. No. 5e-76;
0; Mismatches
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11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
                                                                     Query Match 92.9%;
Best Local Similarity 64.7%;
Matches 174; Conservative
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                                                   399 AA;
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                                  the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
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are useful for clarifying the function of the protein encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 92.9%; Score 870; DB 22; Best Local Similarity 64.7%; Pred. No. 5e-76; Matches 174; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 TEAPTIMIYPLKAISTVKQSWDWTIDMDG 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGNOVVRDKITELRVQ
                                                                                                                                                                                                                                                                                                                                                                                 399 AA;
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30-JUN-2000; 2000US-0215136; (HUMA-) HUMAN GENOME SCI INC Baker KP, Young PE; Ruben SM, Komatsoulls GA,

WPI; 2001-343793/36. N-PSDB; AAD08498:

Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition

Claim 11; Page 440-441; 509pp; English.

AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted

protein genes, and AAE04199-AAE04239 represent the proteins they encode.

AAE0440-AAE04297 represent human secreted protein fragments or variants.

The secreted proteins and their genes are useful for preventing, the secreted proteins and their genes are useful for preventing, the secreted protein in a sample or by determining the presence of amount of the new protein in a sample or by determining the presence of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the sample or the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, hemantopoletic disorders, diseases of the immune system, albeit and adsentable and adseases of e.g., rheumatold arthritis, inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, parkinson's disease, cognitive disorders, schizophrenia, asthma, skin disorders, and infections. The proteins and also be used to aid wound health and and epithelial cell proliferation, to prevent skin againg due to sunburn, to maintain organs before transplantation, for supporting coll cognate ligands or binding partners, and in chemotaxis, and can be used to a for a preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoasays e.g., radioimmunoasay or enzyme linked immunoascabent assay (Elisa). The present sequence represents a human secreted protein of the invention.

399 AA; Sequence

94; Gaps Score 870; DB 22; Length 399; Pred. No. 5e-76; 0; Mismatches 1; Indels 9 Ouery Match
Best Local Similarity 64.7%;
Matches 174; Conservative ( ð

MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60 g

61.GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120 61

121 DGNQVVRDKITELRVQ------121

1 OTNNOEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240 -----KHSSKLLKTK 146

137

RESULT 12 AAE04230

AAE04230 standard; Protein; 399 AA

AAE04230;

(first entry) 09-AUG-2001 Human gene 11 encoded secreted protein HMSOW51, SEQ ID NO:85.

foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzhelmer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; andjogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; chromosome X; binding partner identification. protein; proliferative disorder; cancer; tumour; Human; secreted

Homo sapiens

Location/Qualifiers Peptide

protein" /note- "Mature secreted 1..19 /label= signal\_peptide 20..399

Protein

W0200136432-A2.

25-MAY-2001.

.5-NOV-2000; 2000WO-US31162

19-NOV-1999; 99US-0166415.

(HUMA-) HUMAN GENOME SCI. INC

Young PE; Baker KP, Komatsoulis GA, Ruben SM,

2001-343793/36. N-PSDB; AAD08520

÷. Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition

Claim 11; Page 460-461; 509pp; English.

AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the proteins they encode. AAE04240-AAE04297 represent human secreted protein fragments or variants gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their mutations in the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autolimune diseases (e.g., rheumatoid arthritis), inflammation, alleggies, neurological disorders (e.g., Alzheimer's disease, barkinson's disease, cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriatis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, anglogenic disorders, kidney disorders, chemotaxis, and can be used The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the as a food additive or preservative to modify storage properties cognate ligands or binding partners,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
                                                                                                                                                                                                                                                                                                        GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, a in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (Elish). The present sequence represents a human secreted protein of the invention.
                                                                                                                                                                                                                                                     1 MGILLGELLLGERLIVDIYGRPILEVPESVTGPWKGDVNLPCTYDPLGGYTQVLVKWEVQR 60
                                                                                                                                                                                               94; Gaps
                                                                                                                                                                                                                                1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               limunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human serum albumin, HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antilnfertility; antilnflammatory; antiulcer;
                                                                                                                                                        DB 22; Length 399;
                                                                                                                                                        Query Match 92.9%; Score 870; DB 22
Best Local Similarity 64.7%; Pred. No. 5e-76;
Matches 174; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New fusion protein for treating disease e.g. albumin fused to a therapeutic protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 TEAPTIMIYPLKAISTVKQSWDWTIDMDG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human albumin fusion protein #1162.
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25-APR-2000; 2000US-199384P.
21-DEC-2000; 2000US-256931P.
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                                                                                                                      399 AA;
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The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in tro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders disorders (e.g. acquired immundeficiency syndrome, AlbS), endocrine disorders (e.g. acquired immundeficiency syndrome, AlbS), endocrine disorders (e.g. Alzhehmer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelmer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelmitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). AbBG65518 represent albumin tusion proteins of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder;
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neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.9%; Score 870; DB 23; Length 399; 64.7%; Pred. No. 5e-76;
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Claim 1; Page 1257-1258; 2102pp; English.
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Best Local Similarity 64.7
Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 AA;
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encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to albumin (HA, also known as human serum therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, disease, ulcerative colliss, immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ||||||||
| OTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders
(e.g. diabetes), haematopoietic disorders, neural disorders
(e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,
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                                                                                                                                                                                                                                                                                                                                               an
                                                                                                                                                                                                                                                                                                                                 fusion protein for treating disease e.g. diabetes comprises
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
92.9%; Score 870; DB 23; Length 399;
Best Local Similarity 64.7%; Pred. No. 5e-76;
Matches 174; Conservative 0; Mismatches 1; Indels 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorder; psoriasis; sepsis; diabetes; atherosclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 1258-1259; 2102pp; English.
                                                                                                                                                                                                                                                                                                                                                                       albumin fused to a therapeutic protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TEAPTIMIYPLKATSTVKQSWDWTTDMDG 269
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12-APR-2000; 2000US-229358P.
25-APR-2000; 2000US-199384P.
21-DEC-2000; 2000US-256931P.
                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                   WPI; 2002-010886/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               399 AA;
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skin disorde
                                                                                                                                                                                                 Rosen CA,
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AbD08488-AbD08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAB04199-AAB04239 represent the proteins they encode. AAB04240-AAB04297 represent human secreted proteins and their genes are useful for preventing. The secreted proteins and their genes are useful for preventing. The secreted protein is an encode. The secreted protein is an encode containing the mount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental aborders, hemantopoletic disorders, diseases of the immune system, allos, neurological disorders, diseases of the immune system, allos, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders, disorders, schizophrenia, asthma, and disorders, and infections. The proteins of iseases of disorders, and infections. The proteins can also be used to aid wound health and epithelial cell proliferation, to prevent skin ageing due to subburn, to maintain organs before transplantation, for supporting culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used to and which health and epithelial cell proliferation, to prevent skin ageing due to connate ligands or binding partners, and in chemotaxis, and each of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners of the impartners
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136
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cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemicaxis; food additive; binding partner identification; chromosome X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecule encoding a human secreted protein is, used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSS
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Pred. No. 6.3e-70;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 62.9%;
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-2000; 2000WO-US31162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-NOV-1999; 99US-0166415.
30-JUN-2000; 2000US-0215136.
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                                                                                                                                                                                                                                                                                                            WO200136432-A2
                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                      25-MAY-2001
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121 RVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQQTNNQEPIKVATL 180
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TIMIYPLKA 159		TIMTYPLKA 240
137KHSSKLLKTEAPTTMTYPLKA 159		181 STLLFRPAVIADSGSYPCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMTYPLKA 240
		STLLFKPAVIADSGSYPCT
137		181
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Search completed: March 4, 2003, 14:58:47 Job time: 17.0933 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.	OM protein - protein search, using sw model	March 4, 2003, 14:53:52; Search time 7.87247 Seconds (without alignments) 2137.006 Million cell updates/sec	
	OM protei	Run on:	

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 283224 seqs, 96134422 residues Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result	Score	Ouery	Length	DB	a	Description
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7	104.5	71.7	COF	4	08//80	3,
m	100.5	10.7	355	-1	LKCH	
₹.	100.5	10.7	408	H	LKRT2	
'n	100	10.7	354	н	LKHU	proteoglycan link
9	97.5	10.4	144	7	S36308	
	97.5	10.4	354	י	504243	proteoglycan link
- 00	~	10.4	453	~	B83380	hypothetical prote
o	97.5	10.4		~	153960	ž
10	97.5	10.4	526	~	A37821	butyrophilin - bov
11	97:5	10.4	538	Ŋ	168093	PRR2 delta - human
12	97	10.4	116	~	D24891	T-cell receptor al
13	96	10.3	526	~	S70587	ph11
14	95	10.1	137	~	I46628	ė,
15	94.5	10.1	135	~	S36314	T-cell receptor de
16	94	10.0	118	7	171934	lass II I-A
17	93.5	10.0	142	7	S36307 ·	
.18	92.5	6.6	144	'n	536322	T-cell receptor de
19	92.5	6.6	1643	7	T14274	versican precursor
70	92.5	6.6	3381	7	T42389	versican precursor
. 21	92	9.6	116	Ä	E24891	T-cell receptor al
. 22	92	9.6	132	7	A55410	
23	92	8.6	309		149522	B7-2 prote
24	91.5	8.6	142	~	S04664	.l recepto
25	. 91	9.7	531	~	S20900	titin - mouse (fra
26	89.5	9.6	323	~	A48997	tumor surface anti
27	89	9.5	101	٦,	A29165	•
28	68	. 9.5	145	~	46	
29	8	5	299	~	S56749	. junctional adhesic

R;Thoelen, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M. Blochem. Blophys. Res. Commun. 288, 805-808, 2001 A;Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus rece

coxsackie- and adenovirus receptor - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 02-Apr-2002 #sequence\_revision 02-Apr-2002 #text\_change 02-Apr-2002 C;Accession: JC7780

Ig V-region-like B hyaluronate lyase elastic titin - hu	activated B-cell p myelin/oligodendro	T-cell receptor de probable purine nu	r-cell receptor de secretory componen titin, cardiac mus r-cell receptor al	Ig V-region-like B T-cell receptor al Ig lambda chain	T-cell receptor de
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T28137 A55137 T38346	A48929 A55717	A40131 840131 837928	S36302 ORRBG I38344	C39371 C39371 B24891 S25755	03421
728 A55	A P	8 A A 6	N N N	S 2 2 3	20
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## ALIGNMENTS

RESULT 1  \$42938 proteoglycan link protein precursor - horse proteoglycan link protein precursor - horse  N;Alternate names: cartilage link protein C;Species: Equus caballus (domestic horse) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Jun-1999 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Jun-1999 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Jun-1999 C;Dudhia, J.; Platt, D. Submitted to the EMBL Data Library, March 1994 A;Reference number: \$42938 A;Accession: \$42938 A;Accessi	Query Matches 11.4%; Score 106.5; DB 1; Length 354;  Query Matches 37; Conservative 19; Mismatches 57; Indels 11; Gaps 6;  Matches 37; Conservative 19; Mismatches 57; Indels 11; Gaps 6;  Qy 12 HLTVDTYGRPILEVPES-VTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRGSD 63
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F;21/Binding site: carbohydrate (Asn) (covalent) #status predicted F;56/Binding site: carbohydrate (Asn) (covalent) #status experimental F;61-140,182-253,206-227,280-350,305-326/Disulfide bonds: #status predicted
                                                                                                                         10.7%;
30.7%;
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                                                                                                                                       Best Local Similarity 30.79
Matches 31; Conservative
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Residues: 180-408 <DOE>
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Best Local Similarity
Matches 38; Conserv
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                                                                                                                         Query Match
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                                                                                                site on bovine cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H.; Soos, J.; Dekany, K.; Argraves, W.S.; Spa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deak, F.; Kiss, I.; Sparks, K.J.; Argraves, W.S.; Hampikian, G.; Goetinck, P.F. oc. Natl. Acad. Sci. U.S.A. 83, 3766-3770, 1986
Title: Complete amino acid sequence of chicken cartilage link protein deduced from CDN Reference number: A24881; MUID:86233315; PMID:3459154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: protein
Residues: 40-55,'X',57-59 <WU2>
Note: 39K protein, a minor component of matrix vesicles
Comment: Link proteins stabilize the aggregates of proteoglycan monomers with hyaluron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 extracellular matr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be glycosy
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                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Kiss, I.; Deak, F.; Mestric, S.; Delius, H.; Soos, J.; Dekany, K.; Argraves, Proc. Natl. Acad. Sci. U.S.A. 84, 6399-6403, 1987
Vifile: Structure of the chicken link protein gene: exons correlate with the Accession: A28305; MUD:87317659; PMID:3476955
Residues: 1-355 <KIS>
Cross-reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
                                                                                                                                                                                                                                                                                                       LVKWLVQRGS----DPVTIFLRDSSGDHIQQAKYQ---GRLHVSHK--VPGDVSLQLSTL 103
                                                                                                                                                                                                                                                                                                                                    ---VVRDKITELRVOKHSSKLL----KTKTEAPTTMTY 155
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                 1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPWKGD-VNLPCTY-----DPLQGYTQV 52
                                                                                                                                                                                                                                                                       54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Residues: 40-55, X',57-60, X',62-75, X',77-78, X' <WUA>
Note: 38K protein, a major component of matrix vesicles; Asn-56 appears
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN: AAA48940.1; PID:9212260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A)Note: single copy gene
C;Superfamily: proteoglycan link protein; immunoglobulin homology; link
C;Keywords: cartilage; duplication; extracellular matrix; glycoprotein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-355/Product: link protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID:9212267
                                                                                                                                                                                                                                                            1 MELLLRFLLCGVADFTRGLSI-TTPEOMIEKAKGETAYLPCKFTLGPEDQGPLD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and matrix vesicles in the PMID:1985942
                                                                                              attachment
                                                                                                                                                                               41;
                                                                                                                                       Length 365;
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GB:M35038; NID:9212264; PIDN:AAA48941.1;
                                                            A;Cross-references: GB:AY033651
C;Comment: This protein serves as the primary adenoviral
                                                                                                                                                                             81;
                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :177-254/Domain: link protein repeat homology <LNKI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Experimental source: embryonic sternal cartilage Wu, L.N.Y.; Genge, B.R.; Wuthler, R.E. Biol. Chem. 266, 1187-1194, 1991
Title: Association between proteoglycans and matr Reference number: A39097; MUID:91093230; PMID:198
                                                                                                                                ; Score 104.5; Di
; Pred. No. 0.14;
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :oss-references: GB:M13212; NID:g212259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLRYEWOKLSDSOKLPTSWLPEM 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 PL----KATSTVKOSWDWTTDM 173
                                                                                                                           Ouery Match
11.2%;
Best Local Similarity 27.6%;
Matches 56; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Introns: 34/1; 159/1; 260/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oteoglycan link protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                      A; Molecule type: mRNA
A; Residues: 1-365 <THO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Residues: 1-355 < DEA>
JC7780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lecule type:
  A; Accession:
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rat link prote
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16-408/Product: proteoglycan link protein 2 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neame, P.J.; Christner, J.E.; Baker, J.R.
Biol. Chem. 261, 3519-3535, 1986
Jattle: The primary structure of link protein from rat chondrosarcoma proteoglycan
Reference number: A02869; MUID:86140139; PMID:2419334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeated protein structure
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Comment: This protein was extracted from rat chondrosarcoma.
Comment: Residues 259-277 and 358-376 (approximately) form epitopes for the Comment: Link proteins interact with and stabilize aggregates of hyaluronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Date: 13-Aug-1986 #sequence_revision 24-Oct-1997 #text_change 13-Nov-1998 C.Accession: A28654; A24880; A02869
                                                                        Gaps
                                                                                                                                                                                 GNVTLPCKFYHEHTSTAGSGTHKIRVKWTKLTSDYLKEVDVFV--AMGHHRKSYGKYQGR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 GDVNLPC----TYDPLQGYTQVLVKW--LVQRGSDPVTIFLRDSSGDHIQQ-AKYQGR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDPVTIFLRD-----SSGDHIQ-QAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 SD----YLREVDVFVSMGYHKKTYGGYQGRVFLKGGSDNDASLIITDLTLEDYGRYKCEV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LLLGHLTVDTYGRPILEVPES-VTGPWKGDVNLPCTY--DPL---OGYTQVLVKWLVQRG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
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                                                                     Indels
            Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title: Alternative splicing generates two different mRNA Reference number: A28654; MUID:88198139; PMID:2452158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;110/Binding site: carbohydrate (Asn) (covalent) #status e
F;115-193,235-306,259-280,333-403,358-379/Disulfide bonds:
                                                                                                                                                                                                                                                                                          Molecule type: mRNA
Festidues: 1-408 <RMO.>
Doege, K.; Hassell, J.R.; Caterson, B.; Yamada, Y.
coc. Natl. Acad. Sci. U.S.A. 83, 3761-3765, 1986
Title: Link protein cDNA sequence reveals a tandemly a
Reference number: A24880; MUID:86233314; PMID:3459153
                                                                                                                                                                                                                                                LHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVV 126
                                                                  Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55;
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Score 100.5; I
Pred. No. 0.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhodes, C.; Doege, K.; Sasaki, M.; Yamada,
Biol. Chem. 263, 6063-6067, 1988
Title: Alternative splicing generates two o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteoglycan link protein 2 precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N; Alternate names: cartilage link protein
C; Species: Rattus norvegicus (Norway rat)
                                                                  14;
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proteoglycan link protein precursor [validated] -
N; Alternate names: cartilage link protein
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                                                                                                                                                             1-15/Domain: signal sequence #status predicted <SIG>
16-354/Product: proteoglycan link protein #status experimental <MAT>
54-141/Domain: immunoglobulin homology <IVM>
                                                                                                                                                                                                                                                                                         Superfamily: proteoglycan link protein; immunoglobulin homology; link Keywords: cartilage; duplication; extracellular matrix; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: protein
Residues: 16-38,'X',40-55,57-60,62-65,'X',67,'X',69-80 <NG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: S09309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: mRNA
Residues: 1-92,'A','94-354 <NUC>
Nguyen, O.; Mort, J.S.; Roughley, P.J.
ochem. J. 266, 569-573, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: mRNA
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Accession: S04244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title: The primary structure of human cartilage link protein. Reference number: S14914; MUID:90206798; PMID:2320422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Dec-2000 Accession: S14914; S04244; S03868; A36308; S14926; S09309; S08041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Homo
                                                                                                                                                                                                                                                                                                                                                                                               Map position:
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cchem. J. 259, 61-67, 1989
litle: Degradation of proteoglycan aggregate by a cartilage
reference number: S03868; MUID:89246328; PMID:2719651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: the authors translated the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reference number: $14926; MUID:90245703;
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                                                                         176-253/Domain: link protein repeat homology <LNK1>74-350/Domain: link protein repeat homology <LNK2>
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Johna, J., Hardingham, T.E.
Leic Acids Res. 18, 2214, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sborne-Lawrence, S.L.; Sinclair, A.K.; Hicks, R.C.; Lacey,
omics 8, 562-567, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                         ross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atus: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sidues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-354 <OSB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-35 <NGU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-354 · < DUD>
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predicted
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pmiD:2286376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.W.;
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C; Species: Sus s
C; Date: 28-Feb-J
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBO J. 12, 715-724, 1993
A;Title: Divergent evolution of T cell repertoires:
A;Reference number: S36287; MUID:93178447; PMID:8444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Ovis orientalis aries, Ovis C; Date: 03-Feb-1994 #sequence_revision C; Accession: S36308; S23024
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                                                                                                                                                          A; Title: Immunoglobulin fold and tandem repeat structures A; Reference number: 147145; MUID:89293837; PMID:2738916 A; Accession: 147145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S36308
T-cell receptor delta chain precursor - sheep (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteoglycan link protein precursor -
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                                                                                                     A; Residues:
                                                                                                                          A; Molecule
                                                                                                                                            A;Status:
                                                                                                                                                                                                                                                                                                                                                        A; Title: Appendix. Isolation and
                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: S04243; I47145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-144 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translation not shown
                                                                               A;Cross-references: EMBL:Y00165; NID:g2009; PIDN:CAA68358.1; PID:g2010
                                                                                                                                                                                                                 N;Cross-references: EMBL:Y00165; NID:g2009; PIDN:CAA68358.1; Rerkins, S.J.; Nealis, A.S.; Dudhia, J.; Hardingham, T.E. Mol. Biol. 206, 737-753, 1989
                                                                                                                                                                                                                                        R; Perkins,
                                                                                                                                                                                                                                                                                                                                                                                                   R;Dudhia,
Superfamily: proteogry.....

Superfamily: proteogry.....

;Keywords: cartilage; duplication; ext

;Keywords: signal sequence #status

-1-15/Domain: signal sequence #status
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Best Local S
Matches 32
                                                                                                                                                                                                                                                                               Molecule type: mRNA
Residues: 1-354 <DUD>
                                                                                                                                                                                                                                                                                                                     Accession: S04243
                                                                                                                                                                                                                                                                                                                                        Reference number:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 VNLPCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSGD-HIQQAKYQGRLHVSHKVPGD 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 VSLQLSTLEMDDRSHYTCEVT-----WQTPDGNQVVRDKIT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                        preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                 J.; Hardingham,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNVTLPCKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEVDVFV--SMGYHKKTYGGYQGRV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDVNLPCTY--DPL---QGYTQVLVKW--LVQRGSDPVTIFLRDSSGDHIQ-QAKYQGRL 86
                                                                                                                        type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa domestica
                                                                                                   1-354 <PER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                     990 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cartilage link
                                                                                                                                                                                                                                                                                                                                          S04243
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                                                                                                                                                                                                                                                                                                                                                                                                   T.E.
                                                             link protein; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                 (domestic pig)
evision 28-Feb-1990 #text_change
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                                                                                                                                                                                                                                                                                                                                                            sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 100; DB Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                        extracellular matrix;
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03-Feb-1994
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#text_change
    predicted <MAT>
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nge 23-Jul-1999
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                                                                                                                                                                                                                                                          PID:92010
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                                                                                                                                                                                                                                                                                                                                                                                                                                     22-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                             protein
                                                                                                                                                                                                   N-terminal
                                                                                                                                                                                                                                                                                                                                                            cartilage
                                                             repea
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immunoglobulin homology <IMM>

Gaps

47;

Indels

Length 478;

0.8; 0.8;

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R.Jack, L.J.W.; Mather, I.H.
J. Biol: Chem. 265, 14481-14486, 1990
A;Title: Cloning and analysis of CDNA encoding bovine butyrophilin, an apical glycopr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Bos primigenius taurus (cattle)
Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRV---QKHSSKLLK-TKTEAPTT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 TLALHGLIVEDEGNYTCEFA-TFPKGS-*VRG-MTWLRVIAKPKNQAEAQKVTFSQDPTT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------PDAPANHQNVAAFHPKMGPSFPSPKPGSERLSFVSAKQSTGODTEAELQDA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ILLGLLLGHLTVDTYGRPI-LEVPESVTGPWKGDVNLPC-TYDPLQGYTQVLVKMLVQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: poliovirus receptor; immunoglobulin homology F;276-331/Domain: immunoglobulin homology <IMM>
                                                                                                                                                 A;Cross-references: GB:S79171; NID:g1042202; PID:g1042203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reference number: A37821; MUID:90354441; PMID:2387867
Reference number: I53960; MUID:95347610; PMID:7622062
                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                              Query Match
10.4%; Score 97.5; D.
Best Local Similarity 25.7%; Pred. No. 0.8;
Matches 52; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTYPLKATSTVKQSWDWTTDMD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 VALCISKEGRPPARISWLSSLD 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-526 <JAC>
                                                                                            A; Molecule type: mRNA
A; Residues: 1-478 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: A37821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRR2 delta - human
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                                                                                                                                                                                                                     A; Gene: PRR2alpha
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: 153960
C;Accession: 153960
Gene 159, 267-272, 1995
A;Title: The human PRR2 gene, related to the human pollovirus receptor gene (PVR), is the human PRR2 gene, related to the human pollovirus receptor gene (PVR), is the human PRR2 gene, related to the human pollovirus receptor gene (PVR), is the human PRR2 gene, related to the human pollovirus receptor gene (PVR), is the human PRR2 gene, related to the human pollovirus receptor gene (PVR), is the human PRR2 gene, related to the human pollovirus receptor gene (PVR), is the human PRR2 gene, related to the human pollovirus receptor gene (PVR), is the human PRR2 gene, related to the human pollovirus receptor gene (PVR), is the human PRR2 gene (PVR), is the human PRR2 gene (PVR), is the human PRR2 gene (PVR), is the human PRR2 gene (PVR), is the human PRR2 gene (PVR), is the human PRR2 gene (PVR), is the human PRR2 gene (PVR), is the human PRR2 gene (PVR), is the human PRR2 gene (PVR), is the human PRR2 gene (PVR), is the human PRR2 gene (PVR), is the human PRR2 gene (PVR), is the human PRR2 gene (PVR), is the human PRR2 gene (PVR), is the human PRR2 gene (PVR), is the human PRR2 gene (PVR) (PVR) (PVR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Stover, C.K.; Pham, X.Q.; Ervin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pothetical protein PA2131 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --QLSTLEMDDRSHY 111
                                                                                                                                                                                                                                                                                                                                                                                                     PVTIFLRDSSGDHIQ-QAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                          41 C-----TYDPLOGYTQVLVKWLVQRGS----DPVTIFLRDSSGDHIQQA------KY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DIYGRPILEVPESVTGPW-----KGDVNLP 40
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                      HLIVDIYGRPILEVPES-VTGPWKGDVNLPCTY--DPL---QGYTQVLVKW--LVQRGSD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 LGVLLGLPASGQATCYRVTSVGSETTTSNTQIRP----GEGTAGSWTGACDTCNGSLGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 SVVNVSDESFQPYPTLIASAVAPLTQYGATGGYDPERVFFRCSAGDAVYEMFSTNGDDLY
                                                                                                                                                                                                                                                                                                                                    1: : | :: | :: | :: | 31 HIQAENGPRILVEAEQAKVFSHRGGNVTLPPCKFFRDPTAFGSGTHKIRIKWTKLTSDYLK
               F.176-253/Domain: link protein repeat homology <LNK1>
F:274-350/Domain: link protein repeat homology <LNK2>
F:21,56/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:61-139/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                              58; Indels
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.75;
                                                                                                                                                                Score 97.5; DB Pred. No. 0.55;
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Local Similarity 21.7%; Pred. No. 0.75
Les 50; Conservative 26; Mismatches
                                                                                                                                                                                                                                 20; Mismatches
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Experimental source: strain PAO1
                                                                                                                                                                          10.4%;
                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGILLGLLLLGHLTV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7, S.; Olson, M.V.
406, 959-964, 2000
                                                                                                                                                                                            1 Similarity
35; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: DNA'
Residues: 1-453 <STO>
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                                                                                                                                                                          Query Match
Best Local S
Matches 35
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Matches
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                        61 GSDPVTIFLRDSSGDHIQQAKYQGRLHV--SHKVPGDVSLQLSTLEMDDRSHYTCEVTWQ 118
                                                                                                                                                                                                                                                                                                                                                 A:Gross-references: GB:M3551; NID:g1763685; PIDN:AAB39766.1; PID:g162773 C; Keywords: transmembrane protein
                                                                                                                                                                                           3 ILLGLLLGHLTVDTYG--RPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                   17 ILLOLPKLDSAPFDVIGPQEPIL----AVVGE---DAELPCRLSPNVSAKGMELRWFREK
                                                                                                                                         15;
                                                                                  Length 526;
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          119 TPDGNOVVRDKITELRVQKHSSKLLKTKTEAPTTMT----YP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 ENYEEAIVHLKVAALGSDPHISMKVQESGEIQLECTSVGWYP 171
                                                                                     10.4%; Score 97.5; DB 2;
11arity 24.1%; Pred. No. 0.9;
Conservative 23; Mismatches 85;
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R;Taylor, M.R.; Peterson, J.A.; Cerlani, R.L.; Couto, J.R.
Biochim. Biophys. Acta 1306, 1-4, 1996
A;Title: Cloning and sequence analysis of human butyrophilin reveals a potential rece
A;Reference number: S70587; MUID:96201696; PMID:8611614
A;Accession: S70587
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                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-526 <TAY>
A;Cross-references: EMBL:U39576; NID:g1326082; PIDN:AAC50489:1; PID:g1326083
                 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
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03-Feb-1994 #text_change 23-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDG---NQVVRDKI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVTIFLRDSSGDHIQQ-AKYQGRLHVSHK--VPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAVLVHRDGREQEAEQMPEYRGRATLVQDGIAKGRVALRIRGVRVSDDGEYTC---FFRE 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LIGILLIGHLIVDIYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRGSD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 LLTLILLOLPKLDSAPFDVIGPPEPILAVVGEDAELPCRLSPNASAEHLELRWFRKKVS- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYGRPIL -- EVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRD-SS 73
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J. Immunol. 155, 1981-1993, 1995
A;Title: Diversity of T cell receptor delta-chain cDNA in the thymus A;Reference number: 146623; MUID:95363165; PMID:7636249
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0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45; Indels
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10.1%; Score 95; DB 3
Best Local Similarity 27.0%; Pred. No. 0.28
Matches 34; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 DGN---- OVVRDKITELRVQKHSSKLLKTKTE 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGSYEEALVHLKVAALGSDPHISMQVQENGE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Ovis orientalis aries, Ovis C;Date: 03-Feb-1994 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -cell receptor delta chain
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Best Local Similarity
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Residues: 1-137 <YAN>
                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:| |:
TQLVVE 136
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Eberle, F.; Dubreull, P.; Mattel, M.G.; Devilard, E.; Lopez, M. and 159, 267-272, 1995.
Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is the Reference number: I53960; MUID:95347610; PMID:7622062
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23-116/Product: T-cell receptor alpha chain V region F3.5 #status predicted <VAR>
37-114/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----PDAPANHQNVAAFHPKMGPSFPSPKPGSERLSFVSAKQSTGQDTEAELQDA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRV---QKHSSKLLK-TKTEAPTT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 LLWPLLLL - LLLETGAQDVRVQVLPEVRGQLGGTVELPCHLLPPVPGLYISLVTW - OR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 ILLGLLLLGHLTVDTYGRPI-LEVPESVTGPWKGDVNLPC-TYDPLQGYTQVLVKWLVQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            this sequence was determined from the germline gene the authors translated the codon GGA for residue 18 as Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: immunoglobulin V region; immunoglobulin homology (eywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.4%; Score 97; DB 2; Length 116; 27.6%; Pred. No. 0.15; ive 23; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: pollovirus receptor; immunoglobulin homology; 276-331/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                               Cross-references: GB:S79172; NID:g1042204; PID:g1042205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell receptor alpha chain precursor V region (F3.5)
                                                                                                                                                                                                               Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.4%; Score 97.5; DB 25.7%; Pred. No. 0.92; ive 28; Mismatches
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153 MTYPLKATSTVKQSWDWTTDMD 174 VALCISKEGRPPARISWLSSLD 201

97

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Conservative

Similarity

Query Match Best Local Simi Matches 52;

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1-538 <RES>

PRR2delta

Molecule type: mRNA

butyrophilin precursor - human C;Species: Homo sapiens (man)

RESULT 13

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Conservative

Local Similarity Les 32; Conserva

esidues: 1-116 <CHO>

us-09-763-902b-6.rpr

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A;Status: preliminary; translation not shown
A;Molecule type: MRNA
A;Residues: 1-135 <HEL>
A;Cross_references: EMBL:212986; NID:g2236; PIDN:CAA78330.1; PID:g2237
C;Superfamilly: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
A; Reference number: S36287; MUID:93178447; PMID:8440261
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7; Gaps Query Match
Best Local Similarity 27.7%; Pred. No. 0.3;
Matches 28; Conservative 20; Mismatches 46; Indels

37 VNLPCTYDPLQGYTQVLVKWLVQRGS-DPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGD 95 

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US-09-763-902B-6 936 1 MGILLGLILLGHITVDTYGR.....PLKATSTVKQSWDWTTDMDG 175 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

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	*	Description	⊢	O9qup5 mus musculu	Q99795 homo sapten	rattus	P07354 gallus gall	5 homo sa	2 bos t	P10859 sus scrofa	P18892 bos taurus	. Q92692 homo sapien	homo	homo	Q63345 rattus norv	.P81282 bos taurus	P42082 mus musculu	Q9xt56 bos taurus	Q08722 homo sapien	homo	strep		bos t	Q9g176 sus scrofa	P34244 saccharomyc	Q61885 mus musculu	P01832 oryctolagus	~	Q15746 homo sapien	O70570 mus musculu	Q16653 homo sapien	P55283 homo sapien	nomo	homod	Q62059 mus musculu
		1						:																				,							
SUMMARIES		QI QI	PLK_HORSE	PLK_MOUSE	A33_HUMAN	PLK_RAT.	PLK_CHICK	PLK_HUMAN	PLK_BOVIN	PLK_PIG .	BUTY_BOVIN	PVR2_HUMAN	BUTY_HUMAN	CXAR_HUMAN	MOG_RAT	PGCV_BOVIN	CD86_MOUSE	JAM1_BOVIN	CD47_HUMAN	JAM1_HUMAN	HYSA_STRAG	CD83_HUMAN	MOG_BOVIN	PVR1_PIG	KKK1_YEAST	MOG_MOUSE	PIGR_RABIT	CXAR_MOUSE	KMLS_HUMAN	PIGR_MOUSE	MOG_HUMAN	CAD4_HUMAN	PGCV_HUMAN	- 1	PGCV_MOUSE
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		Match Length	354	356	319	354	355	354	354	354	526	538	526	365	245	3381	309	298	323	299	984	205	246	515	1518	246	773	365	1914	771	247	916	3396	924	3358
ď	Query	Match	11.4	11.1	.11.0	11.0	10.7	10.7	10.4	10.4	10.4	10.4	10.3	10.2	6.6				9.6	9.5	9.5	9.4				9.3			9.5	9.1	9.1	9.1		0.6	0.6
		Score	106.5	103.5	102.5	102.5	100.5	100	97.5	97.5	97.5	97.5		95.5	ä	92.2	92	89.5	89.5	68	88	8	87.5	87.5		87	87	ė	•	'n.	82	82	œ	84.5	. 84
	Result	No.	-	7	m	4		9	7	8		10				14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

							*						
	mus musculu	homo saplen	canis famil	homo sapien	homo sapien	mus musculu	mus musculu	gallus gall	rattus norv	brassica ol	mus musculu	cercopithec	•
	99jhj8	P15151	P33706	P09564	015223	088792	962556	P11799	P54900	P49676	P13373	P32506	-
			٠										
•													
	ICOL_MOUSE	PVR_HUMAN	CD8A_CANFA	CD7_HUMAN	PVR1_HUMAN	JAM1_MOUSE	BUTY_MOUSE	KMLS_CHICK	CIB2_RAT	BGAL_BRAOL	VPR2_MOUSE	PVR_CERAE	
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	322	417	239	240	517	300	524	1906	215	828	142	417	
	8	6.8	6.8	8.9	6 8	8.8	8.8	8.8	8.7	8.7	9.0	8.6	
	83.5	83.5	. 83	83	83	82.5	82.5	82.5	. 81.5	81.5	80.5	80.5	
	34	32	36	37	38	39	40	41	42	43	44	4.5	*

## ALIGNMENTS

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RESULT
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X MEDLINE-21085660; PubMed=11217851;

Kawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi K., Kiyosawa H., Rondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,

A Aizawa K., Maţsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Maţsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchi P., Lewis S., Matsuo T., Gissi C., King B., Rochiwa H.,

Ruchi R., Lewis S., Matsuo Y., Nikaldo I., Pescole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

A Blake J., Boğlunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boğlunga N., Carninci P., Raniya M., Lee N.H.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Raniya M., Lee N.H.,

A Lyons P., Marchhonni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguz I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Saya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
                                                                                                                                                                                                                                                                                                                       91 EVDVFV--SMGYHKKTYGGYQGRVFLKGGSDNDASLVITDLTLDDYGRYKCEVIEGLEDD 148
                                                                                                                                                                                                                                                                                            64 PVTIFLRDSSGDHIQ-QAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDG 122
                                                                                                                                                                       Gaps
                                                                                                                                                                                                            12 HLTVDTYGRPILEVPES-VTGPWKGDVNLPCTY--DPL---QGYTQVLVKW--LVQRGSD 63
                                                                                                                                                                                                                                                   31 HIQAENGPRILVEAEQAKVFSHRGGNVTLPCKFLRDPTAFGSGTHKIRIKWTKLTSDYLK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Characterization and chromosomal location of the mouse link protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLK_MOUSE STANDARD; PRT; 356 AA.
090U75; 09D1G9; 09z1X7;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Proteoglycan link protein precursor (Cartilage link protein) (LP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BALB/C;
Orto J.W., Cs-Szabo G., Kamath R.V., Liu W., Li Y., Glant T.T.;
"Molecular analysis of the murine link protein gene: 5' flanking,
coding and 3' flanking sequence analysis; exon-intron structure;
tissue distribution; and generation of transgenic mice.";
submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

OF CHICKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

D815CBB7816C7172 CRC64:
                                                                                                            Score 106.5; DB 1; Length Pred. No. 0.016; Language 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F., Mates L., Krysan K., Liu Z., Szabo P.E., Mann J.R.,
D.R., Kiss I.;
                                                                                                                                                                   19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ytogenet. Cell Genet. 87:75-79(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-129/Sv;
MEDLINE-20108790; PubMed-10640815;
349 BY
325 BY
21 N-
56 N-
40077 MW;
                                                                                                                            11.4%; 29.8%;
                                                                                                                                                                     37; Conservative
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                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                        149 TAVV 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 TIFLRD-----SSGDHIQ-QAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYALURONIC ACID IN THE EXTRACELLULAR CARTILAGE MATRIX.
--- SIMILARITY: CONTAINS 1 IMMNOGCOBULIN-LIKE V-TYPE DOMAIN.
--- SIMILARITY: CONTAINS 1 IMMNOGCOBULIN-LIKE V-TYPE DOMAIN.
--- SIMILARITY: CONTAINS 2 LINK DOMAINS.
--- CAUTION: Ref. 3 sequence differs from that shown due to a frameshift in position 347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 HLIVDIYGRPILEVPES-VIGPWKGDVNLPCIY--DPL---QGYIQVLVKWLVQRGSDPV 65
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Connective tissue; Extracellular matrix; Cartilage; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; Repeat.
                    Raysshizaki Y.,
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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IG-LIKE V-TYPE DOMAIN.
LINK 1.
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MISSING (IN REF. 2).
3FB4B8F30E28C9F2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF137278; AAF24166.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; AAF24977.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROSITE; PS01241; LINK; 2.
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Matches 37; Conservative
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SMART; SM00445; LINK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     356 AA;
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fam; PF00193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Colon carcinoms, MEDLINE-97165045; Pubwed-9012807; MEDLINE-97165045; Pubwed-9012807; Meath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J., Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C., Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C., Burgess A.M.; "The human A33 antigen is a transmembrane glycoprotein and a novel member of the immunoglobulin superfamily."; Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
                                                                                                                                                                                              Homo saplens (Ruman).
Vertebrata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of posttranslational modifications of human A33 antigen, a novel palmitoylated surface glycoprotein of human gastrointestinal epithelium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POST-TRANSLATIONAL MODIFICATIONS.
MEDLINE-97396159; PubMed-9245713;
Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN. SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; 1g; 2.
SWART; SW00410; 1G_like; 1.
SWART; SW00406; IGv; 1.
Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
Transmembrane; Signal; Antigen.
                                                                                      01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cell surface A33 antigen precursor (Glycoprotein A33).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL) POTENTIAL.
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IG-LIKE C2-TYPE DOMAIN.
POLY-CYP.
POTENTIAL.
POTENTIAL.
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     319 AA.
                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interpro; IPR003006; Ig_MHC.
Interpro; IPR003600; Ig_like.
Interpro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U79725; AAC50957.1; -.
                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGNC: 4445; GPA33.
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2256
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2221
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               A33_HUMAN
Q99795;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKV-PGDVSLQLSTLEMDDRSHYTCEVTWQT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-86140139; Pubmed-2419334;
MEDLINE-86140139; Pubmed-2419334;
Medmary Christner J.E., Baker J.R.;
Meame P.J., Christner J.E., Baker J.R.;
Proteoglycan aggregate.";
J. Blol. Chem. 261:3319-3535(1986).
I- FUNCTION: STABILIZE THE AGGREGATES OF PROTEOGLYCAN MONOMERS WITH
HYALURONIC ACID IN THE EXTRACELLULAR CARTILAGE MATRIX.
I- ALTERNATIVE PRODUCTS: 2 ISOFORMS, A LONG FORM, GHOWN HERE) AND A
SHORT FORM; ARE PRODUCED BY ALTERNATYDE SPLICING.
I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
I- SIMILARITY: CONTAINS 2 LINK DOMAINS.
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                4 LIGILILGHLIYDIYGRPILEVPESVTGPWKG-DVNLPCTYDPLQGYTQVLVKW--LVQR 60
                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhodes C., Doege K., Sasaki M., Yamada Y.;
"Alternative splicing generates two different mRNA species for rat link protein.";
J. Biol. Chem. 263:6063-6067(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-1986 (Rel. 02, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Proteoglycan link protein precursor (Cartilage link protein) (LP).
POTENTIAL.

**LINKED (GLCNAC. . .) (POTENTIAL)

**N-LINKED (GLCNAC. . .) (POTENTIAL)

**N-LINKED (GLCNAC. . .) (POTENTIAL)

**9BPC7AAP45C2408E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 126-354 FROM N.A.
MEDLINE-86233314; PubMed-3459153;
Doege K., Hassell J.R., Caterson B., Yamada Y.;
"Link protein cDNA sequence reveals a tandemly repeated protein
                                                                                                                                                                                     11.0%; Score 102.5; DB 1; Length 319; llarity 27.4%; Pred. No. 0.033; Conservative 26; Mismatches 63; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               roc. Natl. Acad. Sci. U.S.A. 83:3761-3765(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-88198139; Pubmed-2452158;
211 PO
112 N-
200 N-
223 N-
35632 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M22340; AAA41535.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 P-DGNQVVRDKITEL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 DLEGNTKSRVRLLVL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
162
112
200
223
323
319 AA;
                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KCBI_TaxID-10116;
                                                                                                                                                                                                                                               37;
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                                                                                                                                                                                        Query Match
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AAA41536.1; JOINED. AAA41536.1; JOINED. AAA41536.1; JOINED.

EMBL; HSSP;

InterPro; IPR003006; Ig\_MHC. InterPro; IPR003596; Ig\_V. InterPro; IPR000538; Link.

fam; PF00047; 1g; 1. fam; PF00193; Xlink; 2. robom; PD000918; Link; 2.

ProDom; PD000918; Link; SMART; SM00406; IGV; 1. SMART; SM00445; LINK; 2

lternative splicing

JOINED,

EMBL; EMBL; EMBL;

us-09-763-902b-6.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 GNVTLPCKFYHEHTSTAGSGTHKIRVKWTKLTSDYLKEVDVFV--AMGHHRKSYGKYQGR 112
                                                                                                                                    [2]
SEQUENCE FROM N.A.
MEDLINE-87317659; PubMed-3476955;
MEDLINE-87317659; PubMed-3476955;
Kiss I., Deak F., Mestric S., Delius H., Soos J., Dekany K.,
Argraves W.S., Sparks K.J., Goetinck P.F.;
"Structure of the chicken link protein gene: exons correlate with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 GDVNLPC-----TYDPLQGYTQVLVKW--LVQRGSDPVTIFLRDSSGDHIQQ-AKYQGR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                          protein domains.";
Proc. Natl. Acad. Sci. U.S.A. 84:6399-6403(1987)
-!- FUNCTION: STABILIZE THE AGGREGATES OF PROTEGGLYCAN MONOMERS WITH
HYALURONIC ACID IN THE EXTRACELLULAR CARTILAGE MATRIX.
-!- SIMILARITY: CONTRAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 2 LINK DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
N'LINKED (GLCNAC. .) (POTENTIAL).
N'LINKED (GLCNAC. .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01241; LINK; 2. Glycoprotein; Cartilage; Glycoprotein; Connective tissue; Extracellular matrix; Cartilage; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; Repeat. PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                     sequence of chicken cartilage link protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 355;
                                 Deak F., Kiss I., Sparks K.J., Argraves W.S., Hampikian G., Goetinck P.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG-LIKE V-TYPE DOMAIN.
LINK 1.
LINK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 LHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : : | | || :: ::| | || || VFLRESSENDASLIITNIMLEDYGRYKCEVIEGLEDDTAVV 153
                                                                                              deduced from cDNA clones.";
Proc. Natl. Acad. Sci. U.S.A. 83:3766-3770(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.7%; Score 100.5; Di
30.7%; Pred. No. 0.057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Mismatches
TISSUE-Embryonic sternal cartilage;
MEDLINE-86233315; PubMed-3459154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M35035; AAA48941.1; JOINED.
M35036; AAA48941.1; JOINED.
M35037; AAA48941.1; JOINED.
M13212; AAA48940.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40533 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M35038; AAA48941.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A24881; LKCH,
PIR, A28305; A28306.
HSSP; P980066; LISC,
LICERPIC; IPRO03096; IG_MHC,
INTERPIC; IPRO03596;: IG_V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Link; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fam; PF00047; 1g; 1.
fam; PF00193; Xlink; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000918; Link;
SMART; SM00406; IGV; 1.
SMART; SM00445; LINK; 2
                                                                             Complete amino acid
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Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M35036;
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CARBOHYD
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                                                                                                  deduced
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     셤
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IHKIRIKWTKLTSDY -> DCTAFWKLIRGRQRSSASPVG
ILTWPCCFPWRKHYTWKGIKSLKLPSLAISDRTS (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 TIFLRD-----SSGDHIQ-QAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLIVDIYGRPILEVPES-VIGPWKGDVNLPCIY---DPL----QGYIQVLVKWLVQRGSDPV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 HIQAENGPRILVEAEQAKVFSHRGGNVTLPCKFYRDPTAFGSGIHKIRIKW-TKLTSD-- 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1988 (Rel. 07, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Proteoglycan link protein precursor (Cartilage link protein) (LP)
                                                                                                                                                                                                                                                                                                                                                       tissue; Extracellular matrix; Cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.0%; Score 102.5; DB 1; Length 354; nllarity 29.1%; Pred. No. 0.037; Conservative, 21; Mismatches 52; Indels 17
                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01241; LINK; 2. Glycoprotein; Connective tissue; Extracellular matrix; Cartil Glycoprotein; Connective tissue; Extracellular matrix; Cartil Hyaluronic acid; Proteoglycan; Immunoglobulin domain; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
R -> W (IN REF. 3).
23278AEA56273D6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEOGLYCAN LINK PROTEIN.
IG-LIKE V-TYPE DOMAIN.
LINK 1.
LINK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC
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40261 MW;

VARSPLIC CONFLICT SEQUENCE

CARBOHYD

DISULFID DISULFID

ISULFID ISULFID DISULFID

NIWWO

Local Similarity hes 37; Conserv

12 Matches

g ò

Query Match

4

PRT;

STANDARD;

PLK\_CHICK P07354;

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88

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01-APR-1988 %(Rel. 07, Created)

Gallus gallus (Chicken)

RESULT 5
PLK\_CHICK
DD PLK\_C
AC P0735
DT 01-AP
DT 01-NO
DD 01-NO
DD REALL
OC BUKAT
OC BUKAT
OC GAILU
OC GAILU
OC GAILU
OX RCEL

SEQUENCE FROM N.A Gallus. NCBI\_TaxID=9031;

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PROSITE; PS01241; LIKK; 2.
Glycoprotein; Connective tissue; Extracellular matrix; Cartilage;
Hyaluronic acid; Proteoglycan; Immunoglobulin domain; Repeat.
                                                                                                                                                                                                                       PROTEOGLYCAN LINK PROTEIN.
IG-LIKE V-TYPE DOMAIN.
LINK 1.
LINK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          315C96EC3AC2626A CRC64;
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N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          40165 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.7%;
32.0%;
                                               Pfam; PF00047; 19; 1.
Pfam; PF00193; X11nk; 2.
ProDom; PD000918; Link; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 32.0 es 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                         SMART; SM00406; IGV; 1
SMART; SM00445; LINK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                          354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an
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P55252;
                                                                                                                                                                                                                                                                                                                                           DISULFID
                                     nterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                         DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       not removed. Usage by and for commercial reement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91139126; PubMed-2286376; OSBorne-Lawrence S.L., Sinclair A.K., Hicks R.C., Lacey S.W., Eddy K.L. Jr., Byers M.G., Shows T.B., Duby A.D.; "Complete amino acid sequence of human cartilage link protein (CRTL1) deduced from cDNA clones and chromosomal assignment of the gene."; Genomics 8:562-567(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hirakawa S., Oohashi T., Su W.-D., Yoshioka H., Murakami T., Arata J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 276:982-989(2000).
-1- FUNCTION: STABILIZE THE AGGREGATES OF PROTEOGLYCAN MONOMERS WITH
HYALURONIC ACID IN THE EXTRACELLULAR CARTILAGE MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Characterization of the promoter for the rat and human link protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The brain link protein-1 (BRAL1): cDNA cloning, genomic structure, and characterization as a novel link protein expressed in adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hodes C., Savagner P., Line S., Sasaki M., Chirigos M., Doege K.,
                                                                                     01.JUL-1989 (Rel. 11, Created)
1-JAPR-1990 (Rel. 14, Last sequence update)
15.JUN-2002 (Rel. 41, Last anotation update)
Proteoglycan link protein precursor (Cartilage link protein) (LP)

    IISSUE SPECIFICITY: Widely expressed: Weakly expressed in the

                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: CONTAINS 1 IMMUNGELOBULIN-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-Articular chondrocytes;
MEDLINE-90206798; Pubmed-2320422;
Dudhia J., Hardingham T.E.;
"The primary structure of human cartilage link protein.";
Nucleic Acids Res. 18:1292-1292(1990).
                                                   354 AA.
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modified and this statement is not removed.
entities requires a license agreement (See )
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Nucleic Acids Res. 18:2214-2214(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ucleic Acids Res: 19:1933-1939(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY.
MEDLINE-20483618; PubMed-11027579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. 4EDLINE-91232964; PubMed-2030970;
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90245703; PubMed-2336413;
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                                                     STANDARD;
                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                 PLK_HUMAN
P10915;
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POTENTIAL

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                                                                                                                                                                                                                                               55 GNVTLPCKFYRDPTAFGSGIHKIRIKWIKLISDYLKEVDVFV--SMGYHKKTYGGYQGRV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hering T.M., Kollar J., Hoynh T.D., Sandell L.J.;

"Bowine chondrocyte link protein cDNA sequence: interspecies
conservation of primary structure and mRNA untranslated regions.";
comp. Biochem. Physiol. 112B:197-203(1995).

-I. FUNCTION: STABILIZE THE AGGREGATES OF PROTEOGLYCAN MONOMERS WITH
HYALURONIC ACID IN THE EXTRACELLICLAR CARTILAGE MATRIX.

-I. SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

-I. SIMILARITY: CONTAINS 2 LINK DOMAINS.
                                                                                           Gaps
                                                                                                                                                                             35 GDVNLPCTY--DPL---QGYTQVLVKW--LVQRGSDPVTIFLRDSSGDHIQ-QAKYQGRL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0cT-1996 (Rel. 34, Created)
1-0cT-1996 (Rel. 34, Last sequence update)
01-0VT-1997 (Rel. 35, Last annotation update)
Proteoglycan link protein precursor (Cartilage link protein) (LP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea.
                                                                                           10;
; DB 1; Length 354;
0.064;
ches 44; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                              87 HVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 AA
                                                    ; Pred. No. 0.06
14; Mismatches
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entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
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BY SIMILARITY.
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Best Local Similarity 28.2%; Pred. No. 0.11
Matches 35; Conservative 20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                            LINK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40260 MW;
                                                                                                        HSSP, P98066, 1TSG.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR00538; Link.
Pfam; PF00047, ig; 1.
Pfam; PF00193; Xilnk; 2.
ProDom; PD000918; Link; 2.
                                                                EMBL; Y00165; CAA68358.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-Holstein-Friesian;
                                                                                                                                                                                                                                                 SMART; SM00406; IGV; 1
SMART; SM00445; LINK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56
354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 NQVV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 TAVV 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Laryngeal cartilage chondrocytes;
MEDLINE-89293837; PubMed-2738916;
Perkins S.G., Nealis A.S., Dudhia J., Hardingham T.E.;
Perkins S.D., Nealis A.S., Dudhia J., Hardingham T.E.;
"Immunoglobulin fold and tandem repeat structures in proteoglycan N-terminal domatics and link protein.";
J. Mol. Biol. 206:737-753(1989).
-!- FUNCTION: STABILIZE THE AGGREGATES OF PROTEOGLYCAN MONOMERS WITH HYALURONIC ACID IN THE EXTRACELULAR CARTILAGE MATRIX.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 2 LINK DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLTVDTYGRPILEVPES-VTGPWKGDVNLPCTY--DPL---QGYTQVLVKW--LVQRGSD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1989 (Rel. 11, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Proteoglycan link protein precursor (Cartilage link protein) (LP).
                                                                                                                                        Probom; PD000918; Link; 2.
SMART; SM00406; IGV; 1.
SMART; SM00445; LINK; 2.
PROSITE; PS01241; LINK; 2.
Glycoprotein; Connective tissue; Extracellular matrix; Cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (P1g).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

    Immunoglobulin domain; Repeat.
BY SIMILARITY.

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IG-LIKE V-TYPE DOMAIN.
LINK 1.
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065D155378A1283C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40287 MW;
                                   Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
Interpro; IPR00538; Link.
Pfam; PF00047; Ig; I.
EMBL; U02292; AAC04311.1; -.
HSSP; P98066; ITSG.
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Best Local S
Matches 35
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DOMAIN
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Jack E.J.W., Mather I.H., "Cloning and analysis of cDNA encoding bovine butyrophilin, an apical glycoprotein expressed in mammary tissue and secreted in association with the milk-fat globule membrane during lactation.";
J. Biol. Chem. 265:14481-14486(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 EVDVFV - - SMGYHKKTYGGYHGRVFLKGGSDNDASLVIIDLILEDYGRYKCEVIEGLEDD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 PVTIFLRDSSGDHIQ-QAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDG 122
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BUTY_BOVIN STANDARD; PRT; 526 AA.
01-809-1990 (Rel. 16, Created)
15-JUL-1998 (Rel. 36, Last sequence update) .
16-CCT-2001 (Rel. 40, Last annotation update)
BUTYCOPHIN PRECURSOR (BT)
BUTYCOPHIN PRECURSOR (BT)
BUTIAL OR BYN.
BOS taurus (Bovine)
Eukaryora, Metacoa; Chordata; Cranlata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
PROSITE; PS01241; LINK; 2.
Glycoprotein; Connective tissue; Extracellular matrix; Cartilage;
Hyaluronic acid; Proteoglycan; Immunoglobulin domain; Repeat.
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BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL)
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                                                                                                                                 PROTEOGLYCAN LINK PROTEIN, IG-LIKE V-TYPE DOMAIN.
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Pred. No. 0.11;
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130 ENYEEAIVHLKVAALGSDPHISMKVQESGEIQLECTSVGWYP 171

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                                                                                                                                                                                                                                                                                                                                                     Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.; "Site-specific glycosylation of bovine butyrophilin.", J. Biochem. 117:147-157(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
ASSOCIATION WITH THE MILK FAT-GLOBULE MEMBRANE DURING LACTATION
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN,
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Davey H.W., Ogg S.L., Husaini Y., Snell R.G., Korobko I.V., Mather I.H., Wilkins R.J.;
Submitted (MAY-1997), to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Immunoglobulin domain; Signal.
                                                                                                                                                                                             Seyfert H., Luethen F.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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E -> D (IN REF. 1).
A14126802BD19284 CRC64;
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N-LINKED (GLCNAC. ) (
N-LINKED (GLCNAC. ) (
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nterPro; IPR003878; SPRY_domain.
nterPro; IPR003877; SPRY_receptor
                                                                                                                                                                                                                                                                                                                             MEDLINE-95293916; PubMed-7775382;
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SMART; SM00406; IGv; 1.
SMART; SM00449; SPRY; 1
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526 AA;
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fam; PF00622
                                                                                                                                                                  FISSUE-Blood
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InterPro; Il
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Freitas E.M., Zhang W.J., Lalonde J.P., Tay G.K., Gaudieri S., ashworth L.K., Van Bockxmeer F.M., Dawkins R.L.; "Sequencing of 42kb of the APO E-C2 gene cluster reveals a new gene:
                                                                                        092692; 075455; 096J29; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-0CT-2002 (Rel. 40, Last semonation update) Poliovirus receptor related protein 2 precursor (Herpes virus entry mediator B) (HveB) (Nectin 2) (CD112 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA 569, 9:89-101(1998).
-I- FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
-I- SUBCELLULAR LOCATION: TYPE I membrane protein.
-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA AND DELTA (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yoshiura K., Murray J.C.;
"A transcriptional map in the region of 19913 derived using direct
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WWW="http://www.ncbi.nlm.nlh.gov/prow/gulde/204270028_g.htm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM DELTA).
MEDLINE-95347610; PubMed-7622062;
Eberle F., Dubreuil P., Mattei M.-G., Devilard E., Lopez M.;
"The human PRR2 gene, related to the human pollovirus receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whitbeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G., "A cell surface protein with herpesvirus entry activity (HveB) susceptibility to infection by mutants of herpes simplex virus 1, herpes simplex virus type 2, and pseudorables virus."; virology 246:179-189(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SIMILARITY: BELONGS TO THE IMMUNOCLOBULIN SUPERFAMILY.
-i- SIMILARITY: CONTAINS 1 IMMUNOCLOBULIN-LIKE V-TYPE DOMAIN.
-i- SIMILARITY: CONTAINS 2 IMMUNOCLOBULIN-LIKE C2-TYPE DOMAINS.
-i- DATABASE: NAME-PROW; NOTE-PROW 1:74-77 (2000);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing and exon trapping.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PVR), is the true homolog of the murine MPH gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinfo.
the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 449-538 FROM N.A. MEDLINE-99449047; Pubmed-10520737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- TISSUE SPECIFICITY: UBIQUITOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDLINE-98321161; PubMed-9657005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 31-538 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sene 159:267-272(1995).
                                                                                                                                                                                                                                                                                                                                                       lomo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSUE-Brain;
                                                                  PVR2 HUMAN
RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               888888888888
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Gaps

15;

GSDPVTIFLRDSSGDHIQQAKYQGRLHV--SHKVPGDVSLQLSTLEMDDRSHYTCEVTWQ 118 

119 TPDGNQVVRDKITELRVQKHSSKLLKTKTEAPTTMT

17 ILLQLPKLDSAPFDVIGPQEPIL----AVVGE----DAELPCRLSPNVSAKGMELRWFREK 69

ILLGLLLLGHLTVDTYG--RPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Matches

셤 ò g

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 DGN----QVVRDKITELRVQKHSSKLLKTKTE 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 DGSYEEALVHLKVAALGSDPHISMQVQENGE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      interPro; IPR001870; Gamma_carbxylse.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003878; SPRY_domain.
InterPro; IPR003877; SPRY_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                      MEDLINE-96201696; PubMed-8611614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59004 · MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.3%;
24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U39576; AAC50489.1; -. Genew; HGNC:1135; BTN1A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00406; IGV; 1
SMART; SM00449; SPRY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; 19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   526 AA;
                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ransmembrane;
IGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                              Jenew; HGNC:
MIM; 601610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILLRVRRRRKSPGGAGGASGDGGFYDPKAQVLGNGDPVF
WTPVVPGPMEPDGKDEEEEEEEKARKGLMLPPPPALEDDM
SCDLGGSLISRRAVY (IN ISOFORM ALPHA).
MISSING (IN ISOFORM ALPHA).
33R4F83E92F6F624 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGAEEDEDLEGPPSYKPPTPKAKLEAQEMPSQLFTLGASEH
SPLKTPYFDAGASCTEQEMPRYHELPTLEERSGPLHPGATS
LGSPIP -> RASPRDVGPLVWGAYGGTLLVLLLAGGSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                           ntagagatggiiggiiaaiiatavaatgilicroorkeotl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----PDAPANHONVAAFHPKMGPSFPSPKPGSERLSFVSAKQSTGQDTEAELQDA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRV---QKHSSKLLK-TKTEAPTT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 TLALHGLTVEDEGNYTCEFA-TFPKGS--VRG-MTWLRVIAKPKNQAEAQKVTFSQDPTT 179
                                                                                                                                                                                                                             Receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 ILLGLLLLGHLTVDTYGRPI-LEVPESVTGPWKGDVNLPC-TYDPLQGYTQVLVKWLVQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Romo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                    POTENTIAL.
POLIOVIRUS RECEPTOR RELATED PROTEIN
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.4%; Score 97.5; DB 1; Length 538; Llarity 25.7%; Pred. No. 0.18; Conservative 28; Mismatches 75; Indels 4
                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
BRLYFOPHILIN precursor (BT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        526 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVP----
                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                      JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 MTYPLKATSTVKQSWDWTTDMD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 VALCISKEGRPPARISWLSSLD 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             538 M
57742 MW;
                                                                                                                                                                  nterpro; IPR003599; Ig.
nterpro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                          tepeat; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                              fam; PF00047; ig; 2. MART; SM00409; IG; 1. mmunoglobulin domain;
                                                                                                                                            HGNC:9707; PVRL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             480 5
538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 52; Conserv
                                                                                                                                                         600798
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Q13410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                   ISULFID
                                                                                                                                                                                                                                                                                                                                                                                                 SULFID
                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
BUTY_HUMAN
                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                  OMAIN
                                                                                    EMBL;
EMBL;
                                                                                                                EMBL;
EMBL;
                                                         EMBL;
                                                                        EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVTIFLRDSSGDHIQQ-AKYQGRLHVSHK--VPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 PAVLVHRDGREQEAEQMPEYRGRATLVQDGIAKGRVALRIRGVRVSDDGEYTC---FFRE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
(BY SIMILARITY).
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin domain; Signal.
BY SIMILARITY.
BUTYROPHILIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Score 96; DB 1; Length 526;8; Pred. No. 0.24;27; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E9ECA0CF8DAF94D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CXAR_HUMAN STANDARD;
P78310; 000694;
30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
CXAR_HUMAN
ID CXAR_HI
AC P78310
DT 30-MAY
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                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-97250541; PubMed-9096397;
Tomko N.P., Xu R., Philipson L.;
"HCAR and MCAR: the human and mouse cellular receptors for subgroup C adenoviruses and group B coxsackleviruses.";
Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .mmunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97190109; PubMed-9036860; Broguett G., Kurt-Jones E., Estgelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.; "Isolation of a common receptor for Coxsackie B viruses and
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Coxsacklevirus and adenovirus receptor precursor (Coxsacklevirus Sedenovirus receptor) (ACAR) (CVB3 binding protein).
CXADR OR CAR.
                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic organization and chromosomal localization of the human Coxsackievirus B-adenovirus receptor gene."; Hum. Genet. 105:354-359(1999).
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-20008750; Pubmed-10543405;
Bowles K.R., Glbson J., Wu J., Shaffer L.G., Towbin J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                    adenoviruses 2 and 5.";
Science 275:1320-1323(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y07593; CAA68868.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; 1g; 2.;
SMART; SM00410; IG_11ke; 1.
SMART; SM00408; IGC2;.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC: 2559; CXADR
                                                                               Homo sapiens (Human)
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                      owles N.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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13;
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Eur. J. Blochem. 246:39-70(1997).
-!- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-
                                                                                                                                                                                                                                                                                                                                                                                                                                      55 --IEWLISPADNQKVDQVIILY---SGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTN 109
                                                                                                                                                                                                                                                                                                                                                                                                     52 VLVKWLVQRGS----DPVTIFLRDSSGDHIQQAKY---OGRLHVSHK--VPGDVSLQLST 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 LOLSDIGTYOCKVKKAPGVANKKIHLVVLVKPSGARCYVDGSEEIGSDFKIKCE-PKEGS 168
                                                                                                                                                                                                                                                                                  Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 LEMDDRSHYTCEVTWQTPDGNQ----VVRDKITELRVQKHSSKLL----KTKTEAPTTMT 154
                                                                                                                                                                                                                                                                                                                         1 MGILLGLLLLGHLTVDTYGRPI-LEVPESVTGPWKGD-VNLPCTY-----DPLQGYTQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
NCBI_TaxID=10116,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMM OF U. U. MEDLINE=97354172; PubMed=9210466; Albouz-Abo S., Wilson J.C., Bernard C.C.A., von Itzstein M.; A conformational study of the human and rat encephalitogenic myelin "A conformational study of the pluman 35-55.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Myelin/oligodendrocyte glycoprotein is a member of a subset of the immunoglobulin superfamily encoded within the major histocompetibility complex.": Proc. Natl. Acad. Sci. U.S.A. 90.7990-7994(1993).
      COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR
                                                         CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                            1 MALLLCFVLL--CGVVDFARSLSITTPEEMIEKAKGETAYLPCKFTLSPEDQGPLD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pham-Dinh D., Mattel M.-G., Nussbaum J.-L., Roussel G.,
Pontarotti P., Roeckel N., Mather I.H., Artzt K., Lindahl K.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gardinier M.V., Amiguet P., Linington C., Matthieu J.-M.; "Myelin/oligodendrocyte glycoprotein is a unique member of the
                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                    AB01C6346CB7FE64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myelin-oligodendrocyte glycoprotein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 . AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurosci. Res. 33:177-187(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 YPL----KATSTVKQSWDWTTDM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 LPLOYEWOKLSDSOKMPTSWLAEM 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain;
MEDLINE-93376728; PubMed-8367453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93085763; PubMed-1453482;
                                                                                                                                                                                                       40029 MW;
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                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 26.09
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1mmunoglobulin superfami]
                                                                                                                      41
162
106
201
365 AA;
CHAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                             DISULFID
                                                                                                                                                             CARBOHYD
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Q63345;
                                                                                DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I. SUBCELLUAR LOCATION: Secreted; extracellular matrix.
-i. SUBCELLUAR LOCATION: At least 4 isoforms; VO (shown here), VI, V2 and V3; are produced by alternative splicing.
-i. TISSUE SPECIFICITY: Cerebral white matter. VO and V1 are expressed in the central nervous system, and in a number of mesenchymal and epithelial itssues; the major isoform v2 is restricted to the central nervous system.
-i. DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochim. Biophys. Acta 1075:248-258(1991).

-i- FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (By similarity).
--- SMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
--- SIMILARITY: CONTAINS 2 LINK DOMAINS.
--- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
--- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
--- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
--- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                         SEQUENCE OF 21-53; 78-96; 226-250; 262-277; 295-306; 314-324; 329-331
                                                                                                                                                                                                                                                                                                TISSUE-Spinal cord;
MEDIINE-9205052; PubMed-1720020;
PEPTIGES G., Biviano F., Bignami A.;
"Interaction of a brain extracellular matrix protein with hyaluronic
                                                                          "Versican V2 is a major extracellular matrix component of the mature bovine brain.";
                            Schmalfeldt M., Dours-Zimmermann M.T., Winterhalter K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long amodified and this statement is not removed.
                                                                                                                                                            J. Biol. Chem. 273:15758-15764(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sushi_SCR_CCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF060456; AAC24358.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01265; LINKMODULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF060458; AAC24360.1;
AF060459; AAC24361.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lectin_c; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00084; sush1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fam; PF00193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MART
                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on the was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SUBUNIT: MAY FORM HOMODIMERS.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS
LOCALIZED ON THE SURFACE OF WYELIN AND OLIGODENDROCYTE CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 WYRSPPSRVVHLYRNGKDQDAEQAPEYRGRTELLKESIGEGKVALRIQNVRFSDEGGYTC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 WLVQRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGD---VSLQLSTLEMDDRSHYTC 113
                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN. CAUTION: DO NOT CONFUSE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG) WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 LLSLLLLLQLSRSYAGQFRVIGPGHPI----RALVG---DEABLPCRISPGKNATGMEVG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LLGLLLL------GHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVK 55
                                                                                                                                                                   DEVELOPMENTAL STAGE: A PEAK OF EXPRESSION HAS BEEN OBSERVED BETWEEN POSTNATAL DAYS 15 AND 25, COINCIDENT WITH THE PERIOND OF ACTIVE MYELINATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BIN/MOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mmunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYELIN-OLIGODENDROCYTE. GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGCV_BOVIN STANDARD; PRT; 3381 AA.
P81282; 077609; 077610; 077612;
115-DEC-1998 (Rel. 37, Creates sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
(Chondroitin sulfate proteroglycan core protein sulfate proteoglycan core protein sulfate proteoglycan core protein 2) (PG-M) (Gilal hyaluronate-binding protein) (GHAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
N-LINKED (GLCNAC. . ) (POTENTIAL)
C97F8AD60D6a32B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.9%; Score 92.5; DB 1; Length 245; ilarity 27.5%; Pred. No. 0.2; Conservative 16; Mismatches 54; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL) IG-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27881 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMBL; L21995; AAF74786.1; -. InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58
245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity
33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Matches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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and

Usage

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9.9%;
                   Conservative
                                                                                                                                                                                                      Mus musculus (Mouse)
         Similarity
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                 36;
                                                                                                                                 CD86_MOUSE
P42082;
                                                                                                                                                                                                                                                                                                                                       STRAIN-129
 Query Match
Best Local (
                                    23
                 Matches
                                                                                                                  RESULT 15
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                                                                                                                                  SAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT
                                                             Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi; Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain; Hyaluronic acid; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
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EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING.
C-TYPE LECTIN.
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IG-LIKE V-TYPE DOMAIN.
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                 , PS50041; C_TYPE_LECT:

, PS0022; EGF_1; 2.

, PS01186; EGF_2; 1.

, PS01187; EGF_CA: 1.

, PS01241; LINK; 2.
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         PS00615;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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MEDLINE-9430971; PubMed-7513726;
MEDLINE-9430971; PubMed-7513726;
Cault A., Shen L., Nabavi N.;
Chen C., Gault A., Shen L., Nabavi N.;
Cault A., May Park B.72 molecule.";
Cault A., May Plant N. THE COSTIMULATORY SIGNAL ESSENTIAL
FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
BINDING CD28 OR CTLA-4. MAY PLAR A CRITICAL ROLE IN THE BRELY
EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
CELLS WITHIN 24 HONGS APTER ACTIVATED B CELLS,
COLLS WITHIN 124 HONGS APTER ACTIVATED B CELLS.
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                                                                                                                                                                                                                                                                     LRDSSGDHIQQAKYQGRLHV-SH-KVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVV 126
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                      LEVPESVTGPWKGDVNLPC----TYDPLQGYTQ--VLVKW----LVQRGSD--PVTIF 68
                                                                                                                                                                           MEDLINE-96094437; PubMed-7499829;
Dorriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;
"Differential expression of alternate mB7-2 transcripts.";
J. Immunol. 155:5490-5497(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
1 Jymphocyte activation antigen CD86 precursor (Activation B7-2 antigen) (Early T cell costimulatory molecule-1) (ETC-1).
                                                                   17;
   Length 3381;
                                                                      Indels
; Score 92.5; DB 1;
; Pred. No. 4.9;
14; Mismatches 53;
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us-09-763-902b-6.rsp

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; Score 92; DB 1; Length 309;
; Pred. No. 0.29;
33; Mismatches 76; Indels 18; Gaps
AOSITE; PS00290; IG_MHC; FALSE_NEG.
mwnoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
                                                                                                       I LYMPHOCYTE ACTIVATION ANTIGEN CD86 EXTRACELLULAR (POTENTIAL).
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IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
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Best Local Similarity 24.08.
Matches 40; Conservative
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59 QRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQ 118 60 QQKLVLYEHYLGTEKLDSV-NAKYLGRISFDR---NNWTLRLHNVQIKDMGSYDCFIQKK 115 :||:||:||:|| :|:::||
7 MGLAILIFVTV-----LLISDAVSVETQAYFNGTAYLPCPFTKAQNISLSELVVFWQD 59

LGLLLLGHLTVDTYGRPILEVPESVT----GPWKGDVNLPCTYDPLQ--GYTQVLVKWLV 58

119 TPDGNQVVRDKITELRVQKHSSKLLKTKTEAPTTMTYPLKATSTVKQ 165 

Search completed: March 4, 2003, 15:00:00. Job time: 5.18902 secs

Perfect score: Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database :

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O911b8 mus musculu
O911b9 mus musculu
O46535 bos taurus
^011y4 pseudomonas
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                                                   091114 pseudomonas
094006 mus musculu
091458 homo saplen
09144v4 homo saplen
054947 rattus norv
08516 macropus eu
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Langmaese K., Kloos D.U., Colleaux L., Fontes M., Wleacker P.,
"Cloning of a novel human Ig. Superfamily protein.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                     Q8wwt7 | Q8wwt6 | Q8wwt6 | Q8tag5 | Q97111
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43987 MW; 735CA3BC58185035 CRC64;
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Last annotation update)
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Pred. No. 6.6e-77;
0; Mismatches. 1
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09D006
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Q62319
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097111
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01-NOV-1999 (TrEMBLrel. 12, Cx
01-NOV-1999 (TrEMBLrel. 12, La
01-DEC-2001 (TrEMBLrel. 19, La
2391G protein precursor.
2391G OR DA159A1.1.
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SMART; SM00408; IGc2; 1.
SMART; SM00410; IG_like; 1.
Immunoglobulin domain; Signal
SIGNAL
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InterPro; IPR003600; 19_11ke
InterPro; IPR003006; 19_MHC.
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EMBL; AL034397; CAB46921.1
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Best Local Similarity 64.7
Matches 174; Conservative
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Submitted (DEC-1998)
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            Q9h1x9 homo sapien
Q96dn8 homo sapien
Q96xy7 homo sapien
Q96xy2 homo sapien
Q70356.mus musculu
Q8wmv3 bos taurus
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    (without alignments)
    3007.543 Million cell updates/sec
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                        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q96S86
Q9TU80
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:
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homo sapien streptococc

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181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK
                                                                                                                                                                                                                                                                                                                              Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (WAY-2001) to the EMBL/GenBank/DDBJ databases
EMBL, AV037161; AAK67639.1;
Interpro; IPR003006; Ig_MHC.
InterPro; IPR000538; Link.
                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
10-DEC-2002 (TrEMBLrel. 20, Last annotation update)
Proteoglycan link protein.
Homo sapiens (Human):
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.9%; Score 130.5; DB 4 Best Local Similarity 28.4%; Pred. No. 0.00015; Matches 52; Conservative 20; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 AA
                                                                                                                                                                                       241 TEAPTIMIYPLKAISTVKQSWDWTTDMDG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGILLGLLLCHLTVDTYGRP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9TUB0
Q9TUB0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
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Jamers J.M.J., Poller W.;
"Expression of Coxsackie-adenovirus-receptor and alpha v-integrin does not correlate with adenovector targeting in vivo indicating anatomical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 VLVKWLVQRGS----DPVTIFLRDSSGDHIQQAKYQ---GRLHVSHK--VPGDVSLQLST 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 --IEWLLSPADNQKVDQVIILY---SGDKIYDDYYQDLKGRVHFTSNDLKSGDASINVTN 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 LEMDDRSHYTCEVTWQTPDGNQ----VVRDKITELRVQKHSSKLL----KTKTEAPTTMT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGILLGLLLGHLTVDTYGRPI-LEVPESVTGPWKGD-VNLPCTY------DPLQGYTO 51
                                                                                                                                                                                                                                                                        MEDLINE-99422053; PubMed-10490761;
Fechner H., Haack A., Wang H., Wang X., Elzema K., Pauschinger M.,
Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultheiss H.-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MALLLRFVLL--CGVADFTRSLSITTPEQMIEKAKGETAYLPCKFTLSPEDQGPLD----
                                                                                      Eukaryota, Metazoa, Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalla; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL133515; CAC17584.1; -
HSSP; P56276; ITLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BG15303.1 (Similar to C.elegans hemicentin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35422 MW; 85C63A6EC7986965 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11:7%; Score 109.5; DB 6; 27.5%; Pred. No. 0.015; tive 28; Mismatches 77;
                                Coxsackie-adenovirus-receptor homolog (Fragment).
                                                                                                                                                                                                                                                 STRAIN-BREED GERMAN SHEPHERD; TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; its 2. Pfam; Pro0047; ig; 2. SNART; SM00408; iGc2; 1. SMART; SM00410; iG_like; 1. Immunoglobulin domain; Receptor. 319 319 319 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 YPL----KATSTVKQSWDWTTDM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 LPLQYEWQKLSNSQKTPPSWSTDM 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF109645; AAF01256:1; -
InterPro; IPR03598; Ig_c2.
InterPro; IPR03600; Ig_like.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene Ther. 6:1520-1535(1999).
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InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 3
319 AA;
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                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                         Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rector barriers.
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-- DVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKHS 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                927 NSAMILQNPYITVRSDGSLHIERVQLQDGGEYTCVASNVAGTNNKTTSVVVHVLPTIQHG 986
                                                                                                                                                                                           -DVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKHS 139
                                                                                                                                                                                                                                    268 NSAMLLONPYITVRSDGSLHIERVQLQDGGEYTCVASNVAGTNNKTTSVVVHVLPTIQHG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 CEAENOFGKIQSETTVTVTGLVAPLIGISPSVANVIEGQQLTLPCTLLAGNPIPERRWIK 926
                                                         154 PCY---VQGYPEPTIKW---RRLDNMPIFSRPFSVSSISQLRTGALFILNLWASDKGTYI 207
                                                                                                                                               208 CEAENQFGKIQSETTVTVTGLVAPLIGISPSVANVIEGQQLTLPCTLLAGNPIPERRWIK 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GHLTVDTYGRPI-LEVPESVTGPWKGDVNL 39
                  ---GDHI 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.6%; Score 109; DB 4; Length 5636;
19.6%; Pred. No. 0.75;
ive 33; Mismatches 73; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                613660 MW; F000B319CED7B52C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tted (JUN-1999) to the EMBL/GenBank/DDBJ databases. AF156100; AAK68690.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS01186; EGF_2; UNKNOWN_3.
PS01187; EGF_CA; UNKNOWN_8.
PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
PS50092; TSP1; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VSHKVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                             5636 AA
                    40 PCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSS----
                                                                                                                                                                                                                                                                                                            140 SKLLKTKTEAPTTMTYPLKATSTVKQSWDWT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel, 19, Created)
01-DEC-2001 (TrEMBLrel, 19, Last sequ
01-JUN-2002 (TrEMBLrel, 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 19.6%
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rent J.;
Human hemicentin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 QQAKYQ-GRLH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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PROSITE; PS50092,
SEQUENCE 5636 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
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                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ishlbashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y., Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y. Sugiyama T., Irie R., Otsuki T., Sat.o. H., Wakamatsu A., Ishii S., Kamanoto J., Isono Y., Kawai Hio Y., Saito K., Nishikawa T., Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Takahashi Fujii A., Oshima A., Sugiyama A., Kawakami B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------DVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKHS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---GHLTVDTYGRPI-LEVPESVTGPWKGDVNL 39
                                                                                                                                                                                                                                                                ----GHLTVDTYGRPI-LEVPESVTGPWKGDVNL 39
                                                                                                                                                                                                                                                                                                                                                     PCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSS-------GDHI 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suzuki Y., Sugano S., Nagaĥari K., Masuho Y., Nagai K., Isogai T.; "NEDO human cDNA sequencing project."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. BEBL; AKO56336; BAB71154.1; "InterPro; IPR003066; Ig_MGC. InterPro; IPR003066; Ig_WGC. InterPro; IPR003596; Ig_V. PF00047; ig; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 19, Last sequence update)
CDNA FL311774 fis, clone WT2RI2008050, weakly similar to basement membrane-specific heparan sulfate proteoglycan core protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                    ; Score 109; DB 4; Length 390;
; Pred. No. 0.022;
33; Mismatches 73; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.6%; Score 109; DB 4; Length 512;
19.6%; Pred. No. 0.031;
.ive 33; Mismatches 73; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9368150E8A5BD6C8 CRC64;
                                                                                                                               ElF7B5D5BE6E19B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 SKLLKTKTEAPTTMTYPLKATSTVKOSWDWT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 QQILSTIEGIPVTL -- PCKASGNPKPSVIWS 389
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                                                                                                                               42153 MW;
                                                                                                                                                                      Ouery Match
Best Local Similarity 19.6%;
Matches 53; Conservative 3
SMART; SM00409; IG; 4.
SMART; SM00408; IGc2; 4.
SMART; SM00410; IG_like; 1.
Immunoglobulin domain.
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Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                       390
                                                                                                                               390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             78 QQAKYQ-GRLH---
                                                                                                          NON_TER
SEQUENCE
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                                                                                   NON_TER
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096DN8
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MGD; MGI:1859349; bc...
InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                            SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adenovirus receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 AA;
                                                                                                                                272 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem, Biophys,
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                                                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8WMV3
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STREET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prediction of the coding sequences of unidentified human genes. XXI. he complete sequences of 60 new cDNA clones from brain which code for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 GSVVVQT-----APGQVVSHRGGTIVLPCRYHYEAAAHGHDGVRLKW--TKVVDPLAF 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 --IFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 TDVFVA-LGPQHRAFGSYRGRAELQGDGPGDASLVLRNVTLQDYGRYECEVTNELEDDAG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 GHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYD----PLQGYTQVLVKWLVQRGSDPVT- 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rowen L., Qin S., Loretz C., Mix L., Lasky S., Madan A., Hood L.; "Sequence of the mouse major histocompatibility class II region." Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.4%; Score 107; DB 4; Length 412; 28.5%; Pred. No. 0.037; ive 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 AA; 43652 MW; 3657E0AB81BBCA73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    070356 PRELIMINARY; PRT; 272 AA. 070356; 01-AUG-1998 (TrEWBLrel. 07, Created) 01-AUG-1998 (TrEWBLrel. 07, Last sequence update) 01-DEC-2001 (GrEWBLrel. 19, Last annotation update) Butyrophilin-like (Fragment).
                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                    412 AA
                                      140 SKLLKTKTEAPTTMTYPLKATSTVKQSWDWT 170
                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-BRAIN;
MEDLINE-21456161; Pubmed-11572484;
Nagase T., Kikuno R., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prodom; PD000918; Link; 2. PROSITE; PS01241; LINK; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MBL; AB067513; BAB67819.1;
nterpro; IPR003006; Ig_MHC.
nterpro; IPR000538; Link.
                                                                                                                                                                                                                                                 KIAA1926 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 28.5%
les 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xlink; 2.
                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8:179-187(2001)
                                                                                                                                                                                                                                                                                   omo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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165 MVK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 VVR 127
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                                                                                                                                                    096PW2
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070356
                                                                                                              RESULT 7
096PW2
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53 LVKWLVQRGS----DPVTIFLRDSSGDHIQQAKYQ---GRLHVSHK--VPGDVSLQLSTL 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 EMDDRSHYTCEVTWQTPDGNQ----VVRDKITELRVQKHSSKLL----KTKTEAPTIMTY 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 WLVQRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKV--PGDVSLQLSTLEMDDRSHYTC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 WYRAOPTPAVLVFHNGOEOGEVOMPEYRGRIOMVROAIDMGSVALOIQOVQASDDGLYHC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGD-VNLPCTY-----DPLOGYTQV 52
                                                                                                                                                                                                                                                                                                                                                                                                   2 GILLGLILL ----- GHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TIEMBLrel. 20, Last sequence update)
01-JON-2002 (TIEMBLrel. 21, Last annotation update)
Coxsackie virus and adenovirus receptor BCAR.
Bos taurus (Bovine).
Bos taurus (Bovine).
Bos taurus (Bovine).
Bos taurus (Bovine).
Bovinai, Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bov
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                                                                                                                                                                                                                                                                      21;
                                                                                                                                   Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hoelen I., Keyaerts E., Lindberg M., Van Ranst \dot{M}.; Characterization of a cDNA encoding the bovine coxsackie and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 365;
                                                                                                                     Query Match
Best Local Similarity 27.1%; Pred. No. 0.038;
Matches 39; Conservative 23; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
E745E84220343663 CRC64;
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27.6%; Pred. No. 0.055;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 OFT----DGFTSOEVS---MELRV 143
      30335 MW;
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Interpro; IPR003598; Ig.c2.
Interpro; IPR003600; Ig_like.
Interpro; IPR003006; Ig_MHC.
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12;

POTENTIAL

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63 DPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LLGHLTVDTYGRPILEVPESV----TGPWKGDVNLPCTYDPLQGYTQVLVKW--LVQRGS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.8%; Score 101; DB 13; Length 335; 26.9%; Pred. No. 0.11; ttive 22; Mismatches 60; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 CHT1 THYMOCYTE ANTIGEN.
36553. MW; AA640C5CD02CB16D CRC64;
                                                                                 InterPro; IPR003600; Ig_11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
EMBL; Y14063; CAA74390.1; -. HSSP; P06907; INEU.
                                                                                                                                                                                                                       Pfam; PF00047; 1g; 2. SMART; SM00406; IGV; 1. SMART; SMO0410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 26.99 tes 36; Conservative
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22 3
335 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 DPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCE-VTWQTPD 121
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Eukaryota, Makazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ILLGLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRGS 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GNQVVRDKITEL----RVQKHSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 GNAQSSTTVTVLVEPTVSLIKGPDŠLIDGGNE--TVAAICIAATGKPVAHIDWEGDL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Katevuo K.H., Boyd R., Gobel T.T., Bean A., Dunon D., Imhof B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.9%; Score 102; DB 4; Length 549; 26.0%; Pred. No. 0.17; ive 22; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e.";
to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                 549 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-RPRL LINE 0; TISSUE-THYMUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chīl thymocyte antigen precursor.
                                                                                                         170 PLRYEWQKLSDSQKLPTSWLPEM 192
                                                         156 PL----KATSTVKQSWDWTTDM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam: PF00047; 1g; 2.
SMART; SM00409; 1G; 1.
SMART; SM00410; IG_11ke; 1.
SEQUENCE S49 AA; 61002 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF282874; AAF97597.1; ...
Interpro; IPR003599; Ig.
Interpro; IPR003600; Ig_like.
Interpro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 10,
(TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 0:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9NQS3;
01-OCT-2000
01-OCT-2000
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nectin 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09YGH1
                                                                                                                                                                                                                                                                                                                                                                                 Q9NQS3
                                                                                                                                                                                                                                                                                      RESULT 10
Q9NQS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRE RAY RAY REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT REPARENT 
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 LLGHLTVDTYGRPILEVPESV----TGPWKGDVNLPCTYDPLQGYTQVLVKW--LVQRGS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chil, a new IgSF member inhibits thymocyte differentiation at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 LAGHV --- - HG - VVVTVPEKTVNVKTG --- GNATLLCTYTSSQPLGNFFIQWSFYSAKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-H.B19; TISSUE-THYMUS;
Katevuo K.H., Boyd R., Gobel T.T., Bean A., Dunon D., Imhof B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double positive stage.";
Submitted (JUN 1997) to the EMBL/GenBank/DDBJ databases
EMBL, 114064; CARA4391.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHT1 THYMOCYTE ANTIGEN.
AA6159598079B438 CRC64;
                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.8%; Score 101; DB 1
26.9%; Pred. No. 0.11;
tive 22; Mismatches
                                                                                                                                                                           335 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                Created)
                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                            Chil thymocyte antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN 22 335 C
SEQUENCE 335 AA; 36509 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro; IPR003600; Ig_like.
nterPro; IPR003006; Ig_MHC.
nterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13; 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; 19; 2.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_11ke; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                              PRELIMINARY;
123 NOVVRDKITELRVQ 136
                                               125 GOSOKSVIVNVLVK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 36; Conserva
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RESULT 13

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Chretien I., Marcuz A., Courtet M., Katevuo K., Vainio O., Heath J.K. White S.J., Du Pasquier L.;
"CTX, a Xenopus thymocyte receptor, defines a molecular family conserved throughout vertebrates.";
EMBL. J. Immunol. 28:4094-4104 (1998).
EMBL, AF061023; AAD17523.1;
                                          STRAIN-BALB/C, TISSUE-SPLEEN;
MCINTING J.J., Umetsu S.E., Akbari O., Potter M., Barsh G.S.,
Freeman G.J., Umetsu D.T., DeKruyff R.H.;
Freeman G.J., Teell regulatory locus that controls the development
of airway hyperreactivity, cosegregates with variants in a novel gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 ----VTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVT--- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 SACQNTLIWINGHRVTYQKSSRYNLKGHISE -- - GDVSLTIENSVESDSGLYCCRVEIPG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oarius garius (univeni).
Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 GLILLLPGTVDSY----VEVKGVVGHP----VTLPCTYSTYRGITTTC--W--GRGQCPS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 LLGHLTVDTYGRPILEVPESV----TGPWKGDVNLPCTYDPLQGYTQVLVKW--LVQRGS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 GLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRGSDP-
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.7%; Score 100; DB 11; Length 305; Best Local Similarity 28.9%; Pred. No. 0.12; Matches 48; Conservative 16; Mismatches 60; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 335;
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                                                                                                                                                                                     Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF399829; AAL35774.1; -- MGD; MGI:2159680; Timdl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 WQTPDGNQVVRDKITELRVQKHSSKLLKTKTEAPTTMTYPLKATST 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 WEND-----QKVT-----FSLQVKPEIPTRP--PTRPTIT 142
                                                                                                                                                                                                                                                                                                                                                         8F4EA38627FE85FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           071A313C3CE6DCA0, CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.7%; Score 100; DB 13;
1larity 26.1%; Pred. No. 0.14;
Conservative 21; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99077161; Pubmed-9862345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00406; ÍGV; 1.
SMART; SM00410; IG_11ke; 1.
SEQUENCE 335 AA; 36561 MW;
                                                                                                                                                                                                                                                                                                                                SMART; SM00409; IG; 1.
SEQUENCE 305 AA; 33391 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR003600; Ig_like.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                           InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig.MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                            Pfam; PF00047; 1g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P06907; 1NEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 -----VTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVT--- 116
63 DPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 SACONTLIWINGHRVIYQKSSRYNLKGHISE -- - GDVSLTIENSVESDSGLYCCRVEIPG 114
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                                               67 QLHTIYYY-SEGQSYSYGEFKDRITAATS-PGNASITISNMQPSDTGSYTCEVFSPQDDA 124
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sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutharia; Rodentia; Sciurognathl; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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; Pred. No. 0.097;
19; Mismatches 81; Indels 45;
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SMART; SM00409; IG; 1.
SEQUENCE 282 AA; 30968 WW; 7D30EE0698F0ACSF CRC64;
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Last annotation update)
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08VIM2:
01-MAR-2002 (TrEMBLFel. 20,
01-MAR-2002 (TrEMBLFel. 20,
01-JUN-2002 (TrEMBLFel. 21,
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Best Local Similarity 27.1%;
Matches 54; Conservative 1
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125 GOSQKSVIVNVLVK 138
                                                                                              123 NOVVRDKITELRVQ 136
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01-JUN-2002
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42;

- Search completed: March 4, 2003, 15:02:42 Job time: 14.9893 secs

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19-JUN-2000 (first entry)
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Gorgone GA,
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Arabidopsis thalia
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                                                                                         March 4, 2003, 14:50:41; Search time 12:1312 Seconds (without alignments) 1559.740 Million cell updates/sec
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                                                                                                                                                                                            749
1 MATSLDFKTYVDQACRAAEE......NNTVWKIASDCFRFQDWSSS 142
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                                                                                                                                                                                                                                                                                                                                        908470
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                      908470 segs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Drosophila melanog	o o	Arabidopsis thalia	Arabidopsis thalia	Ø	Arabidopsis thalla	Drosophila melanog	Ø	Arabidopsis thalia	S	Arabidopsis thalla	Ø	S	Arabidopsis thalia	Staphylococcus aur	Staphylococcus aur	. Chlamydia pneumoni	Human NTF2 associa	Mature human alpha	Amino acid sequenc	alph	Human nicotinic ac	Human TRICH-15 pro	nto		Human TRICH-6 prot	Nematode 3'-5' exo	S. pneumoniae BSCE	S. pneumoniae deri		Human alpha nicoti	Human pancreatic c	Human differentiat	Propionibacterium
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## ALIGNMENTS

(BODE-) BODE GENE DEV CO LTD SHANGHAI

Xie Y;

Mao Y,

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AAA08035 to AAA08042 encode the human protein transport-associated molecules (PTAMs) given in AAY82317 to AAY82324. The PTAMs have cytostatic, antiarthritic, antiasthmatic, immunosuppressant,
                                                               New numan protein transport-associated polypeptide and poluseful for diagnosis, prevention and treatment of cell proand secretory disorders such as leukemia, cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      r generating hybridisation probes useful occurring genomic sequences.
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                      N-PSDB; AAA08041
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NTF2 associated protein 16. The sequences can be used in the treatment of cancer and HIV infection, as well as other diseases. The present sequence is the protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NFFDTLPSSEFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NFFDTLPSSEFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection; diagnosis; antisense therapy; gene therapy
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                                                                                                                                                                            Polypeptide-human NTF2 associated protein 16 and polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 142;
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Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 749; DB 23;
100.0%; Pred. No. 4.7e-76;
ttive 0; Mismatches 0;
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Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                  Claim 1; Page 26(Disclosure); 32pp; Chinese.
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                                                                                                                                                                                                         encoding it -
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27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                            hepatotropic, antigout, antiinflammatory and antiHTV activities, and regulate protein transport. PTAM proteins and antagonists are useful for preventing or treating a disorder associated with decreased or increased expression or activity of PTAM. PTAM polynucleotides are useful for diagnosing conditions associated with PTAM, comprising detecting PTAM by forming a hybridisation complex, preferably after PCR amplifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      blological sample. Diseases prevented, treated or diagnosed include cell proliferative disorders such as cancers, immune disorders, secretory disorders and other conditions associated with abnormal vesicle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    haemolytic anaemia. Anti-PTAM antibodies may be used as antagonists, as a targeting or delivery mechanism for bringing pharmaceutical agents into cells or tissues expressing PTAM and for diagnosis of PTAM-related disorders. PTAM, its catalytic or immunogenic fragments are useful for drug screening using libraries of compounds. PTAM polynucleotides are
                                                                                                                                                                                                                                                                                                antiarteriosclerotic, antiallergic, antidiabetic, antilipaemic, antirheumatic, osteopathic, dermatological, antianaemic, antipsoriatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; NTF2 associated protein 16; cancer; HIV infection; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NFFDTLPSSEFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQS 120
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                                                                                                               proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              such as allergies, asthma, urticaria and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in mapping the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 749; DB 21;
100.0%; Pred. No. 4.7e-76;
ive 0; Mismatches 0;
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Gaps

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a squence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a compluence and an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the protein and or all agnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the constant and an allow obtaining of the full-length cDNAs assily without any specialized methods. AAR03166 to AAR1328 and AAR06003 and AAR080003  and AAR080003  and AAR080003 and AAR0800003 and AAR080003 and AAR0800003 and AAR080003 and AAR080003 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
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100.0%; Pred. No. 7.2e-76;
7ative 0; Mismatches 0;
                                                                                                                                                           Claim 8; SEQ ID 17707; 2537pp + CD ROM; English.
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full-length cDNAs -
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cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.

17-JAN-2001; 2001WO-US01341

WO200155322-A2 Homo sapiens

02-AUG-2001

diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

Claim 11; SEQ ID No 1180; 980pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice,

rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked include autoimmune diseases e.g. radioimmunoassays or enzyme linked include autoimmune diseases e.g. rhoppasses or enzyme linked include autoimmune diseases e.g. rhoppasses or enzyme linked configurative disorders e.g. rhoppasses of the breast or liver, cardiovascular disorders e.g. recebral ischaemia, anglogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungical and wound healing and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before

transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be as a food additive or preservative to increase or decrease storage

capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention.

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78 02-027-2000; 2000US-0237037

78 02-027-2000; 2000US-0237037

78 02-027-2000; 2000US-023937

78 13-027-2000; 2000US-023937

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71 7-N
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Human, protein transport molecule; PTAM; diagnosis; cytostatic; antiasthmatic; immunosuppressant; antiateriosoierotic; antiallergic; antidiabetic; antilipaemic; antitheumatic; costeopathic; dermatological; antidiabetic; antipsoriatic; hepatotropic; antigout;
                                                                                                                                                                                66 LPSSEFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKOHFFNQNFLLTAQSTPNNT 125
                                                                                                                                                                                                        86 LPSSEFGVNMLDCOPVHEQATGSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNT 145
                                                                                                              26 DFKTYVDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLINGNAVSGLDALNNFFDT 85
                                                                                         6 DEKTYVDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein transport regulator; cancer;
iferative disorder; secretory disorder;
                                               ö
Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         abnormal vesicle trafficking; asthma;
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein transport molecule (PTAM) SEQ ID NO:2.
  97.1%; Score 727; DB 22;
100.0%; Pred. No. 1.6e-73;
11ve 0; M1smatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune disorder; cell proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY82318 standard; Protein; 140 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                urticaria; allergy; abnormal autoimmune haemolytic anaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US19616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiinflammatory; antiHIV;
                                                                                                                                                                                                                                                                                                      146 VWKIASDCFRFQDWSSS 162
                                                                                                                                                                                                                                                                              126 VWKIASDCFRFQDWSSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-2000 (first entry)
    Query Match
Best Local Similarity 100.0
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200012703-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY82318;
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
AAY82318
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New nucleic acid molecules encoding 461 human secreted proteins for

WPI; 2001-488783/53. N-PSDB; AAS26214.

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MAA08035 to AAA08042 encode the human protein transport-associated molecules (PTAMS) given in AAY83317 to AAY8234. The PTAMS have cytostatic, antiathritic, antiathratic, immunosuppressant, antiatricisclerotic, antiallergic, antidabetic, antilipaemic, antiatricisclerotic, antiallergic, antidabetic, antilipaemic, equivation, antigout, antidation, antigout, antidation antiling antiling antiporticis, and creating a disorder associated with decreased or increased expression or activity of PTAM. PTAM polynucleotides are useful for preventing or treating a disorder associated with decreased or increased dagnosing conditions associated with PTAM, comprising detecting PTAM by forming a hybridisation complex, preferably after PCR amplifying the biological sample. Diseases prevented, treated or diagnosed include cell proliferative disorders such as cancers, immune disorders, secretory disorders and other conditions associated with abnormal vesicle trafficking, such as allergies, asthma, uritcarla and autoimmune trafficking, such as allergies, asthma, uritcarla and autoimmune trafficking, such as allergies, asthma, uritcarla and autoimmune a targeting or delivery mechanism for bringing pharmaceutical agents into cells or tissues expressing PTAM and for diagnosis of PTAM: related disorders. PTAM, its catalytic or immunogenic fragment are useful for cuseful for generating mybridisation probes useful in mapping the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                               New human protein transport-associated polypeptide and polynucleotide useful for diagnosis, prevention and treatment of cell proliferative and secretory disorders such as leukemia, cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTLPSSEFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLDFKTYVDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                              Guegler KJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immunosuppressive; antiarthritic; antirheumatic;
                                                                                                                                                          Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human novel secreted protein, Seg ID 1181.
                                                                                                                                                  Tang YT, Lal P, Bandman O, Yue H,
Gorgone GA, Baughn MR, Patterson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  naturally occurring genomic sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 61-62; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228
AAU16228 stan@ard; Protein; 164
98US-0098206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTVWKIASDCFRFQDWSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 NTVWKIASDCFREQDWAS 140
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                                                                       (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                    WPI; 2000-256642/22.
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                                                                                                                                                                                                                                                                                                        N-PSDB; AAA08036.
27-AUG-1998;
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AAU16228
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Ruben SM

Barash SC,

Rosen CA,

WPI; 2001-488783/53. N-PSDB; AAS26215.

(HUMA-) HUMAN GENOME SCI INC 05-JAN-2001; 2001US-0259678

08-DEC-2000; 2000US-0251989 08-DEC-2000; 2000US-0251990 11-DEC-2000; 2000US-0254097

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conceded georeted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They to a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also diagnostic immunosays e.g. radioimmunoasays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, contingentic disorders e.g. rheumatoid arthritis, can liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. nervous system disorders e.g. ardiocans and fungicand ocular disorders e.g. nervous system disorders e.g. and ocular disorders e.g. corneal infection, and many other disorders listed in the specification, and many other disorders listed in the specification, and many other content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 DILPSSEFQVNMLDCQPVHEQAIQSQTIVLVVISGTVKFDGNKQHFFNQNFLLIAQSIPN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SLDFKTYVDQACRAAEEFVNIYYETMDKRRRALIRLYLDKATLIWNGNAVSGLDALNNFF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated nucleic acid molecules and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID No 1181, 980pp; English
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Best Local Similarity 75.4%
Matches 104; Conservative
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Drosophila; developmental biology; cell signalling; insecticide;

Drosophila melanogaster polypeptide SEQ ID NO 21843.

26-MAR-2002 (first entry)

ABB65017;

ABB65017 standard; Protein; 133 AA

RESULT 7 ABB65017

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25-FEB-2000; 2000EP-0301439
06-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides; therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 LPSSEFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 LPSSNHQLNTLDAQPIVDQAVSNQLAYLIMASGSVKFADQQLRKFQQTFIVTAE----ND 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 21843; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48; Indels
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41.4%; Score 310; DB 22;
Best Local Similarity 42.9%; Pred; No. 7.9e-27;
Matches 57; Conservative 24; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                           Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG12073 standard; Protein; 125 AA
                                                                                                                                                                                                                                                                                                                                                                                                           Li PWD,
                                                                                                                                                                                       23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                              23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150
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   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 VWKIASDCFRFQD 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thallana
                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                             (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABL09120.
                                                          WO200171042-A2
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                                                                                                                         27-SEP-2001
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99US-0151080
99US-0151303
99US-0151438
99US-0151930
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90S-0145086
90S-0145088
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99US-0149930
99US-0150566
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                          9US-014
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990S-015
990S-015
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                                   99US-01
99US-01
99US-01
                                                             90s-01
90s-01
                 0-S06
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AEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQ--VNM 75
                                                                       'n
                                                                                                        LDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHF-FNQNFLLTAQSTPNNTVW 127
                                                                                                                         Indels
Score 113.5; DB 21;
Pred. No. 8.2e-05;
21; Mismatches 56;
                                                                                                                                                                         RESULT 9
AAGO5145
ID AAGO5145 standard; Protein; 153 AA.
 15.2%;
ilarity 27.4%;
Conservative 2
 Query Match
Best Local Similarity
Matches 31; Conserva
                                                                                                                                                                                                                             AAG05145;
                                                       18
                                                                                                         9/
                                                                              g
                                                                                                           ò
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Gaps

Arabidopsis thallana protein fragment SEQ ID NO: 1441. 17-OCT-2000 (first entry) 

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

Arabidopsis thalianä

EP1033405-A2

06-SEP-2000.

25-FEB-2000; 2000EP-0301439

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## 25 - FEB - 1999; 9905-0121823.

## 20 - War 1999; 9905-0121803.

## 21 - War 1999; 9905-01221804.

## 21 - War 1999; 9905-01221804.

## 22 - War 1999; 9905-012214.

## 22 - War 1999; 9905-012214.

## 23 - War 1999; 9905-012214.

## 23 - War 1999; 9905-012014.

## 24 - War 1999; 9905-012014.

## 23 - War 1999; 9905-012014.

## 24 - War 1999; 9905-012014.

## 25 - War 1999; 9905-012014.

## 25 - War 1999; 9905-012014.

## 26 - War 1999; 9905-012014.

## 26 - War 1999; 9905-012014.

## 26 - War 1999; 9905-012014.

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## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

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## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905-012014.

## 27 - War 1999; 9905
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PR 12-701-1999; 9905-0142547.

PR 13-701-1999; 9905-0144085.

PR 16-701-1999; 9905-0144085.

PR 16-701-1999; 9905-0144085.

PR 19-701-1999; 9905-0144085.

PR 19-701-1999; 9905-0144332.

PR 19-701-1999; 9905-0144332.

PR 19-701-1999; 9905-0144333.

PR 19-701-1999; 9905-0144334.

PR 20-701-1999; 9905-0144334.

PR 20-701-1999; 9905-0144334.

PR 20-701-1999; 9905-0144884.

PR 20-701-1999; 9905-0144884.

PR 21-701-1999; 9905-0144884.

PR 22-701-1999; 9905-014508.

PR 23-701-1999; 9905-0145192.

PR 23-701-1999; 9905-0149173.

PR 23-701-1999; 9905-014990.

PR 23-701-1999; 9905-0149173.

PR 23-801999; 9905-0149173.

PR 23-801999; 9905-0149173.

PR 23-801999; 9905-0149173.

PR 23-801999; 9905-01999; 9905-01999; 9905-01999.

PR 23-801999; 9905-01999

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capable of detecting 1000 or more genes from brosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176 ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---- OPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNTVWKIASDCF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFVRQYYTLLNKAPNHLHRFYNHNSSYIHGESKLVVGQREIHNRIQ-------CLNFNDC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                          the invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 29004; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match.
15.1%; Score 113; DB 22; Length 688; Best Local Similarity 31.5%; Pred. No. 0.00089; Matches 39; Conservative 14; Mismatches 55; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 24948
                                                                                                                                      Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB66052 standard; Protein; 690. AA.
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11-JUL-2000; 2000US-0614150
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23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                      Venter JC, Adams M,
                                                                                                                                                                                         WPI; 2001-656860/75.
N-PSDB; ABL11507.
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                                                                                (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:||
126 RYQD 129
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ABB66052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 SASLSLKMSQMDPDAVSKAFVEHYYSTFDTNRVGLAGLYQEASMLTFEGGKIQGVGSIVA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ATSLDFKTYVDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 113.5; DB 21;
Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB67404 standard; Protein; 688 AA.
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25.9%; Pred
27; h
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36; Conservative

Nuery Match West Local Similarity

26-MAR-2002 (first entry)

ABB67404;

RESULT 10 ABB67404

23-MAR-2001; 2001WO-US09231

Drosophila melanogaster

40200171042-A2

27-SEP-2001

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3-APR-1
                                                                               3-APR-1
                                                                                              8-APR-
                                                                                                             0-APR-1
                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences genomic DNA sequences (ABLi6176-ABL30511), expressed DNA (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 ---- QPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNTVWKIASDCF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 EFVRQYYTLLNKAPNHLHRFYNHNSSYIHGESKLVVGQREIHNRIQ-------QLNFNDC 71
                                                                                                                                                                                                                                                                                                                                                                                                                              16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 EFVNIYYETMDKRRRALTRLYLDKATLI-WNGNAVSGLDALNNFFDTLPSSEFQVNMLDC 78
                                                                                                                                                   Disclosure; SEQ_ID NO 24948; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 31.5%; Pred: No. 0.00089;
Matches 39; Conservative 14; Mismatches 55; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 6317.
                 Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG08682 standard; Protein; 123 AA.
               PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0121825.
99US-0123548.
99US-0123548.
99US-0125788.
99US-0126264.
99US-0126785.
99US-0127862.
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            Venter JC, Adams M,
                                         WPI; 2001-656860/75.
N-PSDB; ABL10155.
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 690 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 RFQD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:||<sup>-</sup>
128 RYQD 131
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01-APR-1999;
06-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 LDCQPVHEQATQSQTTVLVYTSGTVKFDGNKQHF-FNQNFLLTAQSTPNNTVWKIASDCF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 AEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLP--SSEFQVNM 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKAFVEHYYSTEDTNRVGLAGLYQEASMLTFEGOKIQGVQSIVAKLTSLPFQQCKHHIST 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
15.0%; Score 112.5; DB 21;
Best Local Similarity 27.3%; Pred. No. 0.0001;
Matches 33; Conservative 25; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG08681 standard; Protein; 126 AA.
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990S-0123548.
990S-0125788.
990S-0126264.
990S-0126785.
99US-0159637.
99US-0159638.
99US-0159584.
99US-0160741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-2000; 2000EP-0301439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2000 (first entry)
                                                                        99US-01607
99US-01607
99US-01607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1033405-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 R 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG08681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
AAG08681
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   99US-0144632.
99US-0144884.
99US-0144814.
99US-0145086.
99US-0145089.
99US-0145089.
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-AUG-1
-SEP-1
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PR 06-APR-1999, 9908-0128244
PR 106-APR-1999, 9908-0128144
PR 11-APR-1999, 9908-0122814
PR 11-APR-1999, 9908-0122814
PR 11-APR-1999, 9908-0122405
PR 11-APR-1999, 9908-0122405
PR 11-APR-1999, 9908-0122465
PR 11-APR-1999, 9908-0122465
PR 11-APR-1999, 9908-0122465
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PR 11-APR-1999, 9908-0122465
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PR 11-APR-1999, 9908-0123466
PR 11-APR-1999, 9908-0123466
PR 11-APR-1999, 9908-0123466
PR 11-APR-1999,
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PR 19-JUL-1999 PR 19-10L-1999 PR 19-JUL-1999 PR 20-JUL-1999 PR 20-

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                          76 LDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHF-FNQNFLLTAQSTPNNTVWKIASDCF 134
                                                                                                                                                                                                                                 Gaps
                                                                                                                               18 AEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLP--SSEFQVNM 75
                                                                                                                                                          10 SKAFVEHYYSTEDTNRVGLAGLYQEASMLTFEGGKIQGVQSIVAKLTSLPFQQCKHHIST 69
                                                                                         11;
                                                  15.0%; Score 112.5; DB 21; Length 126; 27.3%; Pred. No. 0.00011; ... tive 25; Mismatches 52; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaltana protein fragment SEQ ID NO: 1443.
                                                                                                                                                                                                                                                                                                                                                                                                                             AAG05147 standard; Protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             990S-0123180.
990S-0123548.
990S-0125788.
990S-0126264.
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                    19US-0162142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2000 (first entry)
                                                                           Best Local Similarity 27.3
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAR-1999;
09-MAR-1999;
28-0CT-1999
29-0CT-1999
                                                                                                                                                                                                                                                                                          135 R 135
                                                                                                                                                                                                                                                                                                                              122 R 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG05147;
                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
AAG05147
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99US-0159330. 99US-0159331. 99US-0159637. 99US-0159638.

99US-015 99US-016 99US-016

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PR 19-70L-1999 900S-0144331

PR 19-70L-1999 900S-0144332

PR 19-70L-1999 900S-0144632

PR 20-70L-1999 900S-0144632

PR 21-70L-1999 900S-0144634

PR 21-70L-1999 900S-0144634

PR 21-70L-1999 900S-0144634

PR 22-70L-1999 900S-0146086

PR 22-70L-1999 900S-0145086

PR 22-70L-1999 900S-0145086

PR 22-70L-1999 900S-0145086

PR 22-70L-1999 900S-0145086

PR 22-70L-1999 900S-0145087

PR 22-70L-1999 900S-0145087

PR 22-70L-1999 900S-0145087

PR 22-70L-1999 900S-0145087

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PR 22-70L-1999 900S-014990

PR 22-70L-1999 900S-014990

PR 22-70L-1999 900S-014990

PR 23-70L-1999 900S-014990
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                             76 LDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHF-FNQNFLLTAQSTPNNTVWKIASDCF 134
                                                                                                                                 18 AEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLP--SSEFQVNM 75
                                                 Indels 11;
Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thallana protein fragment SEQ ID NO: 1442.
Query Match
15.0%; Score 112.5; DB 2
Best Local Similarity 26.8%; Pred. No. 0.00011;
Matches 33; Conservative 26; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG05146 standard; Protein; 134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                              135 RFQ 137
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                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
AAG05146
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990S-0121825. 990S-0123180. 990S-0123548. 990S-0125788.

> 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 25-MAR-1999;

25-FEB-2000; 2000EP-0301439

06-SEP-2000

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990S-019
990S-019
990S-019
990S-019
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PR 12-0CT-1999; 99US-0158369.
PR 13-0CT-1999; 99US-0158369.
PR 13-0CT-1999; 99US-0159294.
PR 13-0CT-1999; 99US-0159294.
PR 14-0CT-1999; 99US-0159295.
PR 14-0CT-1999; 99US-0159330.
PR 14-0CT-1999; 99US-015931.
PR 14-0CT-1999; 99US-0159631.
PR 21-0CT-1999; 99US-0159631.
PR 21-0CT-1999; 99US-0160741.
PR 21-0CT-1999; 99US-0160768.
PR 21-0CT-1999; 99US-0160768.
PR 22-0CT-1999; 99US-0160981.
PR 22-0CT-1999; 99US-0160981.
PR 22-0CT-1999; 99US-0160981.
PR 25-0CT-1999; 99US-0160981.
PR 25-0CT-1999; 99US-0161406.
PR 25-0CT-1999; 99US-0161361.
PR 26-0CT-1999; 99US-0161361.
PR 28-0CT-1999; 99US-016192.
PR 28-0CT-1999; 99US-016192.
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Ouery Match :15.0%; Score 112.5; DB 21; Length 134;
Best Local Similarity 26.8%; Pred. No. 0.00012;
Matches 33; Conservative 26; Mismatches 53; Indels 11; Gaps

135 RFQ 137

:: 122 SWR 124 Search completed: March 4, 2003, 14:58:48 Job time: 13.2741 secs Sequence 6, Ap Sequence 104,

US-09-721-362-112 US-08-308-872B-6 US-09-752-165-104

ALIGNMENTS

Sequence Seq

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US-09-162-021B-12
US-08-486-640A-190
US-08-686-968C-190
US-08-375-992A-190
US-08-375-742D-3
US-08-392-459-32-
PCT-US91-0825-32
PCT-US93-04384-43
PCT-US93-04384-44
PCT-US93-04384-48
US-09-115-444-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: FA

COUNTRY: GA

ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM COMPALIBLE
COMPUTER: IBM COMPALIBLE
COMPUTER: TESTER FOR SYSTEM: DOS
SOFTWARE: FASTER FOR WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Glumi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
APPLICANT: Stodola, Robert
APPLICE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: SmithKline Beecham Corporation
709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                 ce 420, Application US/08858207A No. 6348328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.1%;
23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6348328e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: ADDRESSEE: SmithKline
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Best Local Similarity
                                           STRANDEDNESS:
                                                            US-08-858-207A-420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-858-207A-420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
                                                                                                                                                                                                                                                                                                                                                                                    Patent
                                                                                             March 4, 2003, 14:55:07 ; Search time 4.92282 Seconds (without alignments) 848.711 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 420,
                                                                                                                                                                                     .....NNTVWKIASDCFRFQDWSSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
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Sequence
Sequence
Sequence
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Sequence
Sequence
Sequence
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Sequence
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Sequence
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                                                                                                                                                                                                                                                                                           262574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*/cgn2_6/ptodata/1/1aa/backfiles1.pep:*
               GenCore version 5.1.3 . Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                           262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                    1 MATSLDFKTYVDQACRAAEE.
                                                                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                       US-09-763-902B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match 1
                                                                                                                                                       Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                       OM protein
                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
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Length 238;

76; DB 4; No.0.35;

Score Pred.

us-09-763-902b-7.rai

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he Beecham, Corporation
Recombinant Feline Coronavirus
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                                                                                                                                                                                                                                                                                    IBM PC compatible
                                                                            Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 14-NOV-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (215) 270-5090
NFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 King of Prussia
                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA
                                                                                                                                                                      King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-392-459-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                   APPLICANT: SmithKli
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                            NUMBER OF SEQUENCES
                                                                                                                                                                                                                             19406-2799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION
                                                                                                                                                                                                             USA
Patent No. 628097
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
STREET: 70
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US-08-392-459-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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 Gaps
                                       20 EFVNI - - YYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQVNML - 76
                                                              ---DCQPVHEQATQSQTTVLVVTSGTVKFDGN--KQHFFNQNFLLTAQSTPNNTVWKI 129
                                                                                                                                                     KSDEMEMIRKAMVQMQVSSYVQSSKINKFENNGFRQYFSKENFLICTESDKVNLLEKM 116
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 24;
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 Indels
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APPLICANT: SmithKline Beecham, Corporation
TITLE OF INVENTION: Recombinant Feline Coronavirus S
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 LTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQVNMLD---
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 38;
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                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
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   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.5%; Score 71.5; 27.0%; Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DAIL:
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: .US 07/698,927
FILING DATE: 13-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14 NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/392,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MPUTER: IBM PC compatible
BRATING SYSTEM: PC-DOS/MS-DOS
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US-08-392-459-28
; Sequence 28, Application US/08392459
                                                                                                                                                                                                                                             Sequence 24, Application US/08392459
Patent No. 6280974
 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: King, William T. REGISTRATION NUMBER: 30,954
                                                                | |:: ||| :: : : : EVVDVIGYYELNQEKLKGIDFI---
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INFORMATION FOR SEQ ID NO: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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amino acid
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CORRESPONDENCE ADDRESS:
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JS-08-392-459-24
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APPLICANT: SmithKline Beecham, Corporation
TITLE OF INVENTION: Recombinant Feline Coronavirus
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 54
                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
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; Pred. No. 6.3;
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: King, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: SBC 14532B
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,066
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COMPUTER READABLE FORM:
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protein F17L21.10
nuclear transport
                                                                                                                                                                                                            March 4, 2003, 14:53:52; Search time 6.38795 Seconds (without alignments) 2137.006 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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ABC transport prot	TXBP151 - human	hypothetical prote	transcription fact	E2 glycoprotein pr	myosin alpha heavy	toxin co-requiated	Na+/H+ antiborter	Day at south Day of	DAM-GILECLES DAM P	hypothetical prote	alpha-mannosidase	probable dihydrofl	El protein - human	1	PEP-procein piospii	PEP-protein phosph	phosphoenolpyruvat	71	
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RESULT 1 S00751 placental protein 15 - human N:Alternate names: Pp15 C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: S00751 R;Gruudmann, U.; Nerlich, C.; Rein, T.; Lottspeich, F.; Kuepper, H.A. Nucleic Acids Res. 16, 4721, 1988 A;Title: Isolation of cDNA coding for the placental protein 15 (PP15). A;Reference number: S00751, MUID:88247772; PMID:3380696 A;Accession: S00751 A;Accession: S00751 A;Accession: S00751 A;Cross_references: EMBL:X07315; NID:g35578; PIDN:CAA30278.1; PID:g35579 C;Superfamily: yeast nuclear transport factor NTF2	Query Match Best Local Similarity 27.4%; Score 115; DB 2; Length 127; Best Local Similarity 27.4%; Pred. No. 0.00039; Matches 32; Conservative 18; Mismatches 55; Indels 12; Gaps Qy 21 FVNIYYETMDKRRALTRIZLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQVNMLDC 78 L

probable nuclear transport factor 2 - fission yeast (Schizosaccharomyces pombe) C.Species: Schizosaccharomyces pombe C.Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 15-Sep-2000

C;Accession: T38039; T37728 R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, C.M. submitted to the EMBL Data Library, August 1999 A, Reference number: Z21764

A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-123 <MCD>
A.Cross references: EMBL:AL109951; PIDN:CAB53052.1; GSPDB:GN00066; SPDB:SPAC1B9.01c
A.Cross references: EMBL:AL109951; rosmid clB9
R.Perlin; K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
Submitted to the EMBL Data Library, December 1995

A;Reference number: 221740 A;Accession: T37728

A; Status: preliminary A; Residues: O.; Alon

**Ouery Match** 

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ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A.Title: Sequence number: A86141; MUID:21016719; PMID:11130712
                                                 A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo
Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
Hughes, B.; Huizar, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo wer, J.C.; Bakano, H.; Will, W. D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NID:99802547; PIDN:AAF99749.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 AEEFVNIYYETWDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQ--VNM 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 LDCOPVHEQATQSQTTVLVVTSGTVKFDGNKQHF--FNQNFLLTAQSTPNNTVWKIASDC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 VDCQP-----SGPAGGMLVFVSGNLQLAG-EQHALKFSQMFHLIS----NQGNYVFNDI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 AEEFVNIYYETWDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQVNM-- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tittle: Sequence and analysis of chromosome 1 of the plant Arabidopsis. Accession: H86398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Cross-references: GB:AE005172; NID:g6554189; PIDN:AAF16635.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.0%; Score 105; DB 2; Length 122; Conservative 20; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 VDSQP--SSMAGGGGGILVFVSGSIQLHGEDHPLRFSQTFHL 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 107.5; DB 2;
; Pred. No. 0.012;
17; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 LDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHF-FNQNFLL

    Arabidopsis thallana

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 29.4%;
hes 30; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB: AE005172;
                                                                                                                                                                                                                                                                                                                                                                                                      A Status: preliminary
A Molecule type: DNA
A Residues: 1-522 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: T23J18.22
A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Gene: F17L21.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probable nuclear transport factor 2 (imported) - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Accession: B86405
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EMBL:Z68197; PIDN:CAA92380.1; GSPDB:GN00066; SPDB:SPAC15F9.035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 LDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQ-HFFNQNFLLTAQSTPNNTVWKIASDCF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 AEEFVNIYYETWDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQ--VNM 75
                                                                                                                                                                                                                                                                                                                                                                          sis thallana (mouse-ear cress)
#sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 AEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLP--SSEFQVNM 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Er, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. Reference number: A86141; MVID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                            Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                   Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 126;
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                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                                 15.1%; Score 113; DB 2; 28.1%; Pred. No. 0.00059; Ive 24; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.0%; Score 112.5; DB 2; 27.3%; Pred. No. 0.00068; tive 25; Mismatches 52;
                                                                                                       A. Introns: 3/1; 30/3; 54/3; 88/3
C. Superfamily: yeast nuclear transport factor NTF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 1
C; Superfamily: yeast nuclear transport factor NTF2
                                                                                                                                                                                                                                                                   34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 27.3
hes 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein T23J18.22 [imported]
C;Species: Arabidopsis thalid
C;Date: 02-Mar-2001 #sequenc
C;Accession: H86248
                                                     A; Gene: SPDB:SPAC1B9.01c
                                                                                                                                                                                                                                       Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -126 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           er, M.; Wu, D.; Yu, G
Title: Sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 R 135
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Residues: 1

Query Match

135 R 135 R 122

8 ö RESULT 4

Gaps

Experimental source: clone R05D11

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A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim.
C.A.; Li, J.H.; Li. Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Theologis; A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alor Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: EMBL:268879; PIDN:CAA93082.1; GSPDB:GN00022; CESP:K08F4.2 Experimental source: clone K08F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: F86270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                c;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 QVNMLDCQPV-HEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNTVWKIA 130
                                                                                                                                                                                                                                                                                                                                                                        72 Q--VNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNT-VWK 128
                                                                                                                                                                                                                                                                                                                                                                                                      ---VIINVIGTVNL----RPFLQSFLLGQQGQKK---YYVE 201
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                  18 AEEFVNIYYETMD-----KRRRALTRLY-LDKATLIWNGNAVSGLDALNNFFDTLPSSEF 71
                                                                                                                                                                                                                                                                                                     17 AAEE----FVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLP-SSEF 71
                                                                                                                                                                                                                 19;
                                                                                                                                                              Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 537;
                                                                                                                                                            Query Match
13.3%; Score 99.5; DB 2; Length 13
Best Local Similarity 26.8%; Pred. No. 0.014;
Matches 34; Conservative 27; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, January 1996
A;Reference number: 219746
A;Accession: T23479
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-537 <WIL>
                                                                        A; nncp pustitum: 3, 96/3
A; Introns: 33/1; 63/3; 96/3
C; Superfamily: yeast nuclear transport factor NTF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 4
A;Introns: 66/3; 99/1; 140/3; 161/3; 338/1; 419/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.6%; Score 94; DB 35.0%; Pred. No. 0.26.1ve 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F21F23.16
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                                                                                                                                                                                                                                                                                                                                                                                                                | : ::| ||::::| 71 QRAITVIDSQPLYDGSIQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ypothetical protein KO8F4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 KIOSIKGYPTPHKOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | :: |
SDAFOYID 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDCFRFQD 138
             C,Genetics:
A,Gene: CESP:R05D11.3
A,Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 IASDCFR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: T23479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Petzold, A.S.; Brown, S.S.
ne EMBL Data Library, July 1993
Identification of mutations that are synthetically lethal with altered ye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: SEC3 mutations are synthetically lethal with profillin mutations and cause defedence number: S72237; MUID:9704444; PMID:8889515
                                                                                                                                                                                                                                                                                                                                                                                                                                                            references: EMBL:U18778; NID:9603592; PIDN:AAB64542.1; PID:9603601; MIPS:YER009w
                                                                                                                                                                                                                                                                                                                          scription: The sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lambda ference number: $50459 cession: $50467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Molecule type: DNA
A.Residues: 1-133 <WIL>
A.Cross-references: EMBL:275546; PIDN:CAA99890.1; GSPDB:GN00019; CESP:R05D11.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:9347715
P.; Brown, S.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
Accession: T23921
                                                                                                                                                                                                                            #sequence_revision 12-May-1995 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 DILPSSEFQ--VNMLDCQPVHEQATQSQTTVLVVTSGTVKFD--GNKQHFFNQNFLLTAQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oss-references: EMBL:L22204; NID:g347714; PIDN:AAB49379,1; PID:g347715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -DVLVMITGDLLIDEEQNPQR-FSQVFHL--- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLDFKTYVDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SLDFNT-----LAQNFTQFYXNQFDTDRSQLGNLYRNESMLTFETSQLQGAKDIVEKL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 125;
                                                                                                                                                 yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ireferences: EMBL:L22204; NID:g347714; PIDN:AAB49379.1; E.K.; Corbett, A.; Kweon, Y.; Petzold, A.S.; Sliver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical profein R05D11.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 101.5; DB 2;
Pred. No. 0.008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: yeast nuclear transport factor NTF2
                                                                                                                                                                                                                                                                                                        EMBL Data Library, December 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, June 1996 A.Reference number: 219818 A.Accession: T23921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: SGD:S0000811; MIPS:YER009w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 VSLPFOKVOHRITTLDAOPASPNG-
                                                                                                                                                                                                         Saccharomyces cerevisiae
                                                                                                                                                                                                                                                       Accession: S50467; S41793; S72237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.68; 27.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 STPNNTVWKIASDCFR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - IPDGNSYYVFNDIFR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        r, B.K.; Corbett, A.;
s 144, 495-510, 1996
: SEC3 mutations are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           dues: 1-125 <DIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cule type: DNA dues: 1-84 <HAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ule type: DNA
lues: 1-84 <HAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Map position: 5R
||
FR 118
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A.M.; Sun, H.; Tallo

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on-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: EMBL:271666; NID:91302565; PID:e239594; PID:91302566; MIPS:YNR051
                                                                                                                                                                                                                                                                                       A;Cross_references: GB:AE005173; NID:g7705097; PIDN:AAF67776.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
5;Accession: S63382; S27439; S27440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDFENTKFEVLSVDSQNSLEDG-----IFIMVIGPMTGKDNQRRKFSQMFYLARQNT-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --LPSSEFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 VDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLI--:WNGNAVS--GLDALNNFFDT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDALNNFFD----TLPSSEFQVNMLDCQ---PVHEQATQSQTTVLVVTSGTVKFDGNKQH 108
                                                                                     Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQDICFA---FLQNYYERMRTDPSKLAYFYASTAELTHTNYQSKSTNEKDDVLPTVKVTG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 VPSAQDIAAEFVRQYYHVLGQLPHEARRLYVDASVSRPDVJGTMMSFTSVEAINKHILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         east (Saccharomyces cerevisiae)
protein N3465
                                                                                                                                                                                                                                                                                                                                                                                                             Length 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Length 515,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PID:9553136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:9172081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the Protein Sequence Database, April 1996
A;Reference number: S63346
A;Accession: S63382
                                         A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 VDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGN-
                                                                                                                                                                                                                                                                                                                                                                                                         Score 81; DB
Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 Fred. NO. 4.0;
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cusick, M.E.
ubmitted to the EMBL Data Library, March 1992;Reference number: S27437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NID: 9172079;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 NTVWKIASDCFRFQDWSSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---LVVLNDMLRYVDQEDS 134
                                                                                                                                                                                                                                                                                                                                                                                                                           23.78;
                                                                                                                                                                                                                                                                                                                                                                                                         10.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: EMBL:M88607; Accession: S27440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: SGD:S0005334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N; Alternate names: 'hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: DNA
Residues: 1-316,'T' <CUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 350-441 <CUW>
                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-427 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: DNA
Residues: 1-515 <POH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                      A; Accession: E96716
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                                                                                                                                                                                                                                                                                                                                 A; Gene: F23010.17
A; Map position: 1
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                                                                                                                                                                                                                                                                                                               C; Genetics:
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                                                              H.; Tallon,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zumft, W.G.; Dreusch, A.; Loechelt, S.; Cuypers, H.; Friedrich, B.; Schnelder, B.
ir. J. Biochem. 208, 31-40, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ir. J. Biochem. 208, 31-40, 1992

Title: Derived amino acid sequences of the nosz gene (respiratory N(2)O reducts J. Implications for the Cu(A) site of N(2)O reductase and cytochrome-c oxidase. Reference number: S24382; MUID:92380183; PMID:1324835
                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *Refwords: copper; metalloprotein; oxidoreductase
;589,624,628/Binding site: copper 1 (His, Cys, Cys) #status predicted
;624,626,628,632/Binding site: copper 2 (Cys, His, Cys, His) #status predicted
                                                                                                                                                                                                                              NID:98920577; PIDN:AAF81299.1; GSPDB:GN00141
                                                            Southwick, A.M.; Sun,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNTVWKIASDCFR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable RNA-binding protein F23010.17 (imported) - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  21 FVNIYYETMDKRRRALTRLYLDKATLIWNGN-----AVSGLDALNNFFDTLPSSEFQVNM 75
                                                                                                                                                                                                                                                                                                                                                                                                                                            FVEKYYNLLYKSPŚQVHQFYLDDSVLGRPGSDGEMVSVKSLKAIN---EQIMSFDYEISK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTAFDGRGNAYTTLFLDSQLVKWN-----LDAAIKFHKGDKNAKYVVDRLDLQYQPGHV 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQVNMLDC--OPVHE 83
  Cross-references: EMBL:X65278; NID:938781; PIDN:CAA46383.1; PID:938782
                                                                                                                                                                                                                                                                                                                                                             53; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 13;
                                                                                                                                                                                                                                                                                                                          Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - Alcaligenes eutrophus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 QATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 NASQSET---VAADGKYLAVGCK--FSKDRFLPVGPLHPEN 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: 10-Sep-1999 #sequence_revision 10-Sep-1999
                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                               Score 90.5, DB; Pred. No. 0.43; 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity | 31.7%; Pred No. 188 32; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reductase,(EC 1.7.99.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: nitrous-oxide reductase
                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-428 <STO>;
A/Cross-references: GB:AE005172;
C; Genetics:
                                                                                                                                                                                                                                                                                                                 12.1%;
illarity, 24.8%;
Conservative 2
Rizzo, M.; Rooney, T.; Rowl
A;Authors: Salzberg, S.L.;
Gai, D.; Yu, G.; Fr
                                                                                                                                                                                                                                                                                                                                      Similarity
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408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-643 <2UM>
                                                                                                                                                                                                                                                                     A; Map position: 1
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Chin, C.W.;
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RESULT 11

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In, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, S. D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. Reference number: A84420; MUID:20083487; PMID:10617197
                         ;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GB:AE002093; NID:g4406775; PIDN:AAD20086.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                   pothetical protein At2g03640 [imported] - Arabidopsis thaliana
Species: Arabidopsis thaliana (mouse-ear cress)
Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                        ---MTLOTISN 772
                                                                                                             SYLVOSKTGONLFAGDYYETLLAAAREREYIYRDTARCKQAINLVNGLLQKIN---SLPG 726
                                                                                                                                                                     -SSEFQVNMLDCQPVHE---QATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 FVQEYYNHLYDSTSEVHKFYLEDSMISRPGLDGEIVTIKSLKGINDQIMSIDYKSSRIEI 78
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 QPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNTVWKIASDCFRF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYVDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLP-
                         30;
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                         53; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57;
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                                                                                                                                                                                                                                727 ATSAHKQEMLNATTYYQYSLSVTLNQLTVLESLLAGLK-
llarity 27.9%; Pred. No. 8.7; Conservative 18; Mismatches
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                                                                                                                                                                                                                                                                                                                    NKYDKSVFKIES----FDDW 788
                                                                                                                                                                                                                                                                                   N----TVWKIASDCFRFQDW 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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nes 25; Conserv
     Similarity
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Residues: 1-423 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: H84450
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Gene: At2g03640
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     Best Local
Matches 3
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Job time :
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Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Hickey,
Salzberg,
                                                                                                                                                                                                                                                            - Chlamydophila pneumoniae (strains CWL
                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -references: GB:AE001654; GB:AE001363; NID:94377031; PIDN:AAD18866.1; PID:9437703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fittle: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
Reference number: A81500; MUID:20150255; PMID:10684935
Accession: E81623
                                                                                                                                                                                                                                                                                                                                                     Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, true Genet. 21, 385-389, 1999
Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
Reference number: A72000; MUID:99206606; PMID:10192388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .; Gill, S.R.; Heidelberg, J.F.; White, O.; W.; DeBoy, R.; Kolonay, J.; McClarty, G.;
                                                                                                                                                                                                                                                            conserved hypothetical protein CP0019 [imported] - Chlamydophila pneumoniae
;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
;pate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 SEFQVNMLDCQPVHE---QATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNN- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -MTLOTTSNNK 774
          SILIMATGEMEWTGIPVY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 TYVDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 872;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 81; DB 2;
Pred. No. 8.7;
7; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ad, T.D.; Brunham, R.C.; Shen, C.; Gill, bodson, R.; Gwinn, M.; Nelson, W.; DeBk eic Acids Res: 28, 1397-1406, 2000
                                                                                    109 FFNONFLLTAOSTPNNTVWKIASDCFRF 136
                                                                                                                     115 KFCQTFILLDSS--NGSTFDITNDIRF 140
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perimental source: strain CWL029 ad, T.D.; Brunham, R:C.; Shen, C.

1-872 <ARN>

PNA

RESULT 13

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17;

Conservative

Local Similarity

**datches** 

A; Gene: CPn0727; CP001

ues: 1-872 <REA>

10.8%; 27.5%;

Ouchi, K.; Shiba,

BA000008; NID:98979099; PIDN:BAA98934.1; GSPDB:GN00142 strain J138

A; Experimental source

A; Residues:

Gene: CPj0727 Query Match

Genetics

Length 872;

DB 2;

Score 81;

10.8%;

pneumoniae (strain J138)

Species: Chlamydophila pneumoniae, Chlamydia pneumoniae Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 02-Mar-2001

CT619 hypothetical protein [imported]

Accession: D86581

125 --- TVWKIASDCFRFQDW 139 775 YDKSVFKIES----FDDW 788

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ishirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; ucheic Acids Res. 28, 2311-2314, 2000; Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.; Reference number: A86491; MUID:20330349; PMID:10871362

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

March 4, 2003, 14:51:02 ; Search time 3.39909 Seconds
 (without alignments)
 1732.709 Million cell updates/sec Title: US-09-763-902B-7
Perfect score: 749
Sequence: 1 MATSLDFKTYVDQACRAREE.....NNTVWKIASDCFRFQDWSSS 142 Run on:

112892 seqs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

112892 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Description	homo	Obdzyy mus musculu			09xj54 oryza sativ	P13662 homo sapien	2	Q9c7f5 arabidopsis	P87102 neurospora	s xenobns	Q9p926 candida alb	P33331 saccharomyc	Q21735 caenorhabdi	Q9un86 homo sapien	_	Q59105 alcaligenes	_	Q9gzz6 homo sapien	_	'n	P09287 varicella-z	094260 schizosacch	0		P75990 escherichia	P73376 synechocyst	P10033 feline infe	33	1,	35 buchne	2 human	. 081966 human papil
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<u>e</u>		NXTI MOUSE	1	1	NTF2_ORYSA	NTF2_HUMAN	NTF2_SCHPO	NTF2_ARATH	NTF2_NEUCR	NTF2_XENLA	NTF2_CANAL	NTF2_YEAST	NTF2_CAEEL	G3B2_HUMAN	G3B2_MOUSE	NOSZ_ALCEU	YN8T_YEAST	ACHX_HUMAN	YO68_CAEEL	YDAA_HAEIN	OL25_VZVD	G3BP_SCHPO	FPG_SYNY3	MDCB_ACICA	YCGF_ECOLI	Y50L_SYNY3	VGL2_FIPV	MYH6_HUMAN	TCPD_VIBCH	HOLB_BUCAI	VE1_HPV30	VEL HPV59
08			- ~ - ~	-	7	~ H	7	7	7	-	-	~	-	7	-	-	-	7	Н	Г. Н	-	-	Н	-	-	н	-	_	-	-	H.	
Length	142	140	133	137	122	127	123	126	124	127	124	125	133	485.	482	643	515	450	910	309	579	434	287	292	403	186	1452	1939	278	326	631	644
% Query Match	100.0	78.7	41.4	27.7	16.6	15.4	15.1	15.0	14.5	14.4	14.0	13.6	13.3	11.8	11.8	11.5	10.8	10.5	10.3	10.3	10.3	10.2	9.6	9.7	9.7	9,5	. 9.5	9.5	9.5	9.4	ю	6.9
Score	749	586 586	310	207.5	124	115	113	112.5	108.5	108	104.5	101.5	99.5	88.5	88.5	86.5	81	78.5	77.5	77.	774	76.5	74	73	72.5	71.5	71.5	71.5	71	70.5	70	70
Result No.	; ; ;	7 r	. 4	· ທ	9	7	80	6	10	11	12	13	14	. 15	. 16	17	18	19	. 20	21	22	.23	24	25	56	27	. 28	. 29	30	31	32	33

P32670 escherichia P13339 bacteriopha Q28005 bos taurus Q13281 bomo sapien 032321 bacillus th P5073 human papil O28648 archaeoglob Q02151 lactococcus P97855 mus musculu Q9cg80 lactococcus P12883 homo sapien P79293 sus scrofa
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PT1A_ECOLI VG48_BPT4 LSHR_BOVIN G3BP_HUMAN CKAA_BACUF VG2_HBV7 YG52_ARCPU YMEB_LACLA G3BP_MOUSE TOPI_LACLA MYH7_HUMAN MYH7_HUMAN
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## ALIGNMENTS

RESULT 1

- A T - 4.	25	HUMAN STANDAR 8, Q9H8U0, Q9NRL7	
		(Rel. 40, Created) (Rel. 40, Last sequence update) (Rel. 41, Last annotation update)	
	DE NTF2 GN NXT2	NTF2-related export protein 2 (p15-2 protein) (DC9) (BM025). NXT2.	
	OS Homo	Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	OC Mamm	Primates;	
, pa 14		SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).	
	_		
, H	RX MEDLINE RA Herold	3=20528640; PubMed=11073998; A. Suvama M. Rodriques J.P	
1		Conseca C., Bork P., Izaurralde E.;	
1-4	Kr TAF	o (NAFL) belongs to a multigene lamily of putative KWA exportants with a conserved modular architecture.";	
-		Mol. Cell. Biol. 23:8996-9008(2000).	
	RN [2]	[2] SECULENCE PROM N A (150FORM 1)	
	RT "p15	"p15-2, a homologous protein of p15, interacts with Tap."; Submitted (Mar-2000) to the EMBL/GenBank/DDRI databases	
_		E FROM N.A. (ISOFORM 1).	
	RA L1 Y., RT "Novel	Y., Peng Y., Li N., Gu W., Han Z., Fu G., Chen Z.; Wel genes expressed in human dentritic cell.";	
		ed (NOV-1999) to the EMBL/GenBank/DDBJ o	
	RN [4]	[4] SEOUTENCE FROM N.A. (ISOFORM 1)	
		Ota T., Hayashi K., Sugi	
	RA N1SI	NISDIKAWA I., NAGAI K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.	-
	-	M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi	
•		S., Kimura K., Murakami K.,	
	RA YAME	, Nayanati n., masuno	
_	•	uencing project.";	
	RL Subn	Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.	
		PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).	
	_	one marrow;	
	RA Zhac	Zhao M., Song H., Li N., Peng Y., Han Z., Chen Z.;	
		gene expressed d (DEC-1999) to	
1	RP PAR	PARTIAL SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).	
		r., ed (APR-1999) to the EMBL/GenBank/DDBJ	
- '	는 당	Regulator of protein exp	ä
-	:	AISO piays a role in manA nuclear export.	

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                                                                  A Rawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fibata K., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A slato T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,
A Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
A Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
A Schrim L.M., Staubli F., Suziki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.,
A Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Wastincich S., Hill D., Hofmann M., Mazzarelli J., Mombaerts P.,
A Rodone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sazaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
A Haysshizaki Y.,
A Hayssqua Y., Rawaji H., Kohtsuki S.,
A Hay
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63 EMLPSSEFQISVVDCQPVHDDATPSQTTVLVVICGTVKFEGNKQRDFNQNFILITAQASPS_122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear. Shuttles between the nucleus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transport; Protein transport; mRNA transport; Nuclear protein:
DOMAIN 16 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K -> N (IN REF, 2).
358EAFDC19FE4594 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.2%; Score 586; DB 1;
76.1%; Pred. No. 9.3e-54;
11ve .20; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 40, Created)
(Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -! - SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02136; NTF2; 1.
PROSITE; PS50177; NTF2_DOMAIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 AA; 15847 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF156958; AAD54943.2; -. EMBL; AK003254; BAB22670.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 NTVWKIASDCFRFQDWSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002075; NTF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1929619; Nxtl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the cytoplasm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NXT1_HUMAN
Q9UKK6;
16-OCT-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
NXT1_HUMAN
ID NXT1_HU
AC Q9UKK6,
DT 16-OCT-
DT 16-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               쉽
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                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MATSL -> VTNHVPALCTAGRGPRFAARPAGPTPSLVSSR
FLIPERTLSWEIARGGDVG (IN ISOFORM B).
009B4E8929A6BA6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFFDTLPSSEFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MATSLDFKTYVDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shuttles between the nucleus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Black B.E., Levesque L., Holaska J.M., Wood T.C., Paschal B.M.; "Identification of an NTF2-related factor that binds Ran-GTP and regulates nuclear protein export."
                                                                      the cytoplasm.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are
produced by alternative splicing.
-!- SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ram; PrU1135; NIF2; 1.
PROSITE; PS50177; NIF2_DOMAIN; 1.
Fransport; Protein transport; mRNA transport; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
SUBUNIT: Associates with NXF1, NXF2, NXF3 and NXF5 SUBCELLULAR LOCATION: Nuclear. Shuttles between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 749; DB 1;
Pred. No. 1.3e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0902V9; 0901P7;
16-OCT-2001 (Rel: 40, Created)
16-OCT-2001 (Rel: 40, Last sequence update)
15-JUN-2002 (Rel: 41, Last annotation update)
NTF2-related export protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAB14511.1; ALT_INIT
AAF87325.1; ALT_INIT
CAB41301.1; -.
CAB41302.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-20036817; Pubmed-10567585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulates nuclear protein export
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TPNNTVWKIASDCFRFQDWSSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TPNNTVWKIASDCFRFQDWSSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ277591; CAB96371.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 AA; 16228 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; IPR002075; NTF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02136; NTF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 142; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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MEDLINE-21638749; PubMed-11780052;
MEDLINE-21638749; PubMed-11780052;
MEDLINE-21638749; PubMed-11780052;
MEDLINE-21638749; PubMed-11780052;
MEDLINE-21638749; PubMed-11780052;
MEDLINE-21638749; PubMed-11780052;
MEDLINE-21638749; Maneida J.P., Babbage A.K., Bagguley C.L., Balley J., Barlow K.F., Baezd C.M., Beard D.M., Bearley O.E., Blard C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder N.P.,
Clegg S., Cobley V.E., Coller R.E., Connor R.E., Corby N.R.,
Clegg S., Cobley V.E., Coller R.E., Connor R.E., Corby N.R.,
Clegg S., Cobley V.E., Coller R.E., Connor R.E., Corby N.R.,
Clegg S., Cobley V.E., Coller R.E., Connor R.E., Corby N.R.,
Clegg S., Cobley V.E., Coller R.E., Connor R.E., Corby N.R.,
Clegg S., Cobley V.E., Coller R.E., Connor R.E., Corby N.R.,
Clegg S., Cobley V.E., Coller R.E., Connor R.E., Corby N.R.,
Clegg S., Cobley V.E., Coller R.E., Danmin P.D.,
Clegg S., Cobley V.E., Coller R.E., Connor R.E., Corby N.R.,
Clegg S., Cobley V.E., Coller R.E., Connor R.E., Corby N.R.,
Clegg S., Cobley V.E., Coller R.E., Jeach D.E., Johnson D.,
Clegg S., Rarley J.L., Heath P.D., Ho S., Holden J.L., Monore M.J.F.,
Malle S.A., Mistry D., Moore M.J.F., Mollikin J.C., Nickerson T.,
Coller R., Spann R.M., Sycanore N.T., Scott C.E., Sehra H.K., Shownkeen R., Stans S.,
Swuce C.D., Smith M.L., Soderlund C., Steward C.A., Thomas D.W., Thorpe A.,
Swann R.M., Sycanore N., Taylor R., Thee L., Thomas D.W., Walliams S.A.,
Milling L., Willey P.W., Hubbard T., Durbin R.W., Bentley D.R., Williams S.A.,
Milling D., Wiray P.W., Hubbard T., Durbin R.W., Bentley D.R., Williams S.A.,
Milling S.W., Bentley D.R., Willier B.K., Recer M. Rose R. W., Rocers J.E.,
Malling S.W., Rubbard T., Durbin R.W., Bentley D.R., Williams S.A.,
Milling S.W., Rubbard T., Durbin R.W., Bentley D.R., Williams S.K.,
M. Williams D., Williams S.C., Williams S.J.,
M. Williams D., Williams D., Williams S.J.,
M. Williams S.J., Williams S.J.,
M. Williams S.J., Williams D., Williams S.J.,
M. Williams S.J., Williams S.J.,
M. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dargemont C.; "RanGTP-binding protein NXT1 facilitates nuclear export of different classes of RNA in vitro."; Mol. Cell. Biol. 20:4562-4571(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ossareh-Nazari B., Maison C., Black B.E., Levesque L., Paschal B.M.
                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                          SEQUENCE FROM N.A., num. 10555855, MEDLINE-20036817; Pubmed-1105655855, Black B.E., Levesque L., Holaska J.M., Wood T.C., Paschal B.M.; Identification of an NTF2-related factor that binds Ran-GTP and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Lung, Placenta, and Uterus;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
  15-JUN-2002 (Rel. 41, Last annotation update) NTF2-related export protein 1 (p15 protein).
                                                                                                                                                                                                                                                                regulates nuclear protein export.";
Wol. Cell. Biol. 19:8616-8624(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21160285; PubMed-11259602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20307861; PubMed-10848583;
                                                                                                                                                                       SEQUENCE FROM N.A., AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The DNA sequence and com
Nature 414:865-871(2001).
                                                               sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              he DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rogers
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SUBCELLULAR LOCATION: Nuclear. Shuttles between the nucleus and

SIMILARITY: CONTAINS 1 NTF2 DOMAIN

the cytoplasm

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                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 DTLPSSEFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ||||||||::::||||||||::|:
63 EMLPSSEFQISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLDFKTYVDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20036817; Pubmed-10567585;
MEDLINE-20036817; Pubmed-10567585;
Black B.E., Levesque L., Holaska J.M., Wood T.C., Paschal B.M "Identification of an NTF2-related factor that binds Ran-GTP "Identification of an NTF2-related factor that binds Ran-GTP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 78.0%; Score 584; DB 1; Length 14 Best Local Similarity 75.4%; Pred. No. 1.5e-53; Matches 104; Conservative 22; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               358FA86AC3944594 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         Transport; Protein transport; Nuclear protein. DOMAIN 16 135 NTF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-7UN-2002 (Rel. 41, Last annotation update)
NYT2-related export protein (P15).
NXT1 OR CG12752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulates nuclear protein export.";
Mol. Cell. Biol. 19:8616-8624(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Berkeley;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02136; NTF2; 1.
PROSITE; PS50177; NTF2_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN 16 135 N
SEQUENCE 140 AA; 15847 MW;
                                                                                                                                                                           EMBL; AF156957; AAD54942.1;
EMBL; AL096677; CAC03437.2;
                                                                                                                                                                                                                                        EMBL; BC002687; AAH02687.1;
EMBL; BC003029; AAH03029.1;
EMBL; BC003410; AAH03410.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 NTVWKIASDCFRFQDWSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 NTVWKIASDCFRFQDWAS 140
                                                                                                                                                                                                                                                                                                                                         IPR002075; NTF2.
                                                                                                                                                                                                                       BC000759; AAH00759.1
                                                                                                                                                                                                                                                                                                     HGNC:15913; NXT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NXT1_DROME
                                                                                                                                                                                                                                                                                                                        MIM; 60581
                                                                                                                                                                                                                                                                                                                                             interPro;
                                                                                                                                                                                                                                                                                                       Genew;
                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
NXT1_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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137 AA.

STANDARD;

NXT1\_CAEEL

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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Edwardari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Edwardia P., Brottler P.,
RA Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doub L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferriaz C., Ferriaz S., Felsschmann W.,
RA Harris N.L., Harryey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harryey D., Helman T.J., Hernandez J.R., Houck J.,
RA Jalai M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Kannell B.E., Kodina C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Alali M., Mattel B., McIntosh T.C., McLed M.P., McDherson D.,
RA Luu X., Mattei B., McIntosh T.C., McLed M.P., McDherson D.,
RA Melson D.R., Nablon R.A., Nixon K., Nuskern D.R., Moshrefi A.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shie B.C., Siden Klamos J.S., Shipson M., Skupski M.P., Smith T.,
RA Stirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Yao Q.A.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Yao Q.A.,
RA Hang S.M., Woodage T., Woorley K.C., Wu D., Yang S., Yao Q.A.,
RA Theng Romen sequence of Drosophila melanogaster.";
RTP Genome sequence of Drosophila melanogaster.";
Science 287.2185-2185-2185-21009.
C. TERMA. And MRNA, Ray similativi, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 LPSSEFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 LPSSNHQLNTLDAQPIVDQAVSNQLAYLIMASGSVKFADQQLRKFQQTFIVTAE----ND 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trnh, and mrnh (By similarity).
-i- SUBUNIT: Preferentially binds Ran-GTP (By similarity). Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 DFKTYNDOACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 DLKAKVESCARTADTFTRLYYASVDNRRQQIGRLYLDNATLSWNGNGAIGRQMIESTFQE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transport, Protein transport; mRNA transport, Nuclear protein. DOMAIN 15 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C6E664950AA370AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.4%; Score 310; DB 1; L42.9%; Pred. No. 3.2e-25; Live 24; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50177; NTF2_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15181 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF156959; AAD54944.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0028411; Nxtl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 42.9%
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 VWKIASDCFRFQD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||: |||: |:
|120 KWKVVSDCYRMQE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              am; PF02136; NTF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with NXF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Detween the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61. NFFDTLPSSEFQVNMLDCQPVHEQATQSQT-TVLVVTSGTVKFDGNKQHFFNQNFLLTAQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 EFMKALPSTOHDIQSLDAQRLPEGVTGDMSGGMLLNVAGAVTVDGDSKRAFTQTLLLGVE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 MKTTQEINKEDEELCNESKKFMDVYYDVMDRKREKIGFLYTQVSNAVWNGNPINGYDSIC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MATSLDFKTYVDQACRAABEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALN
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILINE-2008GBT7; Pubmed-10567585;
MEDILINE-2008GBT7; Pubmed-1., Holaska J.M., Wood T.C., Paschal B.M.;
Black B.E., Levesque L., Holaska J.M., Wood T.C., Paschal B.M.;
"Identification of an NTF2-related factor that binds Ran-GTP and
"Identification of an NTF2-related";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
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PROSITE; PS50177; NTF2_DOMAIN; 1.
Transport; Protein transport; mRNA transport; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bradehaw-Cordum H., Scott K., Graves T.;
Submitted. (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Stimulator of protein export for NES-containing
proteins. Also plays a role in the nuclear export of Ul s
trna, and mrna (By similarity)
-!- SUBUNIT: Preferentially binds. Ran-GTP (By similarity)
-!- SUBCELDURA LOCATION: Nuclear (By similarity)
-!- SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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29.5%; Pred. No. 1.4e-14;
ive 35; Mismatches 58;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulates nuclear protein export.";
Mol. Cell: Biol, 19:8616-8624(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF156960; AAD54945.1; -.
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----DGKYKVKSDRFRYVD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WormPep; Y71F9AM.5; CE26780.
InterPro; IPR002075; NTF2.
                                                                                                                         NTF2-related export protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                           Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P13662; 10UN
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Matches 41; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                    NXTI OR Y71F9AM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
NTF2_ORYSA
ID NTF2_ORYSA
AC 09XJ54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123
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SPECIES-Human
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                                                                                                                                                                                                                                                                          FUNCTION: FACILITATES PROTEIN TRANSPORT INTO THE NUCLEUS. COULD BE PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS THAT ASSEMBLE AT THE PORE COMPLEX DURING NUCLEAR IMPORT (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic (By Similarity).
SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 LDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQH--FFNQNFLLTAQSTPNNTVWKIASDC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 AEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSE--FQVNM 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice):
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606, 10090, 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
cor 2 (NTF-2) (Placental protein 15) (PP15).
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                                                                                                                                                                                                                                                      factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 122;
                                                                                                                                                                                                             STRAIN=cv. Nipponbare;
Matsuki R., Iwasaki T., Jiang C., Yamamoto N.;
"Molecular cloning of a cDNA encoding nuclear transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 AA; 13354 MW; 84100EBB62AB1BD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.6%; Score 124; DB 1; 32.0%; Pred. No. 5.2e-06; iive 19; Mismatches 50;
                                                                                                                                                                                                                                                             (NTF2) from rice.",
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nuclear transport factor 2 (NTF-2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1990; (Rel. 13, Created)
01-JAN-1990; (Rel. 13, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fransport; Protein transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB011262; BAA81910.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               562; 1A2K.
IPR002075; NTF2..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human),
Mus musculus (Mouse), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39; Conservative
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NTF2 OR PP15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02136; NTF2;
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                              NCBI_TaxID-4530;
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P13662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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NTF2_HUMAN
AC P13662,
DT 01-JAN
DT 15-JUN
DT 15-JUN
DG NUClea
GN NTF2 01
OS HOMO 81
OS RATUM
OC EUKATY
OC MAMMA1.
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J. Mol. Biol. 277:635-646(1998).

-1- FUNCTION: FACILITATES PROTEIN TRANSPORT INTO THE NUCLEUS.

INTERACTS WITH THE NUCLEOPORIN P62 AND WITH RAN. ACTS AT A

RELATIVELY LATE STAGE OF NUCLEAR PROTEIN IMPORT, SUBSEQUENT TO THE
INITIAL DOCKING OF NUCLEAR. IMPORT LIGAND AT THE NUCLEAR ENVELOPE.

COULD BE PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS THAT

ASSEMBLE AT THE PORE COMPLEX DURING NUCLEAR IMPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stewart M., Kent H.M., McCoy A.J.; "Structural basis for molecular recognition between nuclear transport factor 2 (NTF2) and the GDP-bound form of the Ras-family GTPase
                                                                                                                                                                                                                                                                                                                                                                                               nuclear import that,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adachi J., Alzawa K., Akahira S., Akimura T., Aono H., Arai A., Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Salto R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
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"The 1.6-A resolution crystal structure of nuclear transport factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clarkson W.D., Corbett A.H., Paschal B.M., Kent H.M., McCoy A.J., Gerace L., Silver P.A., Stewart M.; Wuclear protein import is decreased by engineered mutants of nuc transport factor 2 (NFE2) that do not bind GDP-Ran."; J. Mol. Biol. 272:716-730(1997).
                                      Grundmann U., Neilich C., Rein T., Lottspeich F., Kuepper H.A.; "Isolation of cDNA coding for the placental protein 15 (PP15)."; Nucleic Acids Res. 16:4721-4721(1988).
                                                                                                                                                                                                              SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH RAN
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SPECIES-Rat; TISSUE-Kidney;
Kent H.M., Clarkson W.D., Bullock T.L., Stewart M.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ubmitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                       Paschal B.M., Gerace L.; "Identification of NTP2," a cytosolic factor for interacts with nuclear pore Complex protein p62. J. Cell Biol. 129:925-937(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-Mouse; STRAIN-C57BL/6J; TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).</pre>
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MEDLINE-88247772; PubMed-3380696;
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                                                                                                                                                                                                                                                                                                    MEDLINE-95263674; PubMed-7744965;
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MEDLINE-98202576; PubMed-9533885;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                      between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 FVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQ--VNMLDC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 FIQHYYQLFDNDRIQLGAIXIDASCLIWEGQGFGGRAAIVEKLSSLPFQKIQHSITAQDH 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A. Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K. James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Miblett D., Odell C., Oliver K., O'Neil S., Paarson D., Quail M.A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 QPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNTVWKIASDCFR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.4%; Score 115; DB 1; Length 127; 27.4%; Pred. No. 4.7e-05; Indels 11ve 18; Mismatches 55; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN 10 121 NTF2.
SEQUENCE 127 AA; 14478 MW; 817752F20E262FD3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomycetales; Schizosaccharomycetaceae;
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable nuclear transport factor 2 (NTF-2)
PTP2 OR SPACIB9.01C OR SPACISF9.03C.
Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50177; NTF2_DOMAIN; 1.
Transport; Protein transport; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-972;
MEDLINE-21648401; PubMed-11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002075; NTF2. 
Pfam; PF02136; NTF2; 1.
                                                                                                                                                                                                                                                                                             EMBL; X07315; CAA30278.1;
EMBL; X91651; CAA62839.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U43939; AAA85905.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JAN-98.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-4896
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ID NTF2_SCHPO
OT 010100
DT 01-FEB
DT 16-OCT
DT 16-OCT
DT 16-OCT
DC NCBLZ
OC COLAZO
OC COLAZO
OC SCHIZO
OC
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Raeger M., Schaefer M., Mueller Auer S., Abeljens I., Vanstreels E., Raeger M., Schaefer M., Mueller H., Radel D., Hilbert H., Raber D., Moestl D., Hilbert H., Rack A., Lehrach H., Reinhardt R., Pohl T.M., A Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., A Gotfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., A Golibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., A Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., A Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., A Cartuti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., A Cartuti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., A Cartuti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., A Cartuti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., A Cartuti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., A Cartuti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., A Cartuti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., A Cartuti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., A Cartuti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., A Cartuti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., A Cartuti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., A Cartuti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., A Cartuti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., A Cartuti L., Lowe T., McCombie W.R., Paulsen I., Putting S.L., McCombie W.R., Paulsen I., Patting S.C., Murse P., Sumilarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 AEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQ--VNM 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 120 NTF2.
75 76 TT -> SL (IN REF. 1; CAA92380).
123 AA; 14078 MW; F587303CAA3270E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.1%; Score 113; DB 1;
28.1%; Pred. No. 7.2e-05;
ive 24; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear transport factor 2 (NTF-2).
NTF2 OR AT1G27970 OR F13K9.26.
Arabidopsis thaliana (Mouse-ear cre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ransport; Protein transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nterPro; IPR002075; NTF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z68197; CAA92380.2;
P13662; 1A2K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 28.1
nes 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel
16-OCT-2001 (Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTF2_ARATH
Q9C7F5;
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NTF2_ARATH
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us-09-763-902b-7.rsp

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Meyer U., Meyer M., Techel D., Toeken K., Rensing L.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: FACILITATES PROTEIN TRANSPORT INTO THE NUCLEUS. COULD BE
PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS THAT ASSEMBLE
AT THE PORE. COMPLEX DURING NUCLEAR IMPORT (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                           SEQUENCE FROM N.A.
STRAIN-BD-A / FGSC 1858;
             NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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          WEDELINE-21016(119): Pubmed-11130712;
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
A Hosologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
A Mitte O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brocks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
D. Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hulzar L.,
A Hinter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
A Hintscher J., Miranda M., Nguyen M., Narman W.C., Osborne B.I.,
A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
A Bai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
A Utterback T., Wan Aken S., Vaysberg M., Vysotskala V.S., Walker M.,
T. "Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- FUNCTION: FACILITATES PROFEIN TRANSPORT INTO THE NUCLEUS. COULD BE PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS THAT ASSEMBLE AT THE PORE COMPLEX DURING NUCLERR IMPORT (BY SIMILARITY).
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 LDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHF-FNQNFLLTAQSTPNNTVWKIASDCF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLP--SSEFQVNM 75
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Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 126;
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Best Local Similarity 27.3%; Pred. No. 8.4e-05;
Matches 33; Conservative 25; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nuclear transport factor 2 (NTF-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transport; Protein transport.
DOMAIN 9 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AC069471; AAG51491.1;
HSSP; P13662; 10UN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002075; NTF2. stam; PF02136; NTF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 408:816-820(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurospora crassa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 TSLP---FQKVKHEYGPPDAQPTATGGIIILVTGQLIVDDEQRPLGYSQAFQLSQDASGQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DILPSSEFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLDFKTYVDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craníáta; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                    14.5%; Score 108.5; DB 1; Length 124; llarity 26.5%; Pred. No. 0.00021; Conservative 21; Mismatches 63; Indèls 13;
                                                                                                      and
                                                                                                                                                                                                                                                                                                                                              NTF2.
8C7AAF927B0476C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Cytoplasmic (By similarity
                                                                                                        Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nuclear transport factor 2 (NTF-2) (P10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 AA.
                                                                          use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                          entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                Pfam; PF02136; NTF2; 1.
PROSITE; PS50177; NTF2_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                  124 AA; 13726 MW;
                                                                                                                                                                                                                                                                                                                     Transport; Protein transport.
                                                                                                                                                                                                                                             InterPro; IPR002075; NTF2.
                                                                                                                                                                                             EMBL; Y13237; CAA73689.1;
HSSP; P13662; 10UN.
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---WEVFNDIFK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355;
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us-09-763-902b-7.rsp

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8 121 NTF2.
124 AA; 14193 MW; B799DIABA828A049 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  WCBI_TaxID-4932;
                                                                                                                                                                                                                                                                            NTF2_YEAST
P33331;
                                                                  .39;
      DOMAIN
SEQUENCE
                                           Query Match
                                                                                                                                                                                                                                                       RESULT 13
NTF2_YEAST
                                                                                                                                                                                                                                                                  YEAST
                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        noved. Usage by and for commercial (See http://www.isb-sib.ch/announce)
                               This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dominguez A.; *Sequence of Candida albicans and Yarrowia lipolytica homolog of the
                                                                                                                                                                                                                                                                                            21 FVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQ--VNMLDC 78
                                                                                                                                                                                                                                                                                                                   14 FIQOYYQIFDADRIQLAVIYIDASCLIWEGQQYHGKAAIVEKLSLLPFQKIQHSIISQDH 73
                                                                                                                                                                                                                                                                                                                                           79 OPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNTVWKIASDCFR 135
                                                                                                                                                                                                                                                                                                                                                         14 OPTPD-----SCIISMVVGQLKADDDPIMGFHQVFLL----KNIQDAWVCTNDMFR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blanchin-Roland S., Cordero-Otero R., Gaillardin C., Herrero A.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                            Length 127;
                                                                                                                                                                                                                                                                      57; Indels
                                                                                                                                                                                                                    127 AA; 14477 MW; 97110D6828268259 CRC64;
                                                                                                                                                                                                                                              Match 14.4%; Score 108; DB 1; Local Similarity 27.4%; Pred. No. 0.00025; ies 32; Conservative 16; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nuclear transport factor 2 (NTF-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                  124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement
           -i- SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50177; NTF2_DOMAIN; 1
                                                                                                                                                                                                 ransport; Protein transport.
                                                                                                                                                                        PEO2136; NTF2; 1.
PROSITE; PS50177; NTF2_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            40, Created)
                                                                                                                                     EMBL; AF023911; AAB81276.1; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transport; Protein transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF145758; AAF66701.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002075; NTF2.
                                                                                                                                                    ISSP; P13662; 1A2K.
InterPro; IPR002075; NTF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candida albicans (Yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02136; NTF2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-AICC 26555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          6-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                   NTF2_CANAL
Q9P926;
                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                              52 EKLASLPFQKVAHRISTLDAQP----ASANGDILVMVTGELLIDEEQNAQR-YSQVFHL 105
                                                     Gaps
                                                                                                4 SLDFKTYVDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFF 63
                                                                                                                                                   51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=S288C / AB972;
Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aniligan J.T., Benna J., Chen E., Cherry J.M., Alles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Grung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Opetell F.X., Roberts D., Sehl P., Schraum S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nuclear transport factor 2 (NTF-2) (Nuclear transport factor P10).
NTF2 OR YEROODW.
                                                                                                                                 2 SVDFNA-----VATEFCNFYYNQFDSDRSQLGNLYRNESMLTFE---TSQLGGRRDIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                  27;
Length 124;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haarer B.K., Petzold A.S., Brown S.S.;
Submitted (JUL-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics
the European Bioinformatics Institute. There a
                                                       53;
       DB 1;
     Score 104.5; DB 1 Pred. No. 0.00055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      institutions as long
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed-8600522;
                                                          20;
          14.08;
28.18;
                                                                                                                                                                                                                                                                                                           117 TAQSTPNNTVWKIASDCFR 135
                                                                                                                                                                                                                                                                                                                                          |:| : :! ||
----IPDNGSYYVFNDIFR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U18778; AAB64542.1;
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96178681;
                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: FACILITATES PROTEIN TRANSPORT INTO THE NUCLEUS. COULD BE PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS THAT ASSEMBLE AT THE PORE COMPLEX DURING NUCLEAR IMPORT (BY SIMILARITY).

1. SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 DTLPSSEFQ--VNMLDCQPVHEQATQSQTTVLVVTSGTVKFD--GNKQHFFNQNFLLTAQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                               4 SLDFKTYVDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                            Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                       5660D8C00E634714 CRC64;
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                                                                                                                                                                                                                                                                                                                13.6%; Score 101.5; DB 1; 27.9%; Pred. No. 0.0011; .: Live 19; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        send an email to license@isb-sib.ch)
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                                                                    SGD, S0000811, NTF2.
InterPro; IPR002075; NTF2.
Pfan. PF02136; NTF2; IPR0SITE, PS50177; NTF2_DOMAIN; I.
Transport; Protein transport.
                                                                                                                                                                                                                               NTF2
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Transport; Protein transport.
                                                                                                                                                                                                                                                 125 AA; 14453 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROSD11.3; CE06238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002075; NTF2.
L22204; AAB49379.1;
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 27.9
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 STPNNTVWKIASDCFR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1: :: | | |
106 -IPDGNSYYVFNDIFR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02136; NTF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
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021735;
                                                                                                                                                                                                                                                    SEQUENCE
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Length 133;

Score.99.5; DB 1; Pred. No. 0.002; 7; Mismatches 47;

27;

Query Match
Best Local Similarity 26.8%;
Matches 34; Conservative 2

Indels

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1 QRAITVIDSQPLYDGSIQ-----VWVLGQLKTDEDPINPFSQVFIL----RPNNQGSYF 120
                                                                                                                    Q--VNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNT-VWK 128
                                    Tennedy D., Mattick J.S.;
"Characterisation and chromosomal location of G3BP-1 and G3BP-2a/b, members of a novel SH3 domain-binding and RNA-binding protein family implicated in signal transduction ";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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-!- FUNCTION: PROBABLE SCAFFOLD PROTEIN THAT MAY BE INVOLVED IN MRNA TRANSPORT (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

NA Res. 5:169-176(1998).
18 AEEFVNIYYETMD-----KRRRALTRLY-LDKATLIWNGNAVSGLDALNNFFDTLPSSEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G3B2_HUMAN STANDARD; PRT; 482 AA.

G9UN86; 075149; O60606; Q9UPA1;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-UN-2002 (Rel. 41, Last annotation update)

15-UN-2002 (Rel. 41, Last annotation update)

15-UN-2002 (Rel. 41, Last annotation update)

15-UN-2002 (Rel. 2) (G3BP-2).
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MEDLINE-20549669; PubMed=10969074;
Prigent M., Barlat I., Langen H., Dargemont C.;
"IkappaBalpha and IkappaBalpha /NF-kappa B complexes are retain the cytoplasm through interaction with a novel partner, RasGAP SH3-binding protein 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.
Kotani H., Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBUNIT: BINDS TO THE N-TERMINAL DOMAIN OF IKAPPABALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kennedy D., Ru K., Mattick J.S.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R., submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS A AND B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98403880; PubMed-9734811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM B)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                       129 IASDCFR 135
                                                                                                                                                                                                                                                                                                                      121 IGNEIFR 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissue-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISSUE-Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISSUE-B-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suitard E.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> I (IN REF. 3).
2545C6A3F1AAE218.CRC64;
                                                                                        - SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA-BINDING (RRM)
GLU-RICH.
GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50177; NTF2_DOMAIN; 1.
RRSTTE; PS50102; RRM; 1.
RROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.8%; Score 88.5; DB 27.2%; Pred. No. 0.14; Live. 19; Mismatches
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Best Local Similarity 27.2%
Matches 34; Conservative·
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Search completed: March Job time : 5.39909 secs

g

Gaps

63; Indels

ignisista in termiore, si considerati di distribita probabili anticonsiderati di distribita di distribita di di

099504 chlamydia p 092708 chlamydia p 092708 chandia p 092708 chandia p 09035 arabidopsis 09037 mycoplasma 09546 caenorhabdi 016677 caenorhabdi 02446 drosophila 08xst4 raistonia s 090x9 ureaplasma 09py6 ureaplasma 09py6 ureaplasma 09py6 ureaplasma 09py6 ureaplasma 09py6 ureaplasma 09py6 ureaplasma 09py6 ureaplasma 09py6 ureaplasma 09py6 ureaplasma 09py6 ureaplasma 09py6 ureaplasma 09py6 ureaplasma 09py6 ureaplasma 09py6 ureaplasma 09py6 ureaplasma 09py6 ureaplasma 09py6 ureaplasma 09py6 no arabidopsis 09coup clostridium 09sx88 arabidopsis 06038 homo sapien 09u88 homo sapien

85 11.3 646 16 81.5 10.9 579 12 81 10.8 872 16 81 10.8 872 16 80.5 10.7 423 10 78.5 10.5 1144 2 78.5 10.1 130 5 75.5 10.1 685 16 74.5 9.9 387 16 74.5 9.9 387 16 74.5 9.9 387 16 74.5 9.9 674 5	3.5 9.8 814 11 Q91YT6 73 9.7 1062 2 Q8RC22 2.5 9.7 528 16 Q9FWD0 2.5 9.7 557 10 Q9SK88 72 9.6 563 4 Q90I88 72 9.6 747 4 Q90I88 72 9.6 747 4 Q90I88 72 9.6 789 4 Q9BQC5 73 9.6 1931 13 Q91QC5 74 9.5 374 10 Q41235	PRELIMINARY; PRT; 200 AA. 2001 (TrEMBLrel. 16, Created) 2001 (TrEMBLrel. 16, Last sequence update) 2001 (TrEMBLrel. 21, Last annotation update) 2002 (TrEMBLrel. 21, Last annotation update) 2003 (TREMBLrel. 21, Last annotation update) 2004 (TREMBLrel. 23, Last annotation update) 2007 (TREMBLRel. 2000) 2007 (TREMBLRel. 2000) 2007 (TREMBLRel. 2000) 2007 (TREMBLRel. 2000) 2007 (TREMBLRel. 2000) 2007 (TREMBLRel. 2000) 2007 (TREMBLREL. 2000) 2007 (TREMBREL. 2000) 2	Query Match 22.3%; Score 167; DB 3; Length 200; Best Local Similarity 28.0%; Pred. No. 2.1e-09; Matches 33; Conservative 30; Mismatches 47; Indels 8; Gaps Qy 11 VDQACRAAEEFVNIYYETMDKRRALTRIXIZARATLIWIGNAVSGLDALNNFFDTLPSSE 70 1
GenCore version 5.1.3  Copyright (c) 1993 - 2003 Compugen Ltd.  OM protein - protein search, using sw model  Run on: March 4, 2003, 14:53:32 ; Search time 9.72844 Seconds  (without alignments) 3007.543 Million cell updates/sec  Title: US-09-763-9028-7 Perfect score: 749 Sequence: 1 MATSLDFKTYVDQACRAAEENNTVWKIASDCFRFQDWSSS 142 Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 671580 seqs, 206047115 residues  Total number of hits satisfying chosen parameters: 671580  Minimum DB seq length: 0  Maximum DB seq length: 2000000000  Post-processing: Minimum Match 0%  Maximum Match 100%  Listing first 45 summaries	SPTREMBL_21:*  1: Sp_archea:* 2: Sp_bacteria:* 3: Sp_fung1:* 4: Sp_human:* 5: Sp_nammal:* 7: Sp_mammal:* 7: Sp_mammal:* 8: Sp_organelle:* 9: Sp_phage:* 10: Sp_plant:* 11: Sp_rodent:* 12: Sp_virus:* 13: Sp_virus:* 14: Sp_unclassified:* 15: Sp_archeap:* 17: Sp_archeap:* 17: Sp_archeap:* 17: Sp_archeap:* 18: the number of results predicted by changes than or equal to the score of the resuerthan or equal to the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of scor	4 04 N AN A

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us-09-763-902b-7.rspt

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98 PNSVHVVETFDAQPVPSD-DKENPNILITATGKVTYKTTSQHQFFLLVKDPT-NSNL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative nuclear transport factor similar to nuclear transport factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A. Scyenerce and Anallysis of Chromosome 2 of Dictyostellum."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AC115613; AAM10776.1; -2D45B1B20021B298 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 FOVNMLDCOPVHEGATGSGTVLVVTSGTVKFDGNKQHFFNQ-NFLLTAQSTPNNTVWKI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKINSIDCOQTY-----QPGIMITVTGTLIIDGEAK---NQLKFVQVFNLASNNGSFLL 117
                                                                                                                                                                                                                                                                                                                                                                                                                        8 KTYVDQACRAAEEEV-NIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 KKIVETITPRAEVFIKEFYYPKYDSSRADLIGLYKDHSVSIWNGTECKGPEHIGKLLAEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSSEFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNTV
                                                                                                                                                                               Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.0%; Score 150; DB 5; Length 12.
29.4%; Pred. No. 6.8e-08;
Live 22; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gloeckner G., Eichinger L., Szafranski K., Pachebat J.,
                            01-JDN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 19, Kba protein
Dictyostellum discoideum (Silme mold).
Eukaryota: Mycetozoa; Dictyostellium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (NTF2) from.
Dictyostellum discoideum (Slime mold).
Eukaryota: Mycetozoa: Dictyostellida: Dictyostellum
                                                                                                                                                                                                                                                                                                                                                      21.8%; Score 163.5; DB 5; 31.0%; Pred. No. 3.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                            68;
 167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 AA
                                                                                                                                                                                                                                                                                                                                                                                          18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JUN-2002 (TrEMBLrel, 21, Created)
-JUN-2002 (TrEMBLrel, 21, Last seq
-JUN-2002 (TrEMBLrel, 21, Last ann
PRT;
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Best Local Similarity 31.0%
Matches 40; Conservative
PRELIMINARY;
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Best Local Similarity
Matches 37; Conserv
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                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                 CBI_TaxID-44689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-44689;
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68 LDAQPSGEHG----GILVLVTGALLVDEEKN---PMNYTQTFQLMPDGAGSYFVLNDVF 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 AEEFYNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLP--SSEFQVNM 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyceteles;
Saccharomycetales; Dipodascaceae; Yarrowia.
NCBI_TaxID=4952;
                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 125;
                                                                                                                                                                                                                                                                                                                                                                                   Espeso E.A., Penalva M.A.;
"Nuclear transport factor 2 from Aspergillus nidulans.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AV038983; AAK71467.1;
InterPro; IPR002075; NTF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "RPH1 gene from Yarrowia lipolytica.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8FC18BDFC597E2F2 CRC64;
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                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.0%; Score 127.5; DB 3; 29.8%; Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Cordero Otero R.R., Lepingle A., Gaillardin C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rojas Quijano R., Lepingle A., Gaillardin C.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ
EMBL; AF260231; AAF70316.1; -
                                                                                                                                     125 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 AA
                                                                                                                                                                                                                                                                    Emericella nidulans (Aspergillus nidulans).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.8%; Pred. no.
tive 21; Mismatches
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                                                                                                                                                                         Created)
                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13871 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13696 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 15, C
(TrEMBLrel. 15, I
(TrEMBLrel. 21, I
                                                                                                                                                                     01-DEC-2001 (TEMBLE: 19, 01-DEC-2001 (TEMBLE: 19, 01-MAR-2002 (TEMBLE: 20, Nuclear transport factor 2.
                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002075; NTF2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02136; NTF2; SEQUENCE 125 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002075;
Pfam; PF02136; NTF2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
hes 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5072;
130 ASDCFR 135
                                    118 INDFFR 123
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01-JUN-2002
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Matches
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Q9P8H0
                                                                                            RESULT 4
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Annatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E., Annatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E., Annatides P.G., Scherer S.E., It P.W., Hoskins R.A., Galle R.E., Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Ann K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G., Man K.H., Doyle C., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S., Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davlake P., A., Deny I.B., Davlake P., Dew I., Dietz S.M., Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Ferriac C., Ferriacs P., Pleischmann W., A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dokson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., A. Glodek A., Gong F., Gorrell J.H., Gu Z., Kenison J.A., Ketchum K.A., Houston K.A., Howland T.J., Wei M.-H., Ibeeywam C., Alany Y., Lin X., Liu X., Matteil B., McIntosh T.C., Mravitz S., Kulp D., Lai Z., Liang Y., Lin X., Liu X., Matteil B., McIntosh T.C., Mravitz S., Kulp D., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.R., Melson D.R., Nelson D.R., Nelson D.R., Nelson D.R., Pattman G.S., Pan S., Pollard J., Puri V., Rese M., Sher E., Spradling A.C., Stapleton M., Stung R., Shen H., Ralist R., Tector C., Turner R., Vencer E., Wang A.H., Williams R.Y., Tector C., Turner R., Wenner E., Wang A.H., Williams R.Y., Maristock G., Milliams R.Y., Stapleton M., Stung R., Stong R., Stong R., Stong R., Mariston R., Mariston R., Weiller R., Wang Z., Wang Z., Wang Z., Wang R., Mariston R., Waller R., Wang Z., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 HAKISQVDAQATLGNGVVVQVT-GELSNDGQPMRRFTQTFVLAAQSPKK---YYVHNDIF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---- OPVHEQATOSOTTVLVVTSGTVKFDGNKOHFFNONFLLTAOSTPNNTVWKIASDCF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 EFVRQYYTLLNKAPNHLHRFYNHNSSYIHGESKLVVGQREIHNRIQ------QLNFNDC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFVNIYYETMDKRRRALTRLYLDKATLI-WNGNAVSGLDALNNFFDTLPSSEFQVNMLDC 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ye J., Yeh R.-F., Zaverl J.S., Zhan M., Zhang G., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S
Glibbs R.A., Myers E.W., Rublu G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 113; DB 5;
; Pred. No. 0.004;
14; Mismatches 55,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9NH72 PRELIMINARY; PRT;
Q9NH72;
01-OCT-2000 (TrEMBLrel. 15, Created)
                                                     4EDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000504; RNA_rec_mot
Pfam; PF02136; NTF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        688 AA; 74713 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.1%;
31.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MBL; AE003701; AAG22151.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS50102; RRM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 287:2185-2195(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0015778;
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ID 09
AC 05
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"Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC
clone:P0415A04.";
                                                                                                                                                                                                                                    55 VGLPFGQVRHKISDIDAQPASAQGGD----VIVLVTGELCVDGDNPLPYGQVFHL----I 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 Q--VNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHF-FNQNFLLTAQSTPNNT-VW 127
                                                                                                                                                                                                          64 DTLPSSE--FQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQST 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 RHAVCTVDCOP----TPSFPGGILVFVSGNLQLAGEEHQLRFSQMF----QLVPNEQGSF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SLDFKTYVDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFF 63
                                                                                                                                                     2 SVDFNT -----LAKQFCEFYYQTFDTDRSQLGNLYRDHSMLTFTGTQHQGAQAIVEKL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 DQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Embryophyta; Tracheophyta;
                                                     17;
  Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.0%; Score 120; DB.10; Length 146; 30.5%; Pred. No. 0.0001; tive 18; Mismatches 59; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Trach
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                     57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP003345; BAB90110.1; -.
SEQUENCE 146 AA; 15796 MW; 496BE9A02E1E9670 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last sequence update)
Last annotation update)
Query Match 16.2%; Score 121.5; DB 3; Best Local Similarity 27.6%; Pred. No. 5:9e-05; Matches 37; Conservative 23; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putative nuclear transport factor 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                       |::::|||
107 PDGSSYXVENDIFR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=39947
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RIN OR CG9412
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Length 688;

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STRAIN-BERKELEY;
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01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
Q9LPY0
  SSEPPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----QPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNTVWKIASDCF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota: Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidea; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 HAKISQVDAQATLGNGVVVOVT-GELSNDGQPMRRFTQTFVLAAQSPKK---YYVHNDIF 127
                                                                Nasporinio (19412.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 EFVNIYYETMDKRRRALTRLYLDKATLI-WNGNAVSGLDALNNFFDTLPSSEFQVNMLDC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 EFVRQYYTLLNKAPNHLHRFYNHNSSYIHGESKLVVGGREIHNRIQ------QLNFNDC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M.D. &Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chan L.X., Sutton G.G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.
                                                                                                                                                                                                                                                                             Pazaman C., Mayes C.A., Fanto M., Haynes S.R., Mlodzik M.; "Rasputin, the Drosophila homolog of the RasGaP SH3 binding protein, functions in Ras and Rho mediated signaling."; Development 127:1715-1725(2000).
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B., Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Buttis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.1%; Score 113; DB 5; Length 690; 31.5%; Pred. No. 0.004; tive 14; Mismatches 55; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74985 MW; 40C5BD7E9F5FA253 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CG9412 protein (LD31194P):
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                            MEDLINE-20191744; PubMed-10725247;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      PR002075; NTF2.
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PROSITE; PS50102; RRM;
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Matches 39; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

A bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

A bothin K.J., Evagelista C.C., Ferraz C., Ferrac S., Fleischmann W.,

A clodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,

A harris N.L., Harrey D., Heanan T.J., Hernandez J.R., Houck J.,

A Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

A Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

A Liu X., Mattei B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

A Liu X., Mattei B. McIntosh T.C., McLeod M.P., Mosherson D.,

A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

A Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,

A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

She Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

A Wang Z.-Y., Wassarman D.A., Weinschock G.M., Weissenbach D.,

Wang Z.-Y., Wassarman D.A., Weinschock G.M., Weissenbach D.,

Wang Z.-Y., Wassarman D.A., Weinschock G.M., Weissenbach D.,

Wang Z.-Y., Wassarman D.A., Weinschock G.M., Weissenbach D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.M., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stableton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungail C.J., Nunco J., Pacleb J., Paragas V., Perr S., Phouanenavong S., Wan I Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AEO03701; AAL138465.1;
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31.5%; Pred. No. 0.004;
tive 14; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74943 MW; 40C5AC6F9F4EB353 CRC64;
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01-00T-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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InterPro; IPR00504; NN_rec_mot
Pfam; PF02116; NTF2; 1.
Pfam; PF00076; rrm; 1.
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Conservative 1
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Matches 39; Conserv
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13527 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL66888.1;
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SEQUENCE 122 AA;
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        SEQUENCE FROM N.A.
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117 FR 118
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eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                   Genomic sequence for Arabidopsis thaliana BAC T23J18 from chromosome
                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thallana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic sequence for Arabidopsis thaliana BAC F17L21 from chromosome
                                                                  Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Wukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                18 AEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQ--VNM 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J. Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
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                                                                                                                                                                                             Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases EMBL; AC011661; ARF16635.1; -. HSSP; P13662; 10UN: InterPro; IPR002075; NTF2.
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Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                       76 LDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHF-FNQNFLL 116
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14.4%; Score 107.5; E
Best Local Similarity 29.4%; Pred. No. 0.011
Matches 30; Conservative 17; Mismatches
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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OCC...
OX...
OX...
OX...
OX...
SQ. ODR
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khar S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Nguyen M., Karlin-Neumann G., Southwick A., Carninci P., Chen H.,

Chalm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,

Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai

Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Ecker J., Theologis A., Davis R.W.;

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,

Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kaniya A., Kawin

Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Ecker J., Theologis A., Davis R.W.;

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 AEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQVNM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 122;
                                                                                                                                                                                                                                                                                                                                                Theologis A., Ecker J.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E7CDD9486631A1D2 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.0%; Score 105; DB 10;
29.5%; Pred. No. 0.003;
Live 20; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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<u>ن</u>

; Tracheophyta; eudicots; Rosidae;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.

SEQUENCE FROM N.A

NCBI\_TaxID=3702;

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Abril J.F., Agbayani A., An H.-J., Andrews-Frankocon C., Baldwin D., An Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., An Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., An Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I., An Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., An Cherry J.M., Cawley S., Dahlke C., Davense M., Dagan-Rocha S., Dukov B.C., Dunn P., An Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., R. Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K., Goldek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Kanison J.A., Ketchum K.A. Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A. Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A. Jalali M., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Lai Y., Levitsky A.A., Li J., Li Z., Lidang Y., Lin X., Levitsky A.M., Murphy B., Murphy L., Muzny D.M., Nelson D.E., RA Nelson D.R., Nelson K.A., Niwon K., Nusskern D.R., Parler K., Remington K.A., Niwon K., Nusskern D.R., Parler K., Sanders R.D., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Shen H., Spier E., Spradling A.C., Stapleton M., Strong R., Sun R., Shen S., Poll S., Wang Z.-Y., Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --VNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNTVWKIA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 RVITTVDSQPT-----SDGGVLIIVLGRLKCDDDPPHAFSQIFLL----KPNGGSLFVA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 KEFVQQYYAIFDDPANRENVINFYNATDSFMTFEGNQIQGAPKI---LEKVQSLSFQKIA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 EEFVNIYYETMD---KRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQ--- 72
              Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y. H.C., Blazel R.G., Champe M., Pfeiffer B.D. Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G Abril J.F., Agbayanl A., An H.-J., Andrews-Prennkoch C., Baldwhin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.7%; Score 102.5; DB 5; Length 130; 26.5%; Pred. No. 0.0059; ive 19; Mismatches 57; Indels 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14582 MW; 39286FBC5BD7C34E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TIEMBLrel. 13, Created)
1-MAY-2000 (TIEMBLrel. 13, Last sequence update)
01-UNY-2002 (TIEMBLrel. 21, Last annotation update)
Putative RNA-binding protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T1B9.8.
Arabidopsis thaliana (Mouse-ear cress)
MEDLINE=20196006; PubMed=10731132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lyBase; FBgn0032680; CG10174.
nterPro; IPR002075; NTF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 287:2185-2195(2000)
EMBL; AE003659; AAF53669.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 26.5%
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02136; NTF2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 SDCFRFQDWSSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 HDIFRLNIHNSA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE
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09SEV5
1D 09SEV
DC 01-MA
DT 01-MA
DT 01-JU
DE 01-JU
DE T1B9
OS Arabi
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338 SVKITSVISQDSLKQ-GILVVVVKGYLIFNERPARHFIQVFFL----VPQEKGYIVCIDMF 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 MLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNONFLLTAQSTPNNTVWKIASDCF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 EEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFF----DTLPSSEFQVN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                       STRAIN=CV. COLUMBIA;
Lin X., Raul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujil C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thallana chromosome III BAC 11B9 genomic sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC012395; AAF20221.1;
                                                                                                                                                                                                                                                                                                                                                                                         12.8%; Score 96; DB 10; Length 946; 28.2%; Pred. No. 0.35; tive 15; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hembry C.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                        RM; 2.
105623 MW; AD4CD94A16D8A4FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59730 MW; 7C3169BFA71C312F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.6%; Score 94; DB 5; 25.0%; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-99069613; Pubmed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z68879; CAA93082.1;
InterPro; IPR002075; NTF2.
InterPro; IPR000504; RNA_rec_mot
                                                                                                                                                                                                                                          InterPro; IPR002075; NTF2.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF02136; NTF2: 1
Pfam; PF00076; rrm; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21, KO8F4.2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nvestigating biology."; clence 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                      35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fam; PF02136; NTF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00360; RRM; 1. PROSITE; PS50102; RRM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                      SMART; SM00360; RRM; 2
PROSITE; PS50102; RRM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             946 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 RFQD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393 RFVD 396
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Q21351
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                                                                                         96 AAEQVGGAFCHQFYITVSENRKAITKFYGHESKFYLDDQVVTGSQEIVKLYNHLPETTHF 155
                                                                                                                                           72 QVNMLDCQPV-HEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNTVWKIA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; permatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; irosids II; Brassicales; Brassicaceae; Arabidopsis.
    20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Etgu P., Lee J.M., Lenz C., Pham P., ung M., Goldsmith A., Liu A., Smith A., rooks S., Buehler E., Chao Q., Conn L., Johnson-Hopson C., Khan S., Kim C., Lam B. Im C.J., Shinn P., Southwick A., Davis R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the sequence of BAC F21F23 from Arabidopsis thaliana chromosome 1.", 
ubmitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                            17 AAEE----FVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLP-SSEF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 428;
    48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heologis A.;
ubmitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5-2001) to the EMBL/GenBank/DDBJ databases
; AAF81299.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46803 MW; AA862197FE87C68D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score '90.5; DB 10;
; Pred. No. 0.47;
25; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F., Johnson-Hopson C.,
Palm C.J., Shinn P.
                                                                                                                                                                                                                                                                                                                                                                                                               428 AA.
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .16 protein (Atlg13730/F21F23_12)
                                                                                                                                                                                          156 KIQSIKGYPTPHKQG-----VIINVIGTVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rabidopsis thaliana (Mouse-ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.18;
24.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -OCT-2000 (TrEMBLrel. 15, OCT-2000 (TrEMBLrel. 15, JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s cDNA clones."
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hansen N.F
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Matches 30; Conserv
                                                                                                                                                                                                                                                                  131 SDCFRFQD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQUENCE FROM N.A
32;
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Matches
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--- AVSGLDALNNFFDTLPSSEFQVNM 75

21 FVNIYYETMDKRRRALTRLYLDKATLIWNGN-

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76 LDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNTVWKIASDCFR 135
4, 2003, 15:02:44
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Job time : 11.7284 secs
                                                                                                      136 F 136
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36 LTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQVNMLD------CQPVHEQATQS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 ATINVEAPTSGGYIPDG---FSFNNWFLLTNSSTFVSGRFVTNQPLLINCLWPVPS 315
                                                                                                                                                                                                                                                                                                                                                                                                      89 QTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQST-----PN-----NTVWKIAS 131
                                                                                                                                                                                                                                                                      41; Indels 29;
                                                                                                                                                                                                                       Score 71.5; DB 5; Length 748; Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
URRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US91/08525
FILING DATE: 19911114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Application PC/TUS9108525
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTR: 21P; 19406-2799
COMPUTER READABLE FORM: 4VPE; Floppy disk
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 27.0%;
Matches 31; Conservative 1
                    TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                          : 748 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           King of Prussia
                                                                                                                                                         , MOLECULE TYPE: protein
PCT-US91-08525-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 QTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQST-----PN-----NTVWKIAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 ATHVFAPTSGGYIPDG---FSFNNWFLLTNSSTFVSGRFVTNOPLLINCLWPVPS 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Recombinant Feline Coronavirus
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Release #1.0, Version #1.25
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Patentin Release #1.0, Version #1.25
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F: 709 Swedeland Road
King of Prussia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.5%; Score 71.5; DE Best Local Similarity 27.0%; Pred. No. 6.3; Matches 31; Conservative 14; Mismatches
                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13 MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: SBC 14532B
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application PC/TUS9108525
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Cor
                                            APPLICATION NUMBER: US/08/392,459
                                                                                                                                                                                                                                                                                               30,954
                                                                                                                                                                                                                                                                                                                                                                     (215) 270-5015
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTI
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211 VILLYSRSSTATWEYSAAYAYOGVSNF-----TYYKLNNTNGLKTYELCED-YEHCTGY 263
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                                                                                                                                       and Methods for Vaccination
                                                                                                                                                                                                   SmithKline Beecham Corporation - Corporate
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US93/04384
FILING DATE: 19930507
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FILING DATE: 13-MAY-1991
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                                                                                                                                                                                                                                 7: 709 Swedeland Road .King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Schreck, Patrica A. REGISTRATION NUMBER: 33,777 REFERENCE/DOCKET NUMBER: SB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION
FILING DATE: 13-MAI-LOS
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/1
APPLICATION NUMBER: 14-N0V-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-1992
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Matches 31; Conservative
                                                                                                                                                                                                                                                                                                    ZIP: 19406-2799
OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                29; Gaps
                                                      36 LTRLYLDKATLIMNGNAVSGLDALNNFFDTLPSSEFQVNMLD-----COPVHEQATGS 88
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                                                                                                                                                       264 ATNVFAPTSGGYIPDG---FSFNNWFLLTNSSTFVSGREVTNOPLLINCLMPVPS 315
                                                                                                                              89 OTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQST-----PN-----NTVWKIAS 131
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                                    Indels
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              Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                               E: SmithKline, Beecham Corporation 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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JRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08525
FILING DATE: 19911114
                                                                                                                                                                                                                                                          Application PC/TUS9108525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
Best Local Similarity 27.0%; Pr
Matches 31; Conservative 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
PCT-US93-04384-4
; Sequence 4, Application PC/TUS9304384
                                                                                                                                                                                                                                                                                           SmithKline Beecham,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Best Local Similarity 27
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INFORMATION FOR SEQ
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Length 748;

NUMBER OF SEQUENCES:

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211 VILLYSRSSTATWEYSAAYAYQGVSNF-----TYYKLNNTNGLKTYELCED-YEHCTGY 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 ATNVFAPTSGGYIPDG -- - FSFNNWFLLTNSSTFVSGRFVTNQPLLINCLWPVPS 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 1454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
TITLE OF INVENTION: Recombinant Feline Coronavirus
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
  YSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 LTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQVNMLD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.5%; Score 71.5; 1
Best Local Similarity 27.0%; Pred. No. 17;
Matches 31; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 QTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQST---
                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-WAY-1991
PRIOR APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY AGENT INFORMATION:
NAME: King, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: SEC 14532B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/613,066 FILING DATE: 14-NOV-1990 ATTORNEY/AGENT INFORMATION:
                    SOFTWARE: Patentin Release #1.0, vurkent APPLICATION DATA:
APPLICATION NUMBER: US/08/392,459
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: US 07/698,927
13-MAY-1991
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APPLICATION NUMBER: US/08/392,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/08392459
Patent No. 6280974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1454 amino acids
                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     King of Prussia
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APPLICATION NUMBER: (
FILING DATE: 14-NOV-1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-392-459-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 748;
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corporate ADDRESSEE: Patents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22, Application US/08392459
Patent No. 6280974
GENERAL INFORMATION:
APPLICANT: SMITKHINE Beecham, Corporation
TITLE OF INVENTION: Recombinant Feline Coronavirus
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 LTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQVNMLD--
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                                                                                                                                                                                                                                                                                   19930507
N.
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US.07/882,171
FILING DATE: 08-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US.07/698,927
FILING DATE: 13-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/613,066 FILING DATE: 14-NOV-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
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                                                            .709 Swedeland Road
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illarity 27.0%;
Conservative 1
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AMINO ACID
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
                                                                            King of Prussia
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APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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Matches 31; Conserva
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                                                                                                                                                 19406-2799
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US-08-392-459-22
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Query Match

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211 VILLYSRSSTATWEYSAAYAYQGVSNF-----TYYKLNNTNGLKTYELCED-YEHCTGY 263
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29; Gaps
                                          36 LTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQVNMLD------CQPVHEQATQS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 AINVFAPISGGYIPDG---FSFNNWFLLINSSTFVSGRFVINOPLLINCLWPVPS 315
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                                                                                                                                                                    264 AINVFAPTSGGYIPDG---FSFNNWFLLTNSSTFVSGRFVINGPLLINCLWPVPS 315
                                                                                                                                      89 QITVLVVTSGTVKFDGNKQHFFNQNFLLTAQST-----PN----NTVWKIAS 131
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  Indels
                                                                                                                                                                                                                                                                                                                      APPLICANT: SmithKline Beecham, Corporation
TITLE OF INVENTION: Recombinant Feline Coronavirus S
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 LTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQVNMLD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
  41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: SmithKline Beecham Corporation: 709 Swedeland Road King of Prussia
  Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US91/08525
FILING DATE: 19911114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/613,066 FILING DATE: 14-NOV-1990 TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,066
                                                                                                                                                                                                                                                                                          Sequence 26, Application PC/TUS9108525 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 2, Application PC/TUS9304384; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: King, William T.
REGISTRATION NUMBER: 30,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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       31;
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       Matches
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                                                                                                                                                                                                                                                                                                                                            Gaps
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GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
TITLE OF INVENTION: Recombinant Feline Coronavirus
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: SmithKline Beecham Corporation: 709 Swedeland Road
King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 71.5; D
Pred. No. 17;
                                                                                                                                                                                                                                                                                               Ouery Match 9.5%; Score 71.5; Digest Local Similarity 27.0%; Pred. No. 17; Matches 31; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US91/08525
FILING DATE: 19911114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/613,066 FILING DATE: 14-NOV-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/698,927 FILING DATE: 13-MAY-1991 RIOR APPLICATION DATA:
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Sequence 22, Application PC/TUS9108525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPES: Floppy disk
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: King, William T. REGISTRATION NUMBER: 30,954
       30,954
                                            TELECOMMUNICATION INFORMATION
TELEPRA: (215) 270-5015
TELEPRA: (215) 270-5090
INFORMATION FOR SEQ ID NO. 26:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                             : 1454 amino acids
amino acid
       REGISTRATION NUMBER: 3(
REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-392-459-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 199111
CLASSIFICATION: 435
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 29; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 AINVFAPTSGGYIPDG---FSFNNWFLLINSSTFVSGRFVINQPLLINCLWPVPS 315
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                                                                 TITLE OF INVENTION: Compositions and Methods for Vaccination TITLE OF INVENTION: Against Coronaviruses NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Methods for Vaccination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 1454;
                                                                                                                                                                      ADDRESSEE: SmithKline Beecham Corporation - Corporate ADDRESSEE: Patents
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
POT/US93/04384
FILING DATE: 19930507
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9.5%; Score 71.5; DE
Best Local Similarity 27.0%; Pred. No. 17;
Matches 31; Conservative 14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,171
FILING DATE: 08-WAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING BAPE: 13-WAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,066
                                                                                                                                                                                                                                                                            ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miller, Timothy J. Rlepfer, Sharon Reed, Albert Paul Jones, Elaine V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: SB
ELECOMMUNICATION INFORMATION:
Miller, Timothy J.
                    Klepfer, Sharon
Reed, Albert Paul
Jones, Elaine V.
                                                                                                                                                                                                               STREET: 709 Swedeland Road CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schreck, Patrica A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1454 amino acids
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; MOLECULE TYPE: protein
PCT-US93-04384-2
                                                                                                                                              CORRESPONDENCE ADDRESS:
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APPLICANT: Jones, El
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SECUENCES:
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SmithKline Beecham Corporation - Corporate
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                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
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Best Local Similarity 27.0%; Pred. No. 17;
Matches 31; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Schreck Patrica A, REGISTRATION NUMBER: 33,777 REPERENCE/DOCKET NUMBER: SBC H85009-1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19930507
CLASSIFICATION: PRIOR APPLICATION DATE: 19930507
PRIOR APPLICATION DATE: 00 07/862,171
FILING DATE: 08 MAX-1992
PRIOR APPLICATION NUMBER: US 07/698,927
FILING DATE: 13 MAX-1991
PRIOR APPLICATION NUMBER: US 07/613,066
FILING DATE: 14 NOV-1990
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                               SUFTRACE.

URRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04384
FILING DATE: 19930507
                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                         3: Patents
709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 8:
                                                                      · King of Prussla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-04384-8
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                                                                                                                    COUNTRY: USA
ZIP: 19406-2799
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Total number

Database

Searched:

Perfect score: Sequence: Scoring table:

OM protein

Run on:

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Sequence 2, Appl.
Sequence 30, Appl.
Sequence 4, Appl.
Sequence 5, Appl.
Sequence 7, Appl.
Sequence 7, Appl.
Sequence 7, Appl.
Sequence 7, Appl.
Sequence 7, Appl.
Sequence 11, Appl.
Sequence 14, Appl.
Sequence 156, Appl.
Sequence 156, Appl.
Sequence 4, Appl.
Sequence 2, Appl.
Sequence 4, Appl.
Sequence 2, Appl.
Sequence 2, Appl.
Sequence 2, Appl.
Sequence 2, Appl.
Sequence 2, Appl.
Sequence 3, Appl.
Sequence 2, Appl.
Sequence 3, Appl.
Sequence 4, Appl.
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Patent No. US20020132753a1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT23

CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEO ID NOS: 1792

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1180

LENGTH: 162
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10 US-09-877-804-4

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10 US-09-829-378-5

9 US-10-076-157-4

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Patent No. US20020132753A1
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Best Local Similarity 100.
Matches 137; Conservative
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ORGANISM: Homo sapiens
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l to the score of the result being printed
of the total score distribution.
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1 MATSLDEKTYVDQACRAAEE.....NNTVWKIASDCFRFQDWSSS 142
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Cgn2_6/ptodata//pubpaa/pcr_nem_ro.pep:

Cgn2_6/ptodata/2/pubpaa/USO6_NEM_PUB.pep:

Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:

Cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:

Cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:

Cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:

Cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:

Cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:

Cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:

Cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:

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2: Cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:

3: Cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:

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            version 5.1.3
- 2003 Compugen Ltd.
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US-09-925-297-787
US-09-854-799-28
US-09-854-799-34
US-09-854-799-34
US-09-854-799-25
US-09-925-301-977
US-09-925-301-977
US-09-946-239-8
US-09-946-239-8
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US-09-815-242-12522
US-10-156-239-11
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                                                                                                   protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                 March 4, 2003, 14:58:57
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Gapop 10.0 , Gapext 0.5
          GenCore
Copyright (c) 1993
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score greater than or equal to
and is derived by analysis of
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Match Length
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--NGNAVSGLDA 58
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TILE OF INVENTION: Prokaryotes
ILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                            59 LNNFFDTLPSSEFQVNMLDCQPVHEQATQSQTTV-LVVTSGTVKF--
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                                              NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5373
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APPLICATION UNDBER: 60/242,578
TILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
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APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
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US-09-815-242-12522
                                                                                                                                    ORGANISM: Staphylococcus aureus
US-09-815-242-5373
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yskind, Judith W:
all, Daniel
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Grant J.
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FILING DATE: 2000-05-2
APPLICATION NUMBER: 60
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30; Conservative
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Matches 30; Conserva
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Best Local S
Matches 30
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CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1181
                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 164;
                                                                                            Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: P1223 CURRENT APPLICATION NUMBER: US/09/764,864 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NVENTION: Identification of Essential Genes in NVENTION: Prokaryotes
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; Pred. No. 9.5e-59;
22; Mismatches 12;
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FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
APPLICATION NUMBER: 60/242,578
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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10020061569A1
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Zyskind, Judith.W.
Wall, Daniel
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Best Local Similarity 75.4%;
Matches 104; Conservative 2
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Grant J.
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19 EEFVNIYYET-----MDKRRRALTRLYL-----DKATLIWNGNAVSGLDALNNFFDF 65
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                                                                                                                                                                                                                     Length 450;
                                                                                                                                                                                                                                                                                                                                      Indels.
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PAIO.
FULE REFERENCE: PAIO.
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-124,270
PRIOR PRIOR DATE: 1999-03-12
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Patent No. US20020115064A1
GENERAL INFORMATION:
APPLICANT: SMITHKIINE Beecham, Corporation
TITLE OF INVENTION: Recombinant Feline Coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                :||| :|| | ::| | ::| | 1.5 | 106 IPSSLVWRPDIVLYNRADAQP----PGSASTNVVLRHDGAVRWD 145
                                                                                                                                                                                                                                                                                                                                                                                                      ----EFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFD 103
                                                                                                                                                                                                                     Score 78.5; DB 10;
Pred. No. 0.65;
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ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
9.6%; Score 72; DB 1
Best Local Similarity 21.2%; Pred. No. 4.9;
Matches 31; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                  14; Mismatches
         PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 450
TYPE: PRT
ORGANISW: Homo sapiens
US-09-795-693-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 787, Application US/09925297
Patent No. US20020081659A1
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                                                                                                                                                                                                                   10.5%;
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                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens US-09-925-297-787
                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 31; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                      66 LPSS--
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LENGIH: 576
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                                                                                                                                                                                                                                                                                                                                                                                                        ITLE OF INVENTION: NO. US20030036074A1e1 Nucleic Acid Sequences Encoding Human Trans TILE OF INVENTION: ATPASE Molecule, A Human Ubiquitin HydroLase-Like Molecule, A Hu ITLE OF INVENTION: Ubiquitin Conjugating Enzyme-Like Molecule, and Uses Therefor URRENT APPLICATION NUMBER: US/10/156,239

FRENT FILING DATE: 2002-05-24
    --ADKNMOTRIKNKLEDIALIYREFEORIONEFITGEDA 181
                                                                        19 EEFVNIYYET------MDKRRRALTRLYL-----DKATLIWNGNAVSCLDALNNFFDT 65
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TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
TITLE OF INVENTION: 32613, No. US20020068710A1el Human Transporters
FILE REFERENCE: 35800/209292
CURRENT APPLICATION NUMBER: US/09/795,693
CURRENT FILING DATE: 2001-02-28
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                                          59 LINNFFDTLPSSEFQVNMLDCQPVHEQATQSQTTV-LVVTSGTVKF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; DB 9;
0.65;
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29.8%; Pred. No. 0.65
Live 14; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/185,906
FILING DATE: 2000-02-29
APPLICATION NUMBER: 09/809,557
FILING DATE: 2001-03-15
APPLICATION NUMBER: 60/192,018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILING DATE: 2001-03-14
PPLICATION NUMBER: 60/191,790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/795,693
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PPLICATION NUMBER: 09/808,767
                                                                                                                                                                                                                                                                                            Sequence 11, Application US/10156239
Publication No. US20030036074A1
GENERAL INFORMATION:
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FILING DATE: 2000-03-24
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Patent No. US20020068710A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2001-02-28
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Best Local Similarity 29.8%
Matches 31; Conservative
129 DFKKYA-VTPEHLESFI-
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211 VILLYSRSSTATWEYSAAXAYQGVSNF----TYYKLNNTNGLKTYELCED-YEHCTGY 263
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                    41;
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                                                                                                                                                                                                                                                                                                                                                                              %; Score 71.5; DB
%; Pred. No. 7.8;
14; Mismatches
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                                                                                                             REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: SBC 14532B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 QTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQST----
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TITLE OF INVENTION: Recombinant Feline
Proteins
                                 APPLICATION NUMBER: US 07/613,066 FILING DATE: 14-NOV-1990
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                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
08/392,459
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                                                                           ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 27.0%;
Matches 31; Conservative 1
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                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  US-09-854-799-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 748;
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                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 LTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQVNMLD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Mismatches
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/392,459
FILING DATE: «UNKNOWN»
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
                                                                                                                                                                                                               CATION NUMBER: US/09/854,799
G DATE: 14-May-2001
IFICATION: <Unknown>
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Pred. No. 7.
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-854-799-24
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T: 709 Swedeland Road
King of Prussia
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GENERAL INFORMATION:
APPLICANT: SmithKline Beecham,
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                                                                                                       UTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                           CITY: King of Prussia
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Matches 31; Conservation
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INFORMATION FOR SEQ ID NO: 24
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89 QTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQST----
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                                                                                                                               Sequence 26, Application US/09854799 Patent No. US20020115064A1
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IUM TYPE: Floppy disk
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Best Local Similarity 27.09
Matches 31; Conservative
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                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                            89 OTTVLVVTSGTVKFDGNKOHFFNONFLLTAOST-----PN-----NTVWKIAS 131
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SmithKiine Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
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                                                                                                          DB 10;
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REFERENCE/DOCKET NUMBER: SBC 14532B
                                                                                                                                              14; Mismatches
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ilarity 27.0%; Pred. No. 19;
Conservative 14; Mismatches
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APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Recombinant Feline Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/854,799
FILING DATE: 14-May-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                          Score 71.5;
Pred. No. 7.
                           ) MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-854-799-34.
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; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-854-799-22
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Partent No. US20020115064A1
GENEBAL INFORMATION:
APPLICANT: SmithKline Beecham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                      Query Match 9.5%;
Best Local Similarity 27.0%;
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CORRESPONDENCE ADDRESS:
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                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Simi
Matches 31;
                                                                                                                                              31;
                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-09-854-799-22
                                                                                                                                              Matches
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211 VTLLYSRSSTATWEYSAAYAYQGVSNF-----TYYKLNNTNGLKTYELCED-YEHCTGY 263
264 ATNVFAPTSGGYIPDG ---FSFNNWFLLTNSSTFVSGRFVTNQPLLINCLWPVPS 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATNVFAPTSGGYIPDG---FSFNNWFLLTNSSTFVSGRFVTNQPLLINCLWPVPS 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 QTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQST-----PN----NTVWKIAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                     TITLE OF INVENTION: Recombinant Feline Coronavirus S NUMBER OF SPONSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENERGH ANN. Sosen et al. marte of INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 LTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQVNMLD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: King, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: SBC 14532B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 71.5; 1
Pred: No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/854,799
FILING DATE: 14-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acids, Proteir
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/392,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 977, Application US/09925301
Patent No. US20020052308A1
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1 MATSLDFKTYVDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGNAVSGLDALN 60

19; Mismatches

Best Local Similarity Matches 37; Conserva

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Query Match

Score 67.5; Pred. No. 40

; ORGANISM: Streptococcus pneumoniae US-09-815-242-13608

TYPE: PRT

Length 1179;

DB 10;

Indels

669 NSIFIKPELEQLQKEIAEEEASLDSEEVALKTLQDEMARLTESLEAIKSGGEQARIQEGG 728

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114 FLLTAQSTPN----NTVWKIAS---DCFRFQDWSS 141

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CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-301-977
                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 QVNMLDC----QPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNTVW 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 EFVRQYYLLLNQAPDMLHRFYGKNSSYVHGGLDSNGKPADAVYGQKEIHR-----KVM 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 EFVNIYYETMDKRRRALTRLYLDKATLIWNG------NAVSGLDALNNFFDTLPSSEF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TION: Identification of Essential Genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58;
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 68.5; Di
Pred. No. 9.5;
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13608, Application US/09815242 Patent No. US20020061569A1
                                PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILING DATE: 2000-05-23
PPLICATION NUMBER: 60/207,727
ILING DATE: 2000-05-26
PPIECATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-03-21
ER: 60/191,078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prokaryotes
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u, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : :| ||:||
137 -VHNDIFRYQD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 KIASDCFRFQD 138
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
                                                                                                                                                                                                                                                                                 OCATION:
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IITLE OF INVENTION: No. US20020044945Alel Feline Immunodeficiency Virus Nucleotide IITLE OF INVENTION: Polypeptide Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 ILEEKLRACQEVGSTSYKMNML----AQALQQQSQVCQVQQGRGKPQGNNRRPGQSLK 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION: protein encoded by the gag gene of a recombinant vi
INFORMATION: clone constructed from the genomic DNA of a Pallas'
INFORMATION: immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 DFKTYVDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLIWNGN-----AVSGLDALN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NFFDTL-----PSSEFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 498;
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/238,303, US 60/072,927
PRIOR FILING DATE: 1999-01-28, 1998-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411 CFNCGKPGHLARNCRAPRKCNKCGKAGHIATDCWDMO 447
729 LFLAYQQTSQQVEELETLWKLQEEEIDRLSEGDWQA 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.9%; Score 66.5;
21.0%; Pred. No. 17
                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/946,239 CURRENT FILING DATE: 2001-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4, 2003, 15:07:28
                                                                                                               Sequence 8, Application US/09946239
Patent No. US20020044945Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Margaret C.
                                                                                                                                                                                                                                          FILE REFERENCE: 18617.005
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 17
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: March
Job time : 5.39909 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 FFN---
                                                                                                                                                                                                                                                                                                                                                                                              498
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US-09-946-239-8
                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
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; Search time 21.187 Seconds
(without alignments)
1559.740 Million cell updates/sec
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1 MSVSLPLTVMVRERDWIGIH......LRQLRQPRSAQAVAPQPCGC 248
                                                                                                                                                                                                                                                                                                                                                                                             908470
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                 908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
                                                                                                                          March 4, 2003, 14:50:41
                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                          US-09-763-902B-8
                                                                                                                                                                                                        Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                          Scoring table:
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Database :

12: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*

13: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:\*

14: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:\*

15: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:\*

16: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:\*

17: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:\*

18: /SIDS2/gcgdata/geneseqy-embl/AA1996.DAT:\*

19: /SIDS2/gcgdata/geneseqy-embl/AA1999.DAT:\*

20: /SIDS2/gcgdata/geneseqp-embl/AA1999.DAT:\*

21: /SIDS2/gcgdata/geneseqy-embl/AA2000.DAT:\*

22: /SIDS2/gcgdata/geneseqy-embl/AA2000.DAT:\*

23: /SIDS2/gcgdata/geneseqy-embl/AA2000.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human protein trans Novel signal trans Novel signal trans GRab4 amino acid s rRab4b amino acid s Human Rab4b protei Drosophila melanog Amino acid sequenc Amino acid sequenc Human ORFX ORF2487
ID	AAY8224 AAU17547 AAB17127 AAB23762 AAB23763 AAB23761 AAB19164 AAB19166 AAB19166
0.00	2222222222
. % Query Match Length DB	222 222 213 213 213 213 215 215
. & Query Match	00000 00000 00000 00000 00000 00000 0000
Score	1280 1147 1147 1070 1065 1064 828 710 645.5
Result No.	10848901

## ALIGNMENTS

RESULT 1

antiasthmatic; lmmunosuppressant; antiarteriosclerotic; antidiabetic; antilipaemic; antirheumatic; osteopathic; dermatological; antianaemic; antipsoriatic; hepatotropic; antigout; transport regulator; cancer; a disorder; secretory disorder; protein transport molecule; PTAM; diagnosis; cytostatic; Guegler. KJ; vesicle trafficking; asthma; Human protein transport molecule (PTAM) SEQ ID NO:8. Corley NC, Tang YT, Lal P, Bandman O, Yue H, Gorgone GA, Baughn MR, Patterson C; AAY82324 standard; Protein; 248 AA. autoimmune haemolytic anaemia 98US-0098206. 99WO-US19616 19-JUN-2000 (first entry) flammatory; antiHIV; (INCY-) INCYTE PHARM INC WO200012703-A2 26-AUG-1999; 27-AUG-1998; Homo sapiens 09-MAR-2000. urticaria; AAY82324; AAY8232

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oytostatic, antialititic, antialitimatic, immunosuppressant, antialititic, antialititic, antialititic, antialitic, and antialitic, and antialitic, and antialitic, and antialitic, and antialitic, and antialitic, and antialitic, and antialitic, and antialitic, and antialitic, and antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, and antialitic, antialitic, and antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antialitic, antiali
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                                                                                                 New human protein transport-associated polypeptide and polynucleotide useful for diagnosis, prevention and treatment of cell proliferative and secretory disorders such as leukemia, cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAGQERFRSVTRSYYRGAAGAL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLDPEREVTFLEASRFAQENEL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSGIQYGDASLRQLRQPRSAQA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                           transport-associated
                                                                                                                                                                                                                                                                                               molecules (PTAMS) given in AAY82317 to AAY82324. The PTAMS have cytostatic, antiarthritic, antiasthmatic, immunosuppressant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1280; DB 21; Length 248; 100.0%; Pred. No. 8.5e-133; 1ve 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel signal transduction pathway protein, Seg ID 1112.
                                                                                                                                                                                                                                                                     AAA08035 to AAA08042 encode the human protein
                                                                                                                                                                                                               Claim 1; Page 68-69; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     547
AAU17547 Standard; Protein; 222 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 248; Conservative
                       WPI; 2000-256642/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 VAPQPCGC 248
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                                                N-PSDB; AAA08042
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We require transplant rejection, infective, infective disorder; sicked in an auto-degenerative disorder; Altheirant's disorder; sicked in an auto-degenerative disorder; Altheirant's disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked interval disorder; sicked i
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Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders

Ruben SM;

Rosen CA, Barash SC,

WPI; 2001-465460/50. N-PSDB; AAS27464.

(HUMA-) HUMAN GENOME SCI INC

200105-0259678 2000US-0254097

08-DEC-2000; 11-DEC-2000; 05-JAN-2001;

2000US-0251868 2000US-0251869

08-DEC-2000; 08-DEC-2000; 08-DEC-2000;

Claim 1; SEQ ID No 1112; 880pp; English

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-OCT-2000
-OCT-2000
-OCT-2000
-OCT-2000
-OCT-2000
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                                                                                     NOV-200
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The invention relates to novel isolated polypeptides (I), and diagnosing, preventing and treating diseases including immune system diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune transplant rejections and graft versus host disease, infectious diseases transplant rejections and graft versus host disease, infectious diseases c.g. of hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood related disorders (slockle cell anaemia), myeloproliferative disorders (e.g. daucher's disease, parkinson's disease), chromosomal abnormalities (bown syndrome), ischaemic injury (e.g. stroke), renal abnormalities (bown syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (nicasase), reproductive system disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of disorder (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17089-AAU1883 represent novel signal transduction cylenthy protein, amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 VGGKTVKLQİWDTAGQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLAS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNIVVILCGNKKDLDPEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLPVGIPDFGSIWSDFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SLPVGIPDFGSIHSDFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVN 60
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIDSGELDPERMGSGIQYGDASLRQLRQPRSAQAVAPQPCGC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 KIDSGELDPERMGSGIQYGDASLRQLRQPRSAQAVAPQPCGC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU17127 standard; Protein; 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 222; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU17127;
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07-NOV-2001

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Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antilnflammatory; anti-HIV; antibacterial; antilnflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C: blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardlovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS; acquired immune deficiency syndrome.
Novel signal transduction pathway protein, Seq ID 692.
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Homo sapiens.

2000US-0179065. 2000US-0180628. 2000US-0184664. 

7-NOV-'2000;

08-NOV-2000;

-NOV-2000

7-NOV-7

7-NOV-2000

08-NOV-2000

NOV-

08-NOV-2000

- VON - 80

NOV-2

08-NOV-2

-NOV-2000 08-NOV-2000 08-NOV-2000 08-NOV-2000 08-NOV-2000

08-NOV-200

-0CT-200C

WO200154733-A1

02-AUG-2001

17-JAN-2001; 2001WO-US01312

02-OCT-2000

2000US-025039

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The invention relates to novel isolated polypeptides (I), and display to (I) are useful for displayingleotides (II). (II) and the antibody to (I) are useful for displayingling including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune clasorders (e.g. congenital and acquired immunodeficiencies, autoimmune trajections and graft versus host diseases. Infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood related disorders (sickle cell anaemia), myeloproliferative disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. Guorber's disease, Parkinson's disease), chromosomal abnormalities (bown syndrome), ischaemic injury (e.g. stroke), renal alsorders (e.g. globertlonephitis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. arrhythmia), respiratory disorders, (alsorders (cirhosis), liver disorders (cirhosis), as stimulators of B-cell responsiveness to pathogens; activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies eg acquired immune deficiency syndrome (AlDS). AAU17089 appresent novel signal transduction pathone, and sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                      polypeptides useful for diagnosing, treating, preventing and/or saing disorders related to the proteins, including cancers, immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.6%; Score 1147; DB 22;
100.0%; Pred. No. 3.7e-118;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 692; 880pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders and neuronal disorders
                                                                                                                                                                                                                                                                                          Ruben SM;
                                                                                                                                                                                                                                               (HUMA-) HUMÀN GENOME SCI INC
                                                                                                       000US-0251868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 89.6
Best Local Similarity 100.
Matches 222; Conservative
                                                                                                                                                                                                                                                                                          Barash SC,
                                                                                                                                                                                                                                                                                                                             WPI; 2001-465460/50
                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS27044
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                               prognosing
                                                                                                                                                                                                                                                                                          Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                        Novel
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The present invention describes a novel human gene nucleotide sequence and protein designated Rab4b. The human Rab4b protein sequence shows homology with the protein sequences dRab4 and rRab4b (AAB23762 and AAB23763, respectively). The present sequence represents the dRab4 amino acid sequence given in the present invention.

Sequence

Novel human protein and coded sequence, preparation method and use

98CN-0125320 98CN-0125320

dRab4 amino acid sequence

12-JAN-2001

Human; Rab4b; Rab4 Unidentified

CN1257124-A.

21-JUN-2000

Example 2; Fig 1; 22pp; Chinese.

Zhang H, Tu Q;

Yu L,

UYFU-) UNIV FUDAN.

11-DEC-1998;

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41 DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTA 100
                                                                                                                                             6 DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTA 65
                                                                                                                                                                                                                      161 DPEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGS
   Length 213;
                                    Indels
83.6%; Score 1070; DB 21;
llarity 100.0%; Pred. No. 1.1e-109;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                221 GIOYGDASLROLROPRSAQAVAPQPCGC 248
                                                                                                                                                                                                                                                                                                                     186 GIQYGDASLRQLRQPRSAQAVAPQPCGC 213
                                                                                                                                                                                                                                                                                                                                                                                                                               AAB23763 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rRab4b amino acid sequence
                   Best Local Similarity
Matches 208; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human;
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
AAB23763
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87 VGGKTVKLQIWDTAGQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLAS 146 PNIVVILGENKEDLDPEREVIFLEASRFAGENELMFLETSALTGENVEEAFLKCARTILN 206 

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147

64

RESULT 4 AAB23762 ID AAB23762 standard; Protein; 213 AA.

SLPVGIPDFGSIWSDFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVN 86 4 SLPVGIPDFGSIWSDFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVN 63

27

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CN1257124-A

Wed Mar

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The invention relates to an isolated nucleic acid detection reagent. capable of detecting 1000 or more genes from Drosophila. The invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                         42 FLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIMDTAG 101
                                                                                                                                                                                                                                                                                                                                                                                        102 QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEREVIFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
                                                                                                        The present invention describes a novel human gene nucleotide sequence and protein designated Rab4b. The human Rab4b protein sequence shows homology with the protein sequence alkab4 and rab4b. (AAB23762 and AAB23763, respectively). The present sequence represents human Rab4b.
                                                                                                                                                                                                                                                                                                                                     use
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                                    and
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                                                                                                                                                                                                                                       213;
                                  preparation method
                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                    83.1%; Score 1064; DB 21;
llarity 100.0%; Pred. No. 5e-109;
Conservative 0; Mismatches 0;
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                                    Novel human protein and coded sequence,
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                                                                    Claim 4; Page 17; 22pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB61094 standard; Protein; 213
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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N-PSDB; ABL05197.
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                                                                                                                                                                                                                                                   Similarity
N-PSDB; AAA92348
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                                                                                                                                                                                                                                                          Best Local Sim
Matches 207;
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                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127
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2×4×2×20000×3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                   AAB23763, respectively). The present sequence represents the rRab4b amino acid sequence given in the present invention.
                                                                                                                                                                                                                                                                                                                  nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFLFFFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIMDTA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
                                                                                                                                                                                                                                                                                             The present invention describes a novel human gene nucleotide sequence and protein designated Rab4b. The human Rab4b protein sequence shows AAB23763, respectively) The procent negatives of the protein sequences of the protein sequences.
                                                                                                                                                                                                                                         Novel human protein and coded sequence, preparation method and use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPEREVIFLEASRFAGENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1065; DB 21;
Pred. No. 3.9e-109;
0; Mismatches .1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Rab4b protein sequence SEQ ID NO:4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 GIQYGDISLRQLRQPRSAQAVAPQPCGC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein; 213
                                                                                                                                                                                                                                                                            Example 2; Fig 1; 22pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.2%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98CN-0125320
                                                 98CN-0125320
                                                                                       98CN-0125320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                               L, Zhang H, Tu Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-565932/53
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                                                                                                                         (UYFU-) UNIV FUDAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 207; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        213 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Rab4b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang
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                                                   11-DEC-1998;
                                                                                       11-DEC-1998;
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               21-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Wed Mar

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. and useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGIT6-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511). ABB57737-ABB72072) 8888888888888

213 AA; Sequence

41 DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTA 100 Gaps : ~ Length 213; Indels 64.7%; Score 828; DB 22; 77.4%; Pred. No. 6e-83; Live 22; Mismatches 23; Conservative Similarity Query Match Best Local Simi Matches 161; g ò

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DPEREVTFLEASRFAQENELMFLETSALTGENVEBAFLKCARTILNKIDSGELDPERMGS, 220 161

221 GIQYGDASLRQLRQPRSAQAVAPQPCGC 248

186 GIQYGGAALRNL-QTRQRSINKPD-CTC 211

RESULT 8 AAB19164

AAB19164 standard, Protein; 143 AAB19164;

Amino acid sequence of human RAB4B. 19-FEB-2001 (first entry)

RAB protein; GTPase; GTP binding; gene therapy; cancer

Homo sapiens

NO200058464-A2

05-OCT-2000

13-MAR-2000; 2000WO-US06330

·990S-0126083 25-MAR-1999;

(AXYS-) AXYS PHARM INC

useful for mammalian RAB protein Novel Isolated nucleic acid encoding a mammalian RAB prote: identifying homologous or related genes, in producing compo modulates expression or function of RAB for cancer therapy WPI; 2000-647233/62. N-PSDB; AAA96886

Buckler AJ;

Rutter M,

Vega R;

Abel K, McIntosh B,

Allen M,

composition that

English Claim 2; Page 38; 58pp; The present sequence represents a mammalian RAB protein. RAB proteins constitute the largest family of small GTPasses, with over 40 identified isoforms. RAB proteins contain four highly conserved peptide sequences involved in GTP binding and hydrolysis. Compositions comprising RAB nucleic acid are useful for identifying homologous or related genes,

In producing compositions that modulate the expression or function of RAB, for gene therapy, mapping functional regions of the protein and in studying associated physicalogical pathways. In addition, modulation of the gene activity in vivo is used for prophylactic and therapeutic purposes, such as treatment of cancer, and identification of cell type based on expression. The DNA may also be used to identify expression of the gene in a biological specimen. 25555555**x**8

143 AA; Sequence

Gaps ö Length 143; Indels ö 55.5%; Score 710; DB 21; 100.0%; Pred. No. 3.7e-70; 1ve 0; Mismatches 0; Query Match Best Local Similarity 100. Matches 138; Conservative

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DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTA 9 Ġ

101 GOERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160 99 ο. qq

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RESULT 9 AAB19166

AAB19166 standard; Protein; 215 AA.

AAB19166;

(first entry) .9-FEB-2001

Amino acid sequence of human RAB14.

GTP binding; gene

Homo sapiens

WO200058464-A2.

13-MAR-2000; 2000WO-US06330.

99US-0126083 25-MAR-1999;

(AXYS-) AXYS PHARM INC

Buckler AJ; Rutter M, Vega R, Abel K, . McIntosh B, Allen M, 

2000-647233/62. N-PSDB; AAA96888

for identifying homologous or related genes, in producing composition that modulates expression or function of RAB for cancer therapy useful Novel isolated nucleic acid encoding a mammalian RAB protein

Claim 2; Page 41; 58pp; English.

The present sequence represents a mammalian RAB protein. RAB proteins constitute the largest family of small GTPases, with over 40 identified isoforms. RAB proteins contain four highly conserved peptide sequences involved in GTP binding and hydrolysis. Compositions comprising RAB nucleic acid are useful for identifying homologous or related genes, in producing compositions that modulate the expression or function of RAB, for gene therapy, mapping functional regions of the protein and in studying associated physiological pathways. In addition, modulation of the gene activity in vivo is used for prophylactic and therapeutic purposes, such as treatment of cancer, and identification of cell type based on expression. The DNA may also be used to identify expression of

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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthitis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wond;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, open reading frame, ORFX, detection, cytostatic, hepatotropic, vulnerary, antipsoriatic, antiparkinsonian; nootropic, neuroprotective, anticonvulsant, osteopathic, antiarthritic, immunosuppressant, cardiant;
                                                                                                                                                                                             162 PEREVIFLEASRFAGENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
                                                                                     Indels 11; Gaps
                                                                                                                    42 FLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAG 101
                                                                                                                                                                           QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             damage; cartilage damage; antiinflammatory disease; coagulation
                                                                                                                                      10 YIFKYIIIGDMGVGKSCLLHQFTEKKFMADCPHTIGVEFGTRIIEVSGQKIKLQIMDTAG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyrold;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and peptides derived from open reading frame X,
                                                          DB 21; Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ig e.g. cancers, proliferative disord
disorders and cardlovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ORFX ORF2487 polypeptide sequence SEQ ID NO:4974.
                                                       . 50.4%; Score 645.5; DB 21; Ilarity 58.0%; Pred. No. 8.9e-63; Conservative 33; Mismatches 45;
                                                                                                                                                                                                                                                                                              222 IQYGDASLRQLRQPRSAQAVA-PQP----CGC 248
                                                                                                                                                                                                                                                                                                                190 VQHKPSA-----PQGGRLTSEPQPQREGCGC 215
                                                                                                                                                                                                                                                                                                                                                                                                AAB42723 standard; Protein; 215 AA
the gene in a biological specimen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombosis; contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-602362/57.
N-PSDB; AAC76932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for treating
                                                                   Best Local Similarity
Matches 123; Conserv
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                              215 AA;
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                              Sequence
                                                             Ouery Match
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AAB42723
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which represent the munical such as cytostatic, hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiparkinsonian; nootropic; neuroprotective; costeopathic; antiparkinsonian; nootropic; neuroprotective; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic, hypotensive; dermatological; immunosuppressive; antidiabetic, hypotensive; dermatological; immunosuppressive; antidiamatory; antibacterial; antivaria; antithrematic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoinmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal heamoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 FLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWILDARTLASPNIVVILCGNKKDLD 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21; Length 215;
                                                                 AAC74446 to AAC77606 encode the proteins given in AAB40237 to which represent the human ORFX open reading frames 1 to 3161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.4%; Score 645.5; DB 2 58.0%; Pred. No. 8.9e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQYGDASLRQLRQPRSAQAVA-PQP----CGC 248
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Claim 11; Page 4147; 5507pp; English
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Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 AA;
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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immune system disorder; rheumatoid arthritis; inflammatory condition;

Yamamoto J;

Saito K, Y, Otsuki T;

Hayashi K, S A, Nagai K,

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the 5602 mucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to a sequence and an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a oligonucleotide comprises a 1 least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in a gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers also when the proteins encoded by the full-length cDNAs. The primers also when the proteins encoded by the full-length cDNAs. The primers also when the full-length cDNAs allowed the abonc while the full-length cDNAs are present human cDNA sequences; AMB92446 to AMB95893 represent human and sequences; and AAH13612 to AAH13612 represent clause and sequences; and AAH13612 to AAH13612 represent clause and sequences; and AAH13612 to AAH13612 represent clause and sequences; and AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13612 to AAH13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-length coRhs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; SEQ ID 15588; 2537pp + CD ROM; English.
                                                                                             T, Isogai T, Nishikawa T,
Ii S, Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the present invention
                              (HELI-) HELIX RES INST.
                                                                                                                                                                                                      WPI; 2001-318749/34;
                                                                                                                                                                                                                                                                                                                                                                                              full-length cDNAs
                                                                                                                                   Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                 ota.
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Ä Sequence

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102 QERFRSVTRSYYRGAGGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161
                                                                                                                                                                         162 PEREVIFLEASRFAGENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
                                                          42 FLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAG 101
                              Gaps
                                                                          11;
 DB 22; Length 215;
                              45; Indels
50.4%; Score 645.5; DB 2
58.0%; Pred. No. 8.9e-63;
iive 33; Mismatches 45
                                                                                                                                                                                                                                 222 IQYGDASLRQLRQPRSAQAVA-PQP----CGC 248
                                                                                                                                                                                                                                                  190 VQHKPSA-----PQGGRLTSEPQPQREGCGC 215
                              Conservative
              Best Local Similarity
Matches 123; Conserv
Query Match
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AAU17535 standard; Protein; 307 AA.
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Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;

Novel signal transduction pathway protein, Seq ID 1100.

07-NOV-2001 (first entry)

AAU17535;

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organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; isotaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS;
                                                                       reproductive system; gastrointestina acquired immune deficiency syndrome.
                                                                                                                                      WO200154733-A1
                                                                                                                                                                                       17-JAN-2001;
                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                17-MAR-2000;
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Ruben SM

Rosen CA, Barash SC, WPI; 2001-465460/50. N-PSDB; AAS27452.

(HUMA-) HUMAN GENOME SCI INC

11-DEC-2000; 2000US-0254097 05-JAN-2001; 2001US-0259678

2000US-0251856

08-DEC-2000; 08-DEC-2000;

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17-NOV-2000;
17-NOV-2000;
                13-0CT-2000)
20-0CT-2000)
20-0CT-2000)
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-OCT-200
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01-NOV-20
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08-NOV-20
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08-NOV-2
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The invention relates to novel isolated polypeptides (I), and polynucleotides (II). (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood-related disorders (sickle cell anaemia), myeloproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Addison's disease), reproductive system disorders, gastrointestinal disorder (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of r-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-AAU17683 represent novel signal transduction pathway protein, amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                              Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders, primary haematopoletic disorders, hyperproliferative disorders (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders, in wound healing, epithelial cell proliferation, endocrine disorders (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 50.4%; Score 645.5; DB 22; Length 307; Best Local Similarity 58.0%; Pred. No. 1.5e-62; Matches 123; Conservative 33; Mismatches 45; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 1100; 880pp; English.
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162 QERFRAVTRSYYRGAAGALMVYDITRRSTYNHLSSWLTDARNLINPNTVIILIGNKADLE 221

162 PEREVIFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221

222 AORDVIYEEAKOFAEENGLLFLEASAKTGENVEDAFLEAAKKIYONIODGSLDLNAAESG 281

AAB58445 standard; Protein; 312

(first entry

14-MAR-2001

AAB58445; RESULT 13
AAB58445
ID AAB58.
XX
AC AAB58
XX.
DT 14-MA

102 QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161

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42 FLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAG 101

11; Gaps

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cardioactive; immunomodulatory; muscular active; vulnerary; asstrointestinal, nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease.
                                 neuroprotective; cytostatic;
                                                                                                                                                                                                                                                                       Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of diso such as lung cancer
          Lung cancer associated polypeptide sequence SEQ ID 783.
                                                                                                                                                                                                                                                                                                            Claim 11; Page 1315-1316; 1425pp; English.
                                cancer associated protein;
                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC. (ROSE/). ROSEN C A.
                                                                                                                                                    08-MAR-2000; 2000WO-US05918.
                                                                                                                                                                        99US-0124270
                                                                                                                                                                                                                                         2000-587514/55.
                                                                                                                                                                                                                                                   N-PSDB; AAF18321
                                                                                                             WQ200055180-A2
                                                                                                                                                                        12-MAR-1999;
                                                                                        Homo sapiens
                                                                                                                                 21-SEP-2000,
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numerous other
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Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; and immunomodulatory muscular active general; vulnerary; gastrointestinal general; nephrotropic; antilnfective; gynecological; or antibacterial active fitty. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat
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                                                                  42 FLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAG 101
                                                                                                      102 QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161
                                                                                                                                                          PEREVIFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
                              Gaps
 DB 21; Length 312;
                           45;
             1.5e-62,
                        Conservative 33; Mismatches
 50.4%; Score 645.5; 58.0%; Pred. No. 1.5
            Similarity
             Best Local Sim
Matches 123;
Query Match
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312 AA;

Sequence

IQYGDASLRQLRQPRSAQAVA-PQP----CGC 248

222 287

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-POGGRLISEPOPOREGCGC 312

VOHKPSA

189 GVOHRPS--OPSRISLSSEATGAKDOCSC 215

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 GQERFRAVTRSYYRGAAGALMVYDITRRSTYNHLSSWLTDTRNLTNPSTVIFLIGNKSDL 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nsecticides, therapeutics and pharmaceutical drugs. The invention itschoses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 6444; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              discloses genomic DNA sequences (ABL16176-ABL30511), essequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 6444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myers EW;
                       ABB59884 standard; Protein; 215 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                          pharmaceutical
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11-JUL-2000;
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                                                                                  ABB59884;
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ABB5988
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capponishe for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and to produce other types of the invention.

Solidanostic amino acid sequences of the invention.

Solidanostic amino acid sequences of the invention.

Solidanostic and sequences of the invention format directly from WIPO expecification.
                                                                                                                                                                                                                                                                                                                                                                                                  Human, chromosome mapping, gene mapping, gene therapy, forensic;
food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.1%; Score 615.5; DB 22; Length 174; 79.7%; Pred. No. 1.3e-59; ive 10; Mismatches 16; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              claim 20; SEQ ID No 49724; 103pp; English
                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #19356:
                                                                             ABG19365 standard; Protein; 174 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                       18-FEB-2002 (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73.
N-PSDB; AAS83552.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                              ABG19365;
RESULT 15
ABG19365
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96 IWDTAGQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLIDARTLASPNIVVILCG 155

Conservative

Matches 122;

8 . ⋩

Gaps

NKKDLDPEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDP 215

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87 NKKOLDADREVIFLEASRFAQENELMFLETSALIGENVEEAFVQCARKILNKIES---- 141
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216 ERMGSGIQYGDASLRQLRQPRSAQAVAPQPCGC 248 -142 ERMGSGIQYGDAALRQLRSPRRAQAPNAQECGC 174 οχ

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4, 2003, 14:58:50 Search completed: March Job time: 23.3298 secs

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RESULT 1
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                      - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*
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No.
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GTP-binding protei	GTP-binding protei	GTP-binding protei	GTP-binding protei	GTP-binding protei	GTP-binding protei	GTP-binding protei	GTP-binding protei	GTP-binding protei	hypothetical prote	GTP-binding protei		GTP-binding protei		GTP-binding protei	GTP-binding protei	
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449	448	447	447	445	443.5	443	443	443	442.5	442	441	439	439	437.5	436	
30	31	32	33	34	32	36	37	38	39	40	. 41	42	43	44	. 45	
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# ALIGNMENTS

GTP-binding protein rab4b - dog C;Species: Canis lupus familiaris (dog) C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 02-Feb-2001 C;Accession: F36364: S15603
Richavier, P.; Vingron, M.; Sander, C.; Simons, K.; Zerial, M. Mol. Cell. Biol. 10, 6578-6585, 1990 A;Title: Molecular cloning of YPTI/SEC4-related cDNAs from an epithelial cell line. A;Reference number: A36364; MUID:91061765; PMID:2123294
A; Accession: F36364 A; Status: preliminary A; Molecule type: mRNA A; Molecule type: mRNA
A, Kesulues: 1.21 Cuffer A, A, Calludes: 1.21 Cuffer A, Calludes: 1.21 Cuffer A, Calludes: 1.21 Cuffer A, Calludes: 1.21 Cuffer A, Calludes: 1.21 Cuffer A, Calludes: 1.21 Cuffer A, Calludes A, Callu
r:121-124/Region: GIF-Dinding NAAD MOLII F;151-153/Region: GTP-binding SAK/L motif F;211,213/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
Query Match 83.6%; Score 1070; DB 2; Length 213; Best Local Similarity 100.0%; Pred. No. 1.4e-86; Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 DFLEKELVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEEGSRVVNVGGKTVKLQIWDTA 100
QY 101 GQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160 
OY 161 DPBREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGS 220 
Oy 221 GIQYGDASLRQLRQPRSAQAVAPQPCGC 248 
RESULT 2 \$58279
orr binding procein rabab rac. No Alternate names: ras homolog GTPase C;Species: Rattus norvegicus (Norway rat) C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 02-Feb-2001
C;Accession: S58279 R;Schuermann, A.; Muehl-Zuerbes, P.; Lie, C.; Joost, H.G.

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tion factor Tu homology nucleotide binding; P-loo
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C.;atts: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C;Accession: T47160
C;Bulm, H; Baudrsachs, S.; Mewes, H.W.; Well, B.; Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIMDTA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 DADREVTFLEASRFAQENELMFLETSALTGENVEEAFWQCARKILNKIESGELDPERMGS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 GOERFRSVIRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 and 4 cDNAs
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                                                  66 GOERFRSVIRSYYRGAAGALLVYDIISREIYNALINWLIDARMLASQNIVIILCGNKKDL
                                                                                                                                                               126 DADREVTFLEASRFAQENELMFLETSALTGEDVEEAFVQCARKILNKIESGELDPERMGS
                                                                                                                              DPEREVIFILEASRFAGENELMFLETSALIGENVEBAFLKCARTILNKIDSGELDPERMGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A. Title: Four additional members of the ras gene superfamily isolated A. Reference number: A39963; MUID:88068563; PMID:3317403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: GTP binding; lipoprotein; membrane trafficking; nucle F; 9-124/Domain: translation elongation factor Tu homology <ETU> F; 15-22/Region: nucleotide-binding motif A (P-loop) F; 121-124/Region: GTP-binding Name outif F; 151-153/Region: GTP-binding SAK/L motif F; 151, 213/Region: GTP-binding SAK/L motif F; 211, 213/Regions GTP-binding SAK/L motif F; 211, 213/Regions GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-ginding GTP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Title: Complete coding sequences of the ras related rab A:Reference number: S01765, MUID:88143997; PMID:3344209
101 GOERFRSVIRSYYRGAAGALLVYDITSRETYNSLAAWLIDARI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X06890
R;Touchor, N.; Chardin, P.; Tavitian, A.
Proc. Natl. Acad. Sci. U.S.A. 84, 8210-8214, 1987
A;Title: Four additional members of the ras gene s
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                                                                                                                                                                                                                                                                                                             186 GIQYGDAALRQLRSPRRTQAPNAQECGC 213
                                                                                                                                                                                                                                                                        248
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                                                                                                                                                                                                                                                                            GIQYGDASLRQLRQPRSAQAVAPQPCGC
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Matches 179; Conservative
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Residues: 44-213 <TOU>
Cross-references: GB:J03001
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A; Residues: 1-213 <ZAH>
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Nucleic Acids Res. 16,
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binding; P-loop;
                                                                                                                                                                                                                                                                        A; Gene: rab4b
C; Superfamily: ras transforming protein; translation elongation factor Tu homology
C; Superfamily: ras transforming protein; translation elongation; P-loop; prenylated cysteine
C; Keywords: GTP binding; lipoprotein; nucleotide binding; P-loop; F:9-124/Domain: translation elongation factor Tu homology <FTU>F:15-22/Region: nucleotide binding motif A (P-loop)
F:15-22/Region: GTP-binding NKXD motif
F:151-153/Region: GTP-binding SAK/L motif
F:211,213/Region: GTP-binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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Date: 29-Jun-1990 #sequence_revision 29-Jun-1990 #text_change 02-Feb-2001
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                                                                                                                                                                      A;Cross-references: EMBL:X78605; NID:g929829; PIDN:CAA55339.1; PID:g929830
C;Genetics:
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Superfamily: ras transforming protein; translation elongation factor Keyvords: GTP binding; lipoprotein; membrane trafficking; nucleotide 19-124/Domain: translation elongation factor Tu homology <ETU>-15-22/Region: nucleotide-binding motif A (P-loop)
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Biol. Chem. 264, 12394-12401, 1989
;Title: The human Rab genes encode a family of GTP-binding
;Reference number: A34323; MUID:89308668; PMID:2501306
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211,213/Binding site: geranyl-geranyl (Cys) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.3%; Score 938; DB 2; I
86.5%; Pred. No. 5.6e-75;
ive 12; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1065; DB 2;
Pred, No. 3.9e-86;
0; Mismatches 1;
submitted to the EMBL Data Library, April 1994
A; Reference number: S58279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIQYGDASLRQLRQPRSAQAVAPQPCGC 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 83.2%;
Best Local Similarity 99.5%;
Matches 207; Conservative
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nes 180; Conservative
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Residues: 1-213 <ZAH>
                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-213 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary
                                                                                                            A; Status: preliminary
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Matches
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43.4%; Score 556;
              222 IQYGDASLRQLRQPRSAQAVA-PQP
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:Residues: 1-213 <FAB>
                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: S36367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 02-Feb-2001
C;Accession: E42148
R;Elferink, L.A.; Anzal, K.; Scheller, R.H.
Biol. Chem. 267, 5768-5775, 1992
A;Title: rabl5, a novel low molecular weight GTP-binding protein specifically expressed A;Reference number: A42148; MUD:92210533; PMID:1313420
A;Accession: E42148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: ras transforming protein; translation elongation factor Tu homology C; Keywords: GTP binding; lipoprotein; nuclectide binding; P-loop; prenylated cysteine F;12-17/Domain: translation elongation factor Tu homology <FTU>; F12-127/Domain: translation elongation factor Tu homology <FTU>; F18-25/Region: nuclectide-binding maxif A (P-loop) F;124-127/Region: GTP-binding NRXD motif F;154-156/Region: GTP-binding SAK/L motif F;213,215/Binding site: geranyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                              Tu homology
                                  A.Accession: T47160
A.Status: preliminary
A.Molecule type: mnA
A.Residues: 1-215 <AAA
A.Cross references: EMBL:AL162081
A.Experimental source: adult melanoma (MeWo cell line); clone DKFZp762K0911
A.Rote: DKFZp762K0911.1
C.Superfamily: ras transforming protein; translation elongation factor Tu hc
F;12-127/Domain: translation elongation factor Tu hc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 QERFRAVTRSYYRGAGALMYYDITRRSTYNHLSSWLTDARNLTNPNTVIILIGNKADLE 129
                                                                                                                                                                                                                                                                                                                                                                                                     FLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 PEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 YIFKYIIIGDMGVGKSCLLHQFTEKKFWADCPHTIGVEFGTRIIEVSGQKIKLQIWDTAG 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161
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                                                                                                                                                                                                                                                                                                       Ouery Match

So.4%; Score 645.5; DB 2; Length 215;
Best Local Similarity 58.0%; Pred. No. 2.8e-49;
Matches 123; Conservative 33; Mismatches 45; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
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submitted to the Protein Sequence Database, March 2000 A; Reference number: 224379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 50.0%; Score 640.5; DB 2; Best Local Similarity 58.0%; Pred. No. 7.7e-49; Matches 123; Conservative 32; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQYGDASLRQLRQPRSAQAVA-PQP----CGC 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-215 <ELF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
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A;Introns: 36/1; 117/3; 157/2
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-210 <WIL>
A;Cross-references: EMBL:279601; PIDN:CAB01884.1; GSPDB:GN00028; CESP:K09A9.2
A;Experimental source: clone K09A9
                                                                                                                   hypothetical protein K09A9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T23530
R;Swinburne, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTP-binding protein yptV4 - Volvox carteri
C;Species: Volvox carteri
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 PEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
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R; Fabry, S.; Jacobsen, A.; Huber, H.; Palme, K.; Schmitt, R.
Curr. Genet. 24, 229-240, 1993
A; Title: Structure, expression, and phylogenetic relationships
A; Reference number: S36365; MUID:94037148; PMID:821932
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47.3%; Score 606; DB 2; I
Best Local Similarity 55.1%; Pred. No. 8.1e-46;
Matches 114; Conservative 32; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                            R)Swinburne, J.
submitted to the EMBL Data Library, August 1996
A;Reference number: 219753
A;Accession: 172530
A;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;59-66/Region: GTP binding #status predicted
F;116-123/Region: GTP binding #status predicted
F;145-151/Region: GTP binding #status predicted
190 VQHKPSA-----PQGGRLTSEPQPQREGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 IQYGDASLRQLRQPRSAQAVAPQPCGC 248
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C;Superfamily: ras transforming protein; translation elongation factor Tu homology C;Reywords: GTP binding; membrane trafficking; nucleotide binding; P-loop F;7-122/Domain: translation elongation factor Tu homology <FTU>
                                                                                                                                                                                                                                                 Cross-references: EMBL:U46925; NID:g1184982; PIDN:AAA87883.1; PID:g1184983; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 199; Bevan, M.; Rose, M.; Hempel, S.; Entlan, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, ubmitted to the Protein Sequence Database, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; translation elongation factor Tu homology
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Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Feb-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 AHKRAVSKEEGQOFAKEHGLLFLEASARTAQNVEEAFIETAAKILQNIODGVFDVSNESS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GOERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-Dec-1996 #sequence_revision 27-Feb-1997 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 DYLFKYIIIGDIGVGKSCILLQFTDKRFQPVHDLTIGVEFGARMVTVDGRPIKLQIMDTA 63
                                    C; Accession: S71585; T04696; S71233
C; Accession: S71585; T04696; S71233
B; Blermann, B.; Randall, S.K.; Crowell, D.N.
Blant Mol. Biol. 31, 1021-1028, 1996
A; Title: Identification and isoprenylation of plant GTP-binding proteins.
A; Reference number: S71584; MUID: 97000914; PMID: 8843944
A; Reference number: S71585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 211;
                                                                                                                                                                                  Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Keywords: GTP binding; nucleotide binding; P-loop
F;7-122/Domain: translation elongation factor Tu homology <FTU>F;13-20/Region: nucleotide-binding motif A (P-loop)
F;119-122/Region: GTP-binding NRXD motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Experimental source: cultivar Columbia; BAC clone F4B14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uery match
43.0%; Score 550; DB 2;
Best Local Similarity 58.4%; Pred. No. 6.7e-41;
Matches 108; Conservative 29; Mismatches 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        February, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL:X77795; PIDN:CAA54822.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yptm3 - maize
ras-like protein yptm3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 4
A;Introns: 16/1; 62/3; 90/2; 158/3; 181/3
A;Note: F4B14.130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ross-references: EMBL:AL031986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ras transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Data
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                                                                                                                                                                                                                                                                                                                                                                       Reference number: 215380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-210 <DIE>
                                                                                                                                                                                                                         Molecule type: mRNA
Residues: 1-211 <BIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1-211 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: T04362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T04362
                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIQYG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIKIG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Diefenthal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene: ATGB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N; Alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT, 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  원
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R; Dietmaier, W.; Fabry, S.; Huber, H.; Schmitt, R.
Gene 158, 41-50, 1995
A; Title: Analysis of a family of ypt genes and their products from Chlamydomonas reinhan A; Reference number: JC4105; MUID: 95309723; PMID: 7789809
A; Accession: JC4106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         introns: 4/1, 16/2; 62/3; 90/1; 124/3; 158/3; 181/3; introns: 4/1; 16/2; 62/3; 90/1; 124/3; translation elongation factor Tu homology; supportamily: ras transforming protein; translation elongically membrane trafficking; nucleotide binding; P-loop; 7-122/Domain: translation elongation factor Tu homology <FTU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: membrane vesicle transport protein yptC4; ras-like yptC4 protein; sma
C;Species: Chlamydomonas reinhardtii
C;Date: 21-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB:U13167; NID:9806721; PIDN:AAA82726.1; PID:9806722
C; Comment: This protein plays an essential role in the regulation of intracellular membi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 FLEKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLIDARTLASPNIVVILCGNKKDLD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65. QESFRSITRSYYRGAAGALLVYDITRRETENHLASWLEDARQHANPNWTIMLIGNKCDLT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 PEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  predicted
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                                                                                                                                                                                                                                                                                                                                       65 QESFRSITRSYYRGAAGALLVYDITRRETFNHLASWLEDARQHANPNMTIMLIGNRCDLT 124
                                                                                                                                                                                                                                                                                                          221
                                                                                                                                                                                                       102 QERFRSVTŖSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161
                                                                                                      FLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAG 101
                                                       Gaps
                                                                                                                                                     5 YLFKYIIIGDTGVGKSCLLLQFTDKRFQPVHDLTIGVEFGARMINIDGKQIKLQIWDTAG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 PEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG
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13-43/Domain: effector #stætus predicted <EFF>
119-122/Region: GTP-binding NKXD motif
122,213/Binding site: geranyl-geranyl (Cys) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 213;
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                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rab2 protein homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 556; 'DB 2; Lu
Pred. No. 2e-41;
7; Mismatches 49;
                                                         49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTP-binding protein GB2 - Arabidopsis thaliana N.Alternate names: protein F4B14.130; rab2 proteit C.Species: Arabidopsis thaliana (mouse-ear cress)
                                  2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27; Mismatches
                                  Pred. No. 2e-4
7; Mismatches

    Chlamydomonas

                  58.78; ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.48; 58.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 58.7
Matches 108; Conservative
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
JC4106
GTP-binding protein yptC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-213 <DIE>
                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IQYG 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 IKVG 188
                                                                                                                                                                                                                                                                                                                                                                                                                        1QYG 225
                                                                 datches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;7-122/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: yptC4
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rab2 proteins isolated from Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homology
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GTP-binding protein rab2 - dog
GTP-binding protein rab2 - dog
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Accession: A39648; I36364
R;Chavrier, P.; Parton, R.G.; Hauri, H.P.; Simons, K.; Zerial, M.
Cell 62, 317-329, 1990
A;Tille: Localization of low molecular weight GTP binding proteins to exocyt A;Reference number: A39648; MUID:90322428; PMID:2115402
                                                                                                                                                                                                                                               C;Species: Zea mays (maize)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Residues: 1-209 <LAU>
Cross-references: EMBL:U22432; NID:g722325; PIDN:AAA63901.1; PID:g722326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: ras transforming protein; translation elongation factor Tu C; Keywords: GTP binding; membrane trafficking; nucleotide binding; P-loop 77, 1122/Domain: translation elongation factor Tu homology <ETU>F;13-20/Region: nucleotide-binding motif A (P-loop) F;119-122/Region: GTP-binding NKXD motif F;119-151/Region: GTP-binding SAK/L motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QESFRSITRSYYRGAAGALLVYDITRRETFNHLASWLEDARQHANANWTIMLVGNKCDLS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 PEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 FLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIMDTAG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
SRREVKKEEGEAFAREHGLMFMETSAKTASNVEEAFINTAKEIYEKIQEGVFDINNEANG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Molecular cloning of YPTI/SEC4-related cDNAs from an epithelial A;Reference number: A36364; MUID:91061765; PMID:2123294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NID:g164053; PIDN:AAA30888.1; PID:g164054
ander, C.; Simons, K.; Zerial, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
42.2%; Score 540; DB 2;
Best Local Similarity 56.5%; Pred. No. 5e-40;
Matches 104; Conservative 30; Mismatches 5
                                                                                                                                                                                                                                                                                          C.Accession: T02242
R.Laughner, B.J.; Ferl, R.J.; Almira, E.C.
submitted to the EMBL Data Library, March 1995
A.Description: Homologs of mammalian binding GTP
                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: T02242
Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Chavrier, P.; Vingron, M.; Sander,
Mol. Cell. Biol. 10, 6578-6585, 1990
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                                                                                                                                                                                                                                                                                                                                                                                          Reference number: 214636
                                                                                                                                                                                                                        GTP-binding protein rab2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -212 <CHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 IKVG 188
                                                                                                185 IKIG 188
                                                  IQYG 225
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R;Zahraoui, A.; Touchot, N.; Chardin, P.; Tavitian, A.
T. Biol. Chem. 264, 12394-12401, 1989
A;Title: The human Rab genes encode a family of GTP-binding proteins related to yeast YE
A;Reference number: A34323; MUID:89308668; PMID:2501306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 4p15.31-4p15.31
C; Superfamily: ras transforming protein; translation elongation factor Tu homology
C; Superfamily: ras transforming protein; membrane trafficking; nucleotide binding; P-loop;
C; Keywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop;
F; 7-122, Domain: translation elongation factor Tu homology <ETU>
F; 13-20/Region: nucleotide-binding motif A (P-loop)
F; 119-122/Region: GTP-binding NKXD motif
F; 149-151/Region: GTP-binding SAK/L motif
F; 211, 212/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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ssidues: 1-212 <ZAH>
coss-references: GB:J04941; GB:M28213; NID:g550061; PIDN:AAA60241.1; PID:g550062
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C;Date: 29-Jun-1990 #sequence_revision 29-Jun-1990 #text_change 02-Feb-2001
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                                                                                                                                                                                                      seldues: 1-143,'1',145-212 <TAC>
ross-references: EMBL:X12953; NID:g35836; PIDN:CAA31411.1; PID:g35837
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elc Acids Res. 16, 10388, 1988
tle: Nucleotide sequence of a new YPT1-related human
iference number: S01910; MUID:89057482; PMID:3057444
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                                                                         ; Score 544; DB 2;
; Pred. No. 2.3e-40;
30; Mismatches 50
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       GTP-binding NKXD motif GTP-binding SAK/L motif
                                                                            42.5%;
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Best Local Similarity 57.08
Matches 106; Conservative
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     F;119-122/Region:
F;149-151/Region:
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F; 13-20/Region: nucleotide binding motif A (P-loop)
F; 119-122/Region: GTP-binding NXXD motif
F; 149-151/Region: GTP-binding SAK/L motif
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A;Description: RABZ nucleotide sequence in Gallus gallus and its phylogenetic position.
A;Reference number: S52325
                                                                                              C;Superfamily: ras transforming protein; translation elongation factor Tu homology C;Keywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop; F;7-122/Domain: translation elongation factor Tu homology <ETU>F;13-20/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oecies: Gallus gallus (chicken)
ite: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;149-151/Region: GTP-binding SAK/L motif
F;211,212/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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F.149-151/Region: GTP-binding SAK/L motif
F.211,212/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                Score 539; DB 2; Length 212;
Pred. No. 6.3e-40;
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42.1%; Score 539; DB 2;
Best Local Similarity 56.0%; Pred. No. 6.3e-40;
Matches 103; Conservative 30; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                           30; Mismatches
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A; Molecule type: mRNA
A; Residues: 1-38, 'M', 40-212 <CHW>
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Best Local Similarity 56.09
Matches 103; Conservative
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A; Molecule type: mRNA
A; Residues: 1-212 <MON>
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Title: US-09-763-902B-8
Perfect score: 1280
Sequence: 1 MSVSLPLTVMVRERDWIGIH.....LRQLRQPRSAQAVAPQPCGC 248

Run on:

Scoring table: BLOSUM62 Gapext 0.5.

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Description	P22750 homo sapien	P51146 rattus norv	P56371 mus musculu	P20338 homo sapien	rattu	P35287 homo sapten	P36410 dictyostell	_	-	хеа ш	P08886 homo sapten		Q01971 oryctolagus	Q05975 lymnaea sta	P05712 rattus norv			₹*	OJ.	2129 disc	E	· Q15907 homo sapien	Q39434 beta vulgar	P24410 homo sapien	Q9jlx1 mus musculu					P01123 saccharomyc	33	520 nicotla	P31584 VOLVOX CAFE
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SUMMARIES		. A	RB4B_HUMAN	RB4B_RAT	RB4A_MOUSE	RB4A_HUMAN	RB4A_RAT	RB14_HUMAN	RAB4_DICDI	YPT4_CHLRE	YPT4_VOLCA	RB2A_MAIZE	RAB2_HUMAN	RAB2_MOUSE	RAB2_RABIT	RAB2_LYMST	RAB2_RAT	RB2B_MAIZE	YE1B_SCHPO	RAB2_DICDI	YP31_YEAST	R11B_DISOM	R11B_MOUSE	R11B_HUMAN	RAB2_BETVU	R11A_HUMAN	R11A_MOUSE	RIIA_LOTJA	R11D_TOBAC	YPT6_CHLRE	RB1A_ARATH	YPT1_YEAST	R11C_LOTJA	1	I PITT VOLCA
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Ιď	(Rel. 40, Last annotatio
E S	elated protein Rab-4B.
Z (	
S C	Homo sapiens (Human), and Canis familiaris (Dog)
8	vota; Metazo
8	Primates; Catarrhini; Hominidae;
XO	NCBI_TaxID=9606, 9615;
 N C	(I)
R. D.	LUMAN:
RA	., Xu S., Gu W., Wang Y.,
RŢ	pressed in hematopoletic stem/progenit
RI	astic syndromes patient.";
2 2	tollitted (Job-1999) to the EmblyGenbank/Dubby databases.
X X 0	GENTENDE PROM N.A.
S.	SPECIES-C familiaris; STRAIN-Cocker spaniel;
XX.	
RA	., Simons K., Zerial M.;
RT	lar cloning of YPT1/SEC4-related cD1
RŢ	line.";
RI.	
ပ္ပ (	-1- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
ع د	
ខ	SIMILARIII: 10 MAS FROIBINS, BELONGS 10 ING NAD
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ပ္ပ	between the Swiss Institute of Bioinformatics and the EMBL outstation -
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ပ္ပ	s a license agreement (See http://www.isb-si
ខ្ល	to license@
DR.	; AF165522; AA
DR	, X56389; CA
2 2	PIR; F36364; F36364. HSSD: D36017: 1FKO
<u>ر</u> ۾	HGNC:97
D. S.	10; IPR003579;
D.	
Ž, E	InterPro) IPROUD2225; Small_GTP.
ăă	PRINTS; PR00449; RASTRNSFRMNG.
DR	'n.
K D	TIGKFAMS; TIGKUUZ31; SMBII_GTP; I. GTD-binding: Tinonrotein: Prenylation: Protein transport
딢	15 22 GTP (BY SIMILARITY
EL G	é3

0C3D76DC328B0018 CRC64;

.23629 MW;

213 AA;

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the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
modified and this statement is not removed. Usage by and for commerc
                                                                                                                                                                                              DFLFKFLVIGSAGTGKSCLLHQF1ENKFKQDSNHT1GVEFGSRVVNVGGKTVKLQ1WDTA 100
                                                                                                                  Gaps
                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus,
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schuermann A., Muehl-Zuerbes P., Lie C., Joost H.G.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GFP (BY SIMILARITY).
GFPECTOR REGION (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
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-1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
              EFFECTOR REGION (BY SIMILARITY)
GERANYL-GERANYL, (BY SIMILARITY)
GERANYL-GERANYL (BY SIMILARITY)
OC3D76DC3285DB98 CRC64;
                                                                                      Length 213;
                                                                                                                 Indels
                                                                                    Score 1070; DB 1;
Pred. No. 2.3e-83;
 GTP (BY SIMILARITY)
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                      213 AA.
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                                                                                                                 Mismatches
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InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
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                                                        23587 MW;
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TIGRFAMS; TIGR00231; small_
                                                                                      83.68;
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                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                        213 AA;
                                                                                                   Similarity
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                                                                                                               Matches 208;
                                                        SEQUENCE
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or send an email to license@lsb-sib.ch).
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SUBCELULAR LOCATION: GENERALLY ASSOCIATED WITH MEMBRANES;
CYTOPLASMIC WHEN PHOSPHORYLATED BY CDC2 (BY SIMILARITY).
PTM: PHOSPHORYLATED BY CDC2-KINASE DUBING MITOSIS (BY SIMILARITY).
SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                              DPEREVIFICEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGS 220
                                                                                                                                                                                                                              41 DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGYEFGSRVVNVGGKTVKLQIMDTA 100
                                                                                                                                            101 GQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
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                                       Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ikeda H., Ikegami T., Mitsui T., Senda D., Hayasaka K.; "Isolation and sequence determination of cDNA encoding mouse rab and candidate approach for the beige mutation in mice."; Biochem. Mol. Biol. Int. 40:647-651(1996).
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 Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGREAMS; TIGRO0231; small_GTP; 1.
GTP-binding; Lipoprotein; Prenylation; Protein transport;
Phosphorylation.
                                     1; Indels
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Score 1065; DB 1;
Pred. No. 6.1e-83;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
18-related protein Rab-4A.
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InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
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 83.2%;
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                  al Similarity 99.5
207; Conservative
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 Query Match
Best Local
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NP_BIND
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MEDLINE=91218852; PUBAG-1902553;
Bailly E., McCaffrey M., Touchot N., Zahraoui A., Goud B., Bornens M.;
Phosphorylation of two small GTP-binding proteins of the Rab family
                                                                                                                                                                                        DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTA 100
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                                                                                                                                                          Gaps
                                                                                                                                                                                                        PHOSPHORYLATION BY CDC2.
MEDLINE-93049188; PubMed-1425574;
van der Sluijs P., Hull M., Huber L.A., Male P., Goud B., Mellman "Reversible phosphorylation-dephosphorylation determines the localization of rab4 during the cell cycle.";
EMBO J. 11:4379-4382(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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-1- SUBCELLULAR LOCATION: GENERALLY ASSOCIATED WITH MEMBRANES;
CYTOPLASMIC WHEN PHOSPHORYLATED BY CDC2.

-1- PTM: PHOSPHORYLATED BY CDC2-KINASE DURING MITOSIS.

-1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
              EFFECTOR REGION (BY SIMILARITY)
PHOSPHORYLATION (BY CDC2)
(BY SIMILARITY)
GERANYL-GERANYL (BY SIMILARITY)
GERANYL-GERANYL (BY SIMILARITY)
9FEF188966922AD6 CRC64;
                                                                                                                          Length 213;
                                                                                                                        Score 942; DB 1; Length 21
Pred. No. 1.5e-72;
Mismatches 15; Indels
 (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
Res related protein Rab-4A.
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                                                                                                                                                        13; Mismatches
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                           73.68;
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                                                                                                                                                          Matches . 180; Conservative
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                                                                                         213 AA;
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 121
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199
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P20338;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBL_TaxID=10116;
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                                                                                                                                                                                                                                                                           GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
PHOSPHORYLATION (BY CDC2).
GERANYL-GERANYL (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
W; C4F20489D148FAEI CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 938; DB 1;
Pred. No. 3.2e-72;
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InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1
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SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
                                                                                                                                                  InterPro; IPR003579; GTPase_Rab
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124 G
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199 P
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213 G
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09, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                          73.3%;
86.5%;
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Ras-related protein Rab-4A
                                                                            EMBL; M28211; AAA60244.1;
PIR; E34323; E34323.
HSSP; P36017; 1EK0.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                     Genew; HGNC:9781; RAB4A.
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                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                              213
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01-NOV-1988
01-OCT-1996
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Matches 180;
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NP_BIND
DOMAIN
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RB4A_RAT
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Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X., Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H., Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J., Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M., Huang G.-Y., Chen A.-D., Chen J.-L.; "Gene expression profiling in the human hypothalamus-pituitary-adrenal axis and full-length CDNA cloning."
                       Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-Human; TISSUE-placenta;
ISogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
Akamantau A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                            "Cloning and characterization of human small GTPase Rabl4."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blum H., Bauersachs S., Mewes H.-W., Well B., Wiemann S., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                             Prolkas-Cezanne T., Jenkins J.R.;
"Human Rabl4 cloning and intracellular localization to t
biosynthetic/secretory trafficking pathway.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Elferink L.A., Anzai K., Scheller R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-Human; TISSUE-Adrenal gland; MEDLINE-20402571; PubMed-10931946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SPECIES-Human; TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Melanoma;
                                                                                                                                            SPECIES-Human; TISSUE-Liver;
          sapiens (Human), and
                                                                                 NCBI_TaxID=9606, 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2002)
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                                                                                                                         SEQUENCE FROM N.A.
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                       Usage by and for commercial
                                                                                              GQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 GQERFRSVTTSYYRGAAGALLVYDITSRETYNALTNWLTDARMLASQNIVIILCGNKKDL 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
MEDLINE-88143997; PubMed-3344209; Zahraoui A.; Touchot N., Chardin P., Tavitian A.; Zonbree coding sequences of the ras related rab 3 and 4 cDNAs."; Nucleic Acids Res. 16:1204-1204(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 DFLFKFLVIGNAGTGKSCLLHQFIEKKFKDDSNHTIGVEFGQKIINVGGKYVKLQIMDTA
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

EFFECTOR REGION (BY SIMILARITY).

PHOSPHORYLATION (BY CDC2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GERANYL-GERANYL (BY SIMILARITY)
GERANYL-GERANYL (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR00231; small_GTP; 1.
.ng; Lipoprotein; Prenylation; Protein transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RB14_HUMAN STANDARD; PRT; 215 AA. P35287; Q9U111; Q969L0; 01-FEB-1994 (RE1. '28, Created) 01-FEB-1994 (Rel. '28, Last sequence update) 01-FEB-1994 (Rel. '41, Last annotation update) Ras-related protein Rab-14.
                                                                                                                                                                                                                                                                                                     modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 GIQYGDAALRQLRSPRRTQAPSAQECGC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 GIQYGDASLRQLRQPRSAQAVAPQPCGC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>а</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003579; GTPase_Rab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; PR00449; RASTRNSFRMNG.
SM00175; RAB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .86.18;
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Matches 179; Conservative
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67
124
45
199
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PIR; D39963; D39963.
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152
213 AA;
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37
199
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NP_BIND 15
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NP\_BIND DOMAIN

MOD\_RES

LIPID

NP\_BIND

PRINTS;

RRARA RRARA

SMART;

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                                                                                                                                                                                                                                                                                            "Rabl5, a novel low molecular weight GTP-binding protein specifically expressed in rat brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN WHOLE BRAIN, SPINAL CORD, HEART, KIDNEY AND LUNG.
-1- SIMILARITY: TO RAS PROTEINS, BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 267:5768-5775(1992).
-I- FUNCTION: MAY BE INVOLVED IN VESICULAR TRAFFICKING AND NEUROTRANSMITTER RELEASE.
Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                      SPECIES-Rat; STRAIN-Sprague-Dawley; TISSUE-Brain; MEDLINE-92210533; PubMed-1313420;
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RAB14.

Seppe

RB14\_HUMAN

RESULT 6

161

101

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 GOERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
     discoldeum colocalizes with
s of the contractile vacuole
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-1- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
   "A Rab4-like GFPase in Dictyostellum discoideum colocalizes wi
V-H(+)-ATPases in reticular membranes of the contractile vacuo
complex and in lysosomes.";
J. Cell Sci. 107:2801-2812(1994).
-! - SUBCELLUAR LOCATION: ASSOCIATED WITH THE SPONGIOMES OF
CONTRACTILE VACUOLE COMPLEX.
-! - SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
GERANYL-GERRNYL (BY SIMILARITY).
W; 2BF51383A73724F1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; DB 1; Length 205;
1.2e-45;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
GTP-binding protein YPTC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dietmaier W., Fabry S., Huber H., Schmitt R., "Analygis of a family of ypt genes and their Gene 158:41-50(1995).
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TIGRFAMS; TICR0021; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Interpro; IPR001806; Ras_trnsfrmng
Interpro; IPR005225; Small_GTP.
Pfan; PF00071; ras; 1.
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hes 115;
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Q39570;
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Matches
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YPT4_CHLRE
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   noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

EFFECTOR REGION (BY SIMILARITY).

GERANYL-GERANYL (BY SIMILARITY).

GERANYL-GERANYL (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                Prenylation; Protein transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nolta K., Rodriguez-Paris J., Kaufmann N., Ruscetti T., Temesvari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FIId=VAR_012986.
B435AAC6F562B007 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyostelium discoldeum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 50.4%; Score 645.5; DB 1; Best Local Similarity 58.0%; Pred: No. 1.6e-47; Matches 123; Conservative 33; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Ras-related protein Rab4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 IQYGDASLRQLRQPRSAQAVA-PQP----CGC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 VQHKPSA-----PQGGRLTSEPQPQREGCGC 215
                                    or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                               IPR003579; GTPase_Rab.
IPR001806; Ras_trnsfrmng.
IPR005225; Small_GTP.
0071; ras; 1.
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Bush J.M. IV, Nolta K., Rodriguez
                                                                                                                                                                                                                                                                                                                                                       PR00449; RASTRNSFRMNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23927 MW;
modified and this statement entities requires a license
                                                                           EMBL; AF152463; AAF00150.1;
                                                                                                                                                                                      BC006081; AAH06081.1;
                                                                                                                                AL162081; CAB82414:1
                                                                                                                                                   BAB14598.1
                                                                                                                                                                                                                                                                                                                                                                                                                Lipoprotein;
                                                                                                                                                                                                           AAA41994.1;
                                                                                                                                                                                                                                                                  RAB14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00175; RAB; 1
TIGRFAMS; TIGR00231; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 AA;
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                                                                                                                                                                                                           M83680;
                                                                                                                                                                                                                                                                                                                                                                                                                GTP-binding;
                                                                                                                                                                                                                                                                                                                                      PF0007
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphism
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P36410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-AX3;
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                                                                                                                                                                      EMBL;
EMBL;
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                                                                                                                                    EMBL;
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Gaps

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us-09-763-902b-8.rsp

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-i- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR TRAFFIC (BY SIMILARITY)
-i- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                          EMBL; L08130; AAA34253.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 58.7
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
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213 A
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P49103;
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NP_BIND
DOMAIN
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                                                                   this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bukaryotat Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvocaceae; Volvox.
NCBL_TaxID=3067;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (PROBABLE).
GERNYL-CERRANYL (BY SIMILARITY).
GERANYL-GERRANYL (BY SIMILARITY).
W; CB9B3AAAE4E8BB76 CRC64;
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MEDLINE-94031148; PubMed-8221932;
MEDLINE-94031148; PubMed-8221932;
Fabry S., Jacobsen A., Huber H., Palme K., Schmitt R.;
"Structure, expression, and phylogenetic relationships of a fypt genes encoding small G-proteins in the green alga Volvox
                                       BELONGS TO THE RAB SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.4%; Score 556; DB 1; 58.7%; Pred. No. 5.6e-40; tive 27; Mismatches 49
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01-JUN-1994 (Rel. 29, Last sequence update)
01-EE-1996 (Rel. 33, Last annotation update
GTP-binding protein yptV4 (RAB2 homolog).
                                                                                                                                                                                                                                                                                                                               InterPro; IPR001806; Ras trnsfrmng.
InterPro; IPR005225; Small GTP.
                    TRAFFIC (BY SIMILARITY).
SIMILARITY: TO RAS PROTEINS.
                                                                                                                                                                                                                                                                                                             InterPro; IPR003579; GTPase_Rab
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                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
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65
122
43
212
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213
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TIGRFAMS; TIGR00231; sm
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Best Local Similarity
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P36863;
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YPT4_VOLCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC clade;
Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 FLEKFLVIGSAGTGKSCLLHQFIENKFKQDSNHŢIGVEFGSRVVNVGGKTVKLQIWDTAG 101
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Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
TRAFFIC (BY SIMILARITY).
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (PROBABLE).
GERANYL-GERANYL. (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
W; FFE43AAAE4EBB5E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS; TIGR00231; small_GTP; 1.
GTP-binding; Lipoprotein; Prenylation; Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49; Indels
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01-FEB-1996 (Rel. 33, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
Ras-related protein Rab-2-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 556;
Pred. No. 5
                                                                                                                                                                         or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                  ; IPR001806; Ras_trnsfrmng; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                     PIR; S36367; S36367.
HSSP; P05713; 3RAB.
InterPro; IPR003579; GTPase_Rab.
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65 GT
122 GT
43 EF
212 GE
213
23697 MW;
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SM00175; RAB; 1.
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MIM; 179509;
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                                                                                                                                                                                                                                                                                                                                      SOPRENOID
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NP_BIND
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                   line.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 PEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
SUBCELLULAR LOCATION: ASSOCIATED WITH A STRUCTURE HAVING THE CHARACTERISTICS OF AN INTERMEDIATE COMPARTMENT BETWEEN THE ENDOPLASMIC RETICULUM AND THE GOLGI APPARATUS (BY SIMILARITY). SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-Human;
MEDLINE-89057482; PubMed-3057444;
Tachibana K., Umezawa A.; Kato S., Takano T.;
"Nucleotide sequence of a new YPT1-related human cDNA which belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canis familiaris (Dog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxiD=9606, 9615;
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                                                                                                                                                                                                                                                                                         GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GERECTOR REGION (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                             Length 209;
                                                                                                                                                                                                                                                                              Lipoprotein; Frenylation; Protein transport
                                                                                                                                                                                                                                                                                                                                                                                                                    50; Indels
                                                                                                                                                                                                                                                                                                                                                                                        .42.2%; Score 540; DB 1;
llarity 56.5%; Pred. No. 1.2e-38;
Conservative 30; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
101-NOV-2002 (Rel. 41, Last annotation update)
Ras_related protein Rab-2.
                                                                                                                                                                                       InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                   SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; small_GTP; 1
                                                                                                                                                                                                                                                                                                                                                     208 GE
23001 MW;
                                                                                                                                                                                                                                         PRINTS; PRO0449; RASTRNSFRMNG.
                                                                                                                                                        EMBL; U22432; AAA63901.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                               l; ras; 1.
                                                                                                                                                                     3RAB.
                                                                                                                                                                                                                                                                                                                                                                  209 'AA;
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                MaizeDB; 121973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 IQYG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKVG 188
                                                                                                                                                                                                                            fam; PF0007
                                                                                                                                                                                                                                                                               GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAB2_HUMAN
                                                                                                                                                                                                                                                                                                      NP_BIND
NP_BIND
DOMAIN
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Best Local
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AC PO8865,
DT 01-NOV-
DT 15-UNV-
DT 15-UNV-
DT 15-UNV-
DE RAS-rel
GN RAB2.
GN HOMO 26
CO HOMO 26
CO MAMPAN
CO MAMPAN
RN (1)
RN (1)
RN SECUEN
RN REDLIN
RX MEDLIN
RY TACALLA
RAB2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=C.familaris; STRAIN=Cocker spaniel;
MEDLINE=91061765; PubMed=2123294;
Charrier P., Vingron M., Sander C., Simons K., Zerial M.;
"Molecular cloning of YPT1/SEC4-related cDNAs from an epithelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                               proteins related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Khosravi Far R., Lutz R.J., Cox A.D., Conroy L., Bourne J.R., Sinensky M., Balch W.E., Buss J.E., Der C.J.;
"Isoprenoid modification of rab proteins terminating in CC or CXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRAFFIC (BY SIMILARITY).

-1- SUBCELULAR LOCATION: ASSOCIATED WITH A STRUCTURE HAVING THE CHARACTERISTICS OF AN INTERMEDIATE COMPARAMENT BETWEEN THE ENDOPLASMIC RETICULUM AND THE GOLGI APPARATUS.

-1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
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-I- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SPECIES=C.familiaris;
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Zahraou1 A., Touchot N., Chardin P., Tavitian A.;
The human Rab genes encode a family of GTP-binding prote
to yeast YPTI and SEC4 products involved in secretion.",
J. Biol. Chem. 264:12394:12401(1989).
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EFFECTOR REGION (BY SI
GERANYL-GERANYL.
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to the ras gene superfamily.";
Nucleic Acids Res. 16:10368-10368(1988).
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SM00175; RAB; 1.
Ms; TIGR00231; small_GTP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X12953; CAA31411,1; -.
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PIR; A39648; A39648.
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PIR; B34323; B34323
PIR; I36364; I36364
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NP_BIND
NP_BIND
                                                                     Matches 103;
LIPID
SEQUENCE
                                        Query Match
                                                         Local
                                                                                                                                                                                                                                                                                                                                    RESULT 13
RAB2_RABIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROF entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                          162 PEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
                                                                                                                                                                                                                                  125 SRREVKKEEGGEAFAREHGLIFMETSAKTASNVEEAFINTAKEIYEKIQEGVFDINNEANG 184
                                                                                                     42 FLEKFLVIGSAGTGKSCLLHOFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIMDTAG 101
                                                                                                                                                           102 QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRAFFIC (BY SIMILARITY).

--- SUBCELLULAR LOCATION: ASSOCIATED WITH A STRUCTURE HAVING THE CHARACTERISTICS OF AN INTERMEDIATE COMPARTMENT BETWEEN THE ENDOPLASMIC RETICULUM AND THE GOLGI APPARATUS.

--- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostómi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .i- FUNCTION: PROTEIN TRANSPORT, PROBABLY INVOLVED IN VESICULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prenylation; Protein transport.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
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                                                 Score 539; DB 1; Length 212;
Pred. No. 1.5e-38;
0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
        144 144 I -> M (IN REF. 2).
212 AA; 23545 MW; F8731E3F6FB399A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
Ras-related protein Rab-2.
                                                                                                                                                                                                                                                                                                                                                                           212 AA.
                                                                             Conservative 30; Mismatches
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InterPro:#IPR003579; GTPase_Rab.
InterPro: IPR001806; Ras_trnsfrmng.
InterPro: IPR005225; Small_GTP.
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PR00449; RASTRNSFRMNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X95403; CAA64684.1;
                                                        42.1%;
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                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-NIH SWISS;
                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00071
PRINTS; PR004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTP-binding;
                                                                                                                                                                                                                                                                                  222 IQYG 225
                                                                                                                                                                                                                                                                                                             185 IKIG 188
                                                                                                                                                                                                                                                                                                                                                                                   RAB2_MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laufer W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP_BIND
NP_BIND
DOMAIN
                                                                           Best Local Sin
Matches 103;
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                  CONFLICT
                                                            Query Match
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                                                                                                                                                                                                                                         42 FLEKFLVIGSAGTGKSCLLHOFIENKFKODSNHTIGVEFGSRVVNVGGKTVKLQIMDTAG 101
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRAFFIC (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: ASSOCIATED WITH A STRUCTURE HAVING THE CHARACTERISTICS OF AN INTERMEDIATE COMPARTMENT BETWEEN THE ENDOPLASMIC RELICULUM AND THE GOLGIA PAPARATUS.

-1- TISSUE SPECIFICITY: BRAIN AND PARIETAL CELLS.

-1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                  162 PEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92359934; PubMed-1323270; Goldenring J.R.; Tang L.H., Stoch S.A., Modlin I.M., Goldenring J.R.; "identification of rab2 as a tubulovesicle-membrane-associated protein in rabbit gastric parietal cells."; Biochem. J. 285:715-719(1992).
GERANYL-GERANYL (BY SIMILARITY)
58231E3F9EF007A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR00231; small_GTP; 1. ng; Lipoprotein; Protein transport.
                                                               Length 212;
                                                                                                                  51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTP (BY SIMILARITY)
GTP (BY SIMILARITY)
                                                                    ; Score 539; DB 1;
; Pred: No. 1.5e-38;
30; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 25, Last sequence update)
(Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR003579; Grpase_Rab.
Interpro; IPR001806; Ras_trnsfrmng.
Interpro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 25, Created)
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                  212 G
23547 MW;
                                                                               42.1%;
56.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1994 (Rel. 30, Last
Ras-related protein Rab-2.
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                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S23979; S23979.
HSSP; P05713; 3RAB.
                  212
212 AA;
                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993
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001971;
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ÜRRÜKEN KANTEN K

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                                                                                                                                                                                                                                                                                                                           102 QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161
                                                                                                                                                                                                                               42 FLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAG 101
                                                                                                                                                                                                                                                                                                                                                     Lymnaea ștagnalis (Great pond snail).
Eukaryotă; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94039042; PubMed-8223561;
Agterberg M., van Die I., Yang H., Andriessen J.A.,
Van Tetering A., van den Eijnden D.H., Ploegh H.L.;
"Isolation and characterization of three cDNAs coding for Rab proteans from the abbumen gland of the mollusc Lymnaea stagnalis.";
Eur. J. Blochem. 217:241-246(193).
-I- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
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-1- SUBCELLULAR LOCATION: ASSOCIATED WITH A STRUCTURE HAVING THE CHARACTERISTICS OF AN INTERMEDIATE COMPARTMENT BETWEEN THE ENDOPLASMIC RETICULM AND THE GOLG! APPARATUS (BY SIMILARITY).

-1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                       162 PEREVIFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG
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  GTP (BY SIMILARITY).

EFFECTOR REGION (BY SIMILARITY).

GERANYL-GERANYL (BY SIMILARITY).

F$731E3F8B68B9A3 CRC64;
                                                                                                                                            Length 212;
                                                                                                                                                                                        Indels
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                                                                                                                 42.1%; Score 539; DB 1; L/56.0%; Pred. No. 1.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
Ras-related protein Rab-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long amodified and this statement is not removed.
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InterPro; IPR005223; Small_GTP.
Pfam; PP00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interPro; IPR003579; GTPase_Rab
                                                                                            23531 MW;
                                                                                                                                                             Best Local Similarity 56.0% Matches 103; . Conservative
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SMART; SM00175; RAB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lymnaeidae; Lymnaea.
NCBI_TaxID=6523;
                                           211
212
212 AA;
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Q05975;
                                                                                            SEQUENCE
                                                                                                                                       Query Match
NP_BIND
DOMAIN
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LIPID
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RAB2_LYMST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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-!- SUBCELLULAR LOCATION: ASSOCIATED WITH A STRUCTURE HAVING THE CHARACTERISTICS OF AN INTERMEDIATE COMPARTMENT BETWEEN THE ENDOPLASMIC RETICULUM AND THE GOLGI APPARATUS (BY SIMILARITY).
-!- SIMILARITY: TO RAS PROFEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                         Touchot N., Chardin P., Tavitian A.;
Four additional members of the ras gene superfamily isolated by
oligonucleotide strategy: molecular cloning of YPT-related cDNAs
a rat brain library.
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-1- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
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                                                       GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
GERANYL.GERNAYL (BY SIMILARITY).
GERANYL-GERNAYL (BY SIMILARITY).
M; FS878EDBA976752C CRC64:
                                                                                                                                                                                                                                                                             Length 212;
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1.8e-38;
51; Indels
                                  transport.
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01-NOV-1988 (Rel. 09, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
Ras_related_protein Rab-2.
                                                                                                                                                                                                                                                                          Score 538; DB; Pred. No. 1.8e
                             Lipoprotein; Prenylation;
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Ras_trnsfrmng.
Small_GTP.
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                                                                                                                                                                                                                      23534
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 56.0°
Matches 103; Conservative
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122
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InterPro; IPR001806;
InterPro; IPR005225;
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211
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212 AA;
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TIGRFAMS; TIGR GTP-binding; I NP_BIND HP_BIND 
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P05712;
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                                                                                                                                                                                                                                                                                          20 GTP (BY SIMILARITY).
65 GTP (BY SIMILARITY).
122 GTP (BY SIMILARITY).
43 EFECTOR REGION (BY SIMILARITY).
211 GERANYL-GERANYL (BY SIMILARITY).
212 GERANYL-GERANYL (BY SIMILARITY).
23535 MW; B68AAFF894DBEB19 CRC64;
                                                                                                                                                                                                            Length 212;
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRANG.
SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
GTP-binding; Lipoprotein; Prenylation; Protein transport.
NP_BIND 13 20 GTP (BY SIMILARITY).
NP_BIND 6 5 GTP (BY SIMILARITY).
                                                                                                                                                                                                                                           51; Indels
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Best Local Similarity 55.4%; Pred. No. 2.7e-38;
Matches 102; Conservative 31; Mismatches 51.
                                                                                                                                                                                    212 AA;
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Search completed: March 4, 2003, 15:00:03 Job time: 6.93644 secs

185 IKIG 188

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	GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.	
M protein - pr	OM protein - protein search, using sw model	
Run on:	<pre>March 4, 2003, 14:53:32 ; Search time 16.9905 Seconds     (without alignments)     3007.543 Million cell updates/sec</pre>	
litle: Perfect score: Sequence:	US-09-763-902B-8 1280 1 MSVSLPLTVWVRERDWIGIHLRQLRQPRSAQAVAPQPCGC 248	
scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5	
searched:	671580 segs, 206047115 residues	
otal number of	otal number of hits satisfying chosen parameters: 671580	
Inimum DB seq aximum DB seq	11nimum DB seq length: 0 Aaximum DB seq length: 200000000	
ost-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	

Q39844 glycine max Q18335 drosophila Q9smq6 arabldopsis Q08147 pisum sativ Q9lmr7 arabidopsis

ALIGNMENTS

Database :

09sip2 carica papa 09xeel sporobolus 09065 gallus gall 090157 ceenorhabdi 041596 oryza gativ 044596 oryza gativ 09466 plasmodium 040208 lotus japon P92963 arabidopsis 039824 glycine max 099043 tetrahymena 0904351 arabidopsis 023561 arabidopsis 023561 arabidopsis 02551 arabidopsis 02951 arabidopsis 02951 arabidopsis 029693 trypanosoma 026693 trypanosoma 026693 trypanosoma 026693 trypanosoma 09675 mus musculu 026691 cetrahymena 08504 oryza sativ 096622 tetrahymena 096622 diardia lam 096623 glardia lam

# 9: sp\_phage:\* 10: sp\_phage:\* 11: sp\_rodent:\* 12: sp\_virus:\* 14: sp\_urlassified:\* 15: sp\_virus:\* 16: sp\_bacteriap:\* 17: sp\_archeap:\* 17: sp\_archeap:\* 17: sp\_archeap:\* 17: sp\_archeap:\* 18: sp\_archeap:\* 19: sp\_archeap:\* 10: sp\_archeap:\* 10: sp\_archeap:\* 11: sp\_archeap:\* 12: sp\_archeap:\* 13: sp\_archeap:\* 14: sp\_archeap:\* 15: sp\_archeap:\* 16: sp\_archeap:\* 17: sp\_archeap:\* 18: sp\_archeap:\* 19: sp\_archeap:\* 19: sp\_archeap:\* 10: sp\_archeap:\* 10: sp\_archeap:\* 11: sp\_archeap:\* 12: sp\_archeap:\* 13: sp\_archeap:\* 14: sp\_archeap:\* 15: sp\_archeap:\* 16: sp\_archeap:\* 17: sp\_archeap:\* 17: sp\_archeap:\* 18: sp\_archeap:\* 18: sp\_archeap:\* 19: sp\_archeap:\* 19: sp\_archeap:\* 19: sp\_archeap:\* 19: sp\_archeap:\* 10: sp\_archeap:\* 11: sp\_archeap:\* 12: sp\_archeap:\* 13: sp\_archeap:\* 14: sp\_archeap:\* 15: sp\_archeap:\* 16: sp\_archeap:\* 17: sp\_archeap:\* 17: sp\_archeap:\* 18: sp\_archeap:\* 18: sp\_archeap:\* 19: sp\_archeap:\* 19: sp\_archeap:\* 10: sp\_arc

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Secription	Oghbré homo sanien	rl mus musculu			5 drosophila	044213 trichinella	41 mus musculu	6 drosophila	6 drosophila	4 caenorhabd1	3 echinococcu	5 drosophila	238922 arabidopsis	1 homo sapien	018333 drosophila	050019 zea mays (m
RIES	Descri	14460	091zr1	Q9bq44	09h0z8		04421	A160 .	. 01833	Q8±04(	093874	. 60gb3	0 Spsn60	.68EQ	D8wnd.	01833	.0050
SUMMARIES	TD TD		1 0912R1	098044	8Z0H6Ö	09V3L5	044213	11 091V41	018336	\$ Q8T046	093874	5 Q9GP33	3 Q905D5	10 . 038922	1 Q8WUD1	5 018333	10 - 050019
	% Query Match Length DB	248	213	218 4	198	213	213	215	215	215	210	223	213	211	216	213	210
	% Query Match	00-	81.6	74.0	6.89	64.7	57.7	50.4	48.6	48.2	47.3	45.8	43.0	43.0	42.7	42.6	42.5
	Score	1280	1045	947	882.5	828	738	645.5	622.5	617.5	909	586.5	550.5	550	546	545.5	544
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	Euteleostoml; Homo.  Zhang P.P., I H.N., Yu Y.,	MILY.	248;
	; Euteleo e; Homo. ., Zhang Li H.N.,	ting canc	Length 248; Indels 0
pdate) update	tebrata ominida ang H.Q L.P.,	nhibiti THE RA THE CA ein.	
; 248 AA. ed) sequence update) annotation update)	Craniata; Vertebrata; Eutel. Catarrhini; Hominidae; Homo Zhou X.M., Jiang H.Q., Zhan. Qian L.F., He L.P., Li H.N.	L/GenBank/DDBJ da BELONGS TO THE mng.	ω
PRT eat st st		e EMBL/GenBank/DDBJ d DTEINS. BELONGS TO THE L: L: L: L:GTP. WANG. LGTP; 1. Protein; Lipoprotein. MW; 69EBDC77A684EAC6	Score 1280; Pred. No. 1. 0; Mismatches
16, 16, 21, ote1	Chordata; Primates; Primates;	to the EMBL/G AS PROTEINS. B 7228.1; - GTPASE_RAD. GTPASE_RAD. ASS_LINGTP. 1 TRNSFRANG. TRNSFRANG. TRNSFRANG. TRNSFRANG. TRNSFRANG. TRNSFRANG. TRNSFRANG.	800
PRELIMINARY; (TrEMBLrel. 16, Cr (TERMBLrel. 21, La 27.5 kDa protein.	luman). Izoa; Ch eria; Pr 5; 1.A. F., Zha	L.H.;  n cDNA.clon DEC-1999 985; AG172 7; 1EK0. 7; 1EK0. PR001806; FPR001806; FPR001806; FPR001806; FPR001806; FPR001805; FPR005285; 271; ras; 1.175; RASTF 1175;	/at
PRE 2001 (Tr 2001 (Tr 2002 (Tr	iens (F ia; Meta i; Euthe ID=9606 FROM R Wan D	luman of the control	Simila 18; Cor
T 1 6 09HBR6 09HBR6; 01-MAR-2001 01-MAR-2001 01-JUN-2002 Hypothetical	Homo sapiens (Human). Eukaryota; Matazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. GUU J.R., Wan D.F., Zhao X.T., QID W.X., Huang Y., Qiu X.K.,	Yu J., Han L.H.;  Nu J., Han L.H.;  Nuvel Human CDNA clones with function of inhibiting cancer cell  growth.", Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  HILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.  HSSP; P36017; 1EK0.  HILLEPPO: JENGO13579; GPASSE RAB.  InterPro: JENGO13579; GMALLGTP.  FRAM; PRO005125; SMALLGTP.  FRAM; PRO0071; ras; 1  FRAM; PRO00715; RAS; 1  SWART: SM00175; RAS; 1  TIGREAMS; TIGRO0231; small_GTP; 1.  GTP-binding: Hypothetical protein; Lipoprotein.  SEQUIENCE 248 AA; 27506 MW; 69EBDC77A684EAC6 CRC64;	Query Match Best Local Similarity Matches 248; Conserv
HBR		K K K K K K K K K K K K K K K K K K K	Que Bes Mat

1 MSVSLPLTVWVRERDWIGIHLFSLYLSLPVGIPDFGSIWSDFLFKFLVIGSAGTGKSCLL 60

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01-JUN-2002 (TrEMBLrel. 21, Last annotation update) RAB4, member RAS oncogene family. Homo sapiens (Human).
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InterPro; IPR001806; Ras_trnsfrmng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RINTS; PRO0449; RASTRNSFRMNG
                                                                                                                                                                                                                                                                                                                                               AAH02438.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                        ISSUE-UTERUS
                                                                                                                                                                                                                                                                                                                                                                   P36017;
                                                                                                                                                                                                                                                    ISSUE-SKIN
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Q9H0Z8;
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                                                         181 MFLETSALIGENVEEAFLKCARTILNKIDSGELDPERMGSGIQYGDASLRQLRQPRSAQA 240
                                                                                                                                                                                                             66 GQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAGQERFRSVTRSYYRGAAGAL 120
                                                                                                                LVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLDPEREVTFLEASRFAQENEL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 DFLFKFLVIGSÄGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 GOERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 DPEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGS 220
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1 MSVSLPLTVMVRERDWIGIHLFSLYLSLPVGIPDFGSIWSDFLFKFLVIGSAGTGKSCLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mus musculus GTP-binding protein (RAB4) mRNA.";
Submitted (AGG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF408432; AAL11725.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 AA; 23554 MW; 9FF249DC329E0A27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1045; DB 11;
Pred. No. 3.6e-87;
0; Mismatches 4;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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InterPro; IPR0010806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
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Q91ZR1;
Q1-DEC-2001 (TrEMBLrel. 19, Cr
01-DEC-2001 (TrEMBLrel. 19, La
01-JUN-2002 (TrEMBLrel. 21, La
GTP-binding protein RAB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel, 17, (TrEMBLrel, 17,
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Best Local Similarity 98.1%;
Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                    241 VAPQPCGC 248
                                                                                                                                                                                                                                                                  241 VAPQPCGC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001
01-JUN-2001
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09B044;
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Q9BQ44
ID Q9BQ
AC Q9BQ
DT 01-J
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71 GQERFRSVTRSYYRGAAGALLVYDITSRETYNALTNWLTDARMLASQNIVIILCGNKKDL 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY
EMBL; AL117350; CAC17572.1; -.
HSSP; P05713; 12BD.
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DJ803J11.1 (RAB4, member RAS oncogene family) (Fragment)
                                                                                                                                                                                                       Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTP-binding: Lipoprotein.
SEQUENCE 218 AA; 24389 MW; 983D65E1162741B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 74.0%; Score 947; DB 4; Best Local Similarity 87.5%; Pred. No. 3.1e-78; Matches 182; Conservative 11; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIQYGDASLRQLRQPRSAQAVAPQPCGC 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nterPro; IPR001806; Ras_trnsfrmng
nterPro; IPR005225; Small_GTP.
fam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00175; RAB; 1.
IIGRFAMS; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nterPro; IPR003579; GTPase_Rab
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Query Match
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthman J. R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfennkoch C., Baldwin D.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Bulter H., Cadleu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos, B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A de Pablos, B., Delcher A., Dong Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K.W. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Fosler C., Gabriellan A.E., Garrell J.H., Gu Z., Gluan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Nei M.-H., Ibegwam C.,
H., Hostin D., Houland T.J., Nei M.-H., Ibegwam C.,
                                                                                                                                                                                                                                                                                                                                                                        61 RSVTRSYYRGAAGALLVYDITSRETYNALTNWLTDARMLASQNIVIILCGNKKDLDADRE 120
                                                                                                                                                                                                                                                                   46 FLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAGQERF 105
                                                                                                                                                                                                                                                                                                                                                 RSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLDPERE 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -121 VTFLEASRF-----LMFLETSALTGENVEBAFVQCARKILNKIESGELDPERMGSGIQYG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOSLIM D., MOLECOL. M. S. A. Kennison J.A., Ketchum K.A. Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A. Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
                                                                                                                                                                                                                                                                                        VTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSGIQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ina N.V., Mobarry C., Morris J., Moshrefi A., Murphy B., Murphy L., Muzny D.M., Nelson D.L.
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                                                                                                                                                                                         Length 198;
                                                                                                                                                                                                                               Indels
                                                                                                                                             566A2C25BB57A496 CRC64;
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Last annotation update)
                                                                                                                                                                                     Query Match 68.9%; Score 882.5; DB 4; Best Local Similarity 84.7%; Pred. No. 2e-72; Matches 172; Conservative 11; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last seq
1-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly)
                                                    SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
GTP-binding; Lipoprotein.
NON_TER
SEQUENCE 198 AA; 22037 MW; 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 DASLRQLRQPRSAQAVAPQPCGC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 DAALROLRSPRRAQAPNAQECGC 198
IPR005225; Small_GTP
                  Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
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Mount S.M
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SO PET SO STA
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Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V. Reese M.G., Reinert K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Shith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Syriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.Y., Wang Z.-Y., Wassarman D.A., Welistock G.M., Weissenbach J., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhu X., Zhu S., Zhu X., Smith H.O. (Zibs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Dorsophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 GQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 DPEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGS 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Addriguez E., Bonay P., Fresno M., Garate T.;
"cloning and characterization of Rab and Ran/TC4 cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23; Indels
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Trichinellidae, Trichinella.
NCBI_TaxID=6337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTP-binding; Lipoprotein.
SEQUENCE 213 AA; 23573 MW; A5735BE325E8D3F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.7%; Score 828; DB 5; 77.4%; Pred. No. 2e-67; 11ve 22; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 GIQYGDASLRQLRQPRSAQAVAPQPCGC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Ras_trnsfrmng; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00175; RAB; 1.
Ms; TIGR00231; small_GTP; 1.
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                                                                                                                                                                                                                                                                                                                                                                     Satoh A.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR003579; GTPase_Rab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO041; ras; 1.
PRO0449; RASTRNSFRMNG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0016701; Rab4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rab4A-like protein.
Trichinella pseudospiralis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 161; Conservative
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Ozaki K., Shimizu H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF0007
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cDNA collection.";

us-09-763-902b-8.rspt

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MEDLINE-21085660; PubMed-11217851;
RIKEN FANTOM Consortium;
"Functional annotation of a full-length mouse
Nature 409:685-690(2001).
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TISSUE-BREAST TUMOR;
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                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 QERFRSLIKNYYNGRACALLVYDITCRQSFNAIAQMLSDARSLASPQIIVILIGNKKDLE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 PEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42. FLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adachi J., Alzawa K., Akahira S., Akimura T., Aono H., Arai A., Arakama T., Arahira S., Fukuda S., Fukunishi Y., Furuno M., Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanaqaki T., Hara A., Hayetsu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                               Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UDN-2002 (TrEMBLrel. 21, Last senotation update)
Adult male kidney CDNA, RIKEN [111-length enriched library, clone: 0610030624, full lnsert sequence (Unknown) (Protein f
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTP-binding; Lipoprotein.
SEQUENCE 213.Aa; 24065 MW; 48BA45507605756D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 57.7%; Score 738; DB 5; Best Local Similarity 67.2%; Pred. No: 3.2e-59; Matches 131; Conservative 41; Mismatches 23
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                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001806; Ras_trnsfrmng
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00175; RAB; 1.
IIGRFAMS; TIGR00231; small_GTP; 1.
                   Parasitol. Res. 85:607-611(1999)
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STRAIN-C57BL/6J; TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003579; GTPase_Rab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0449; RASTRNSFRMNG.
                                                                                                                                                                                                                                                                       EMBL; Y11881; CAA72626.2; -. HSSP: P05713; 3RAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 IQFGHVEMKPIKNDR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ras; 1.
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                                                                                       SEQUENCE FROM N.A.
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                                                                                                                              STRAIN-GARKAVI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGC:6512).
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STRAIN-C57BL/6J; TISSUE-KIDNEY;
MEDLINE-20499374; PubMed-11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazati Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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MEDLINE=C57BL/G1 TISSUB-KIDNEY;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
Sumi N., Ishil W., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishil Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwayi K. Fujiwake S., Inoue K., Toawa M., Ohara E., Watshiki M. Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J. Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
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58.0%; Pred. No. 8.5e-51;
ive 33; Mismatches 45; Indels
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                                                                    Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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InterPro; IPR005225; Small_GTP.
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TIGRFAMS; TIGR00231; small_GTP; 1.
STRAIN-C57BL/6J; TISSUE-KIDNEY;
MEDLINE-99279253; PubMed-10349636;
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         RAHREY RAHRAN BARAN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                      01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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41 DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIMDTA 100
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira
Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang
Zieran L.L., Rubin G.M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                      FEBS Lett. 404 (65-69(1997).
-!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
EMBL, AE003403; AAF53390.1; -
EMBL, AE003409; AAF44870.1; -
EMBL, D84316; BAA21709.1; -
HSSP; P05713; 3RAB.
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                                                                                                                    STRAIN-OREGON R; TISSUE-HEAD;
MEDLINE-97228579; PubMed-9074639;
Satch A.K., Tokunaga F., Ozaki K.;
"Rab proteins of Drosophila melanogaster: novel members
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTP-binding; Lipoprotein.
SEQUENCE 215 AA; 24256 MW; 8BA09B7FFB41637F CRC64;
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Last annotation update)
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InterPro; IPR0013579; GrPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
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TIGRFAMS; TIGR00231; small_GTP; 1.
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01-JUN-2002 (TrEMBLrel. 21,
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Matches 121; Conserv
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Best Local Similarity
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Q9U5D5;
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Q9GP33
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                                                कुं व
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 PEREVIFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 FLFRFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 YIFKYIIIGDMGVGKSCLLHQFTEKKFMADCPHTIGVEFGTRIIEVSGQKIKLQIMDTAG 69
                                                                                                           DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTA 100
                                                                                                                                                                                   GOERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
                                                                                                                                                                                                         DPEREVIFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGS 220
                                                                                                                                                                                                                                                                                   9 NYIFKYIIIGDMGVGKSCLLHQFTEKKFMANCPHTIGVEFGTRIIEVDDKKIKLQIMDTA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                               Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lipoprotein.
0 AA; 23388 MW; DBDE4B52E447656D CRC64;
9EB59B7FEE546CDA . CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
                                 Query Match
48.2%; Score 617.5; DB 5;
Best Local Similarity 57.4%; Pred. No. 3e-48;
Matches 120; Conservative 30; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 606; DB 5;
; Pred. No. 3.3e-47;
32; Mismatches 55
                                                                                                                                                                                                                                                                                                                                         221 GIQYGDASLRQLRQPRSAQAV-APQPCGC 248
                                                                                                                                                                                                                                                                                                                                                                 189 GVQHRPS--QPSRTSLSSEATGAKDQCSC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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IPR001806; Ras_trnsfrmng.
IPR005225; Small_GTP.
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TIGRFAMS; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99069613; PubMed-9851916;
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 24230 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match (47.3%)
Best Local Similarity 55.1%;
Matches 114; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-FEB-1997 (TrEMBLrel. 02, 11-FEB-1997 (TrEMBLrel. 02, 11-JUN-2002 (TrEMBLrel. 21, 09A9.2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nvestigating biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fam; PF00071; ras; 1
   215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .binding;
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   SEQUENCE
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093874
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101 GQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 DELEKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTA 100
brehm K., Jensen K., Frosch M.; mRNA trans-splicing in the human parasitic cestode Echinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.8%; Score 586.5; DB 5; Length 223; 56.6%; Pred. No. 2.1e-45; Live 37; Mismatches 45; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   multilocularis.";
J. Balol. Chem. 275:38311-38318(2000).
--II-SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY
EMBL; AJ292375; CAC18549.1; --
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Platyhelminthes, Cestoda, Eucestoda;
Cyclophyllidea, Taeniidae, Echinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9EE6D6166E2089A4 CRC64;
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Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37; Mismatches
                                                                                                                                                                                                                       223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                 222 IQYGDASLRQLRQPRSAQAVAPQPCGC 248
                                                                                                   190 VQ-----PKQNLPRAAENNGKKDCNC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR0013579; GTP@se_Rab.
Interpro; IPR001806; Ras_trnsfrmng.
Interpro; IPR005225; Small_GTP.
Pfan; PP00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0449; RASTRNSFRANG.
SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GSGIQYGDASLRQLRQPRSAQAVA 242
                                                                                                                                                                                                                                                                                                                                   Putative ras-related protein RAB4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20556267; PubMed=10973970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24454 MW;
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                                                                                                                                                                                                                                                                  (TrEMBLrel, 16, C
(TrEMBLrel, 16, I
(TrEMBLrel, 21, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Lipoprotein.
223 AA; 24454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAB2 OR DRAB2 OR CG3269.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF0007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002
01-MAR-2002
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Q8WUD1;
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Q8WUD1
ID Q8WUD
AC Q8WUD
DT 01-MA
DT 01-MA
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124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                        of Drosophila genes encoding
                                                                                                                                     SEQUENCE FROM N.A.
MEDILINE-97340933; Pubmed-9197407;
Sasamura T., Kobayashi T., Kojima S., Qadota H., Ohya Y., Masai I.,
Hotta Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-Dinding protein ATGB2 (GTP-binding protein GB2) (Putative GTP-binding protein GB2)
F4B14.130 OR AT4G35860.
FAB14.130 OR AT4G35860.
FWAINOTAL VIIIDIAINA (Mouse-ear cress).
Eukaryota, Viiidiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidieurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAMLTDARTLASPNIVVILCGNKKDLD
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                                                                                                                                                                                 "Molecular cloning and characterization of Drosophila genes enternal Grpases of the rab and rho families.";
Mol. Gen. Genet. 254:486-494(1997).
-I- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
EMBI; AB033352; BAA87878.1; -
HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                 Sasamura T.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biermann B.J., Randall S.K., Crowell D.N.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                    Lipoprotein.
3 Aa; 23537 MW; 669B03897679CC02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          43.0%; Score 550.5; DB 5;
53.4%; Pred. No. 3.8e-42;
Live 28; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                          IGRFAMS; TIGRO0231; small_GTP; 1.
QSITE; PSO0675; SIGMA54_INTERACT_1; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 IQYGDA-SLRQLRQPRSAQAVAPQPCGC 248
                                                                                                                                                                                                                                                                                             PR001806; Ras_trnsfrmng.
PR002078; Sig54_interact
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                                                                                                                                                                                                                                                                                                                       PR005225; Small_GTP
                                                                                                                                                                                                                                                                                                                                 Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRANG
                                                                                                                                                                                                                                                                  lyBase; FBgn0014009; Rab2
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 43.0%
Best Local Similarity 53.4%
Matches 111; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          GTP-binding; Liport
                                                                                    SEQUENCE FROM N.A.
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InterPro; II
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SEQUENCE FROM N.A. Rotian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 GQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL.160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheuk R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamada K., Banh J., Chang C.H., Chang E., Dale J.M., Goldsmith A.D. Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk F. Hayashizaki Y., Tishida J., Jones T., Kamiya A., Karlin Neumann G., Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Shinn B., Lin J., Meyers M.C., Miranda M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A., Submitted (Dec-2001) to the EMBL/GenBank/DbBJ databases.

"Full Length CDNA of gene At4935860 (GI:15233367) ";

"Full Length CDNA of gene At4935860 (GI:15233367) ";

"Full Submitted (Dec-2001) to the EMBL/GenBank/DbBJ databases.
-I - SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jesse T.,
C.;
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Bevan M., Rose M., Hempel S., Entlan K-D., Hohelsel J., Heljnen L., Vos P., Mewes H.W., Mayer K.F.X., Schueller Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                      EU Arabidopsis sequencing project; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                       EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipoprotein.
1 Aa; 23175 MW; 71B5036D4B9A158E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.0%; Score 550; DB 10; 58.4%; Pred. No. 4.1e-42; Ive 29; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGREAMS; TIGRO0231; small_GTP; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Ras_trnsfrmng.
3; Sig54_interact.
5; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR003579; GTPase_Rab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL031986; CAA21472.1; -. AL161588; CAB81495.1; -. AY065262; AAL38738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0449; RASTRNSFRMNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20,
20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3est_Local Similarity 58.4%
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00175; RAB; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3RAB
                                                                                                                                                                                                                                                                                                [5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                     [3]
SEQUENCE FROM N.A.
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Query Match
Best Local &
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Amanatide P.G., Scherer S.E., Il P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayzaktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A.,
Chandra I.,
A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 FLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 PEREVIFLEASRFAQENELMFLETSALIGENVEEAFLKCARTILNKIDSGELDPERMGSG
                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
42.7%; Score 546; DB 4; Length 21
Best Local Similarity 57.6%; Pred. No. 9.8e-42; 
Matches 106; Conservative 29; Mismatches 49; Indels
                                                                                                                                                                                                                     Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2003).
InterPro: BC0208939; AR420839.1; -
InterPro: IPR001579; GTPase_Rab.
InterPro: IPR001806; Ras_trnsfrmng.
InterPro: IPR001086; Sas_trnsfrmng.
Pfam; PF00071; ras; I.
                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0449; RASTRNSFRMG.
SMART; SM00175; RAB; 1.
PROSITE; PS00675; SIGMAS, INTERACT, 1; UNKNOWN, 1.
PROSITE; A214 MW; 80A73F6D259701D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Similar to RIKEN CDNA 1500012D09 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 AA.
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                                                    Homo sapiens (Human).
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                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                        NCBI_TaxID=9606;
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RA Hostin N.D., Haivey D., Heilman T.J., Herrandez J.K., Houck J., RA Hostin D., Houston R.A., Howland T.J., Wei M.-, Ibegwam C., Aulahi M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Rimmel B.E., Kodira C.D.; Kraft C., Kravitz S., Kulp D., Lai Z., Ra Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Matcei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nalson D.L., RA Melson D.R., Nelson K., Niskern D.R., Pacleb J.W., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Rahe B.C., Siden-Kiamos I., Simpson M., Strong R., Smith T., RA Spier E., Spradling A.C., Stapeleton M., Strong R., Smith T., RA Spier E., Spradling A.C., Stapeleton M., Strong R., Sun E., Syradling A.C., Stapeleton M., Strong R., Wang A.H., Wang X., RA Williams S.M., Woodage T., Wonley K.C., Mu D., Yang S., Yao Q.A., RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.M., Zhong W., Zhau S., Zhu X., Smith H.O., RA Zheng X.H., Myers E.W., Rubin G.W., Venter J.C.; RT The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 FLFKFLVIGSAGTGKSCLLHOFIENKFKODSNHTIGVEFGSRVVNVGGKTVKLOIWDTAG 101
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harrey D., Helman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Satoh A.K., Tokunaga F., Ozaki K.;
"Rab proteins of Drosophila melanogaster: novel members of the Rab-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.YLFKYIIIGDTGVGKSCLLLQFTDKRFQPVHDLTIGVEFGARMITIDGKQIKLQIWDTAG
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-!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
EMBL; AE003789; AAF57381.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGR00231; small_GTP; 1.
PROSITE; PSO0675; SIGMAS4_INTERACT_1; UNKNOWN_1.
GTP-binding; Lipoprotein.
SEQUENCE 213 AA; 23560 MW; 61029D8EEFE7CC02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: March 4, 2003, 15:02:46 Job time : 18.9905 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIYBASE; FB900014009; Rab2.
InterPro; IPR003579; GTPASE_RAb.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR002078; S1954_interact
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-OREGON R; TISSUE-HEAD;
MEDLINE-97228579; PubMed-9074639;
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PRINTS; PR00449; RASTRNSFRMNG.
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HSSP; P05713; 3RAB.
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Matches 110; Conservative
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US-08-511-525-51
US-08-511-525-25
US-08-718-270A-25
US-08-511-525-10
US-08-511-525-10
US-08-511-525-35
US-08-531-525-35
US-09-075-454-3
US-08-531-525-19
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371.5
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                                                             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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### ALIGNMENTS

262574

Total number of hits satisfying chosen parameters:

262574 segs, 29422922 residues

Searched:

Title: Perfect score: Sequence:

OM protein

Run on:

Scoring table:

Oncogenic Action

Sequence

RESULT 1 US-08-531-525-20	; Sequence 20, Application US/US331323 ; Patent No. 5840683 ; GENERAL INFORMATION: APPLICANT: Hlavka, Joseph J.	APPLICANT: Pincus, Matthew R. APPLICANT: No. 58406831e, John F. APPLICANT: Abajian, Henry B. APPLICANT: Kende, Andrew S. TITLE OF INVENTION: Peptides Inhibiting the Oncoge: TITLE OF INVENTION: of P21 Ras NUMBER OF SEQUENCES: 52 CORRESCONDENCE ADDRESS:	ADDRESSEE: Greenlee and Winner, P.C. STREET: 5370 Manhattan Circle, Suite 201 STATE: Colorado	REAL TYPE	COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PRIGHT Release #1.0, Version #1.30	CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/531,525 ; FILING DATE: 21-SEP-1995	CLASSIFICATION: 530 ; ATTORNEY/AGENT INFORMATION: ; NAME: Ferber, Donna M.	F > 5 %	2 5 m F	TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein HYDOMETHEATER: NO	CONGANISM: Rattus norvegicus CORGANISM: Rattus norvegicus US-08-531-525-20  Query Match Conf. Par. Rattus CORGANISM: Rattus norvegicus CORGANISM: Rattus norvegicus CORGANISM: Rattus norvegicus
ngth: 0 ngth: 20000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	<pre>Database : Issued_Patents_AA:* 1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:* 2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:* 3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:* 4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:* 5: /cgn2_6/ptodata/1/laa/FUCJ_COMB.pep:* 6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*</pre>	pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES Result Query No Score March Length DB ID Score March Length DB ID	869.5 67.9 208 2 869.5 67.9 208 2	539 42.1 212 4 US-09-399-913-67 Sequence 67, 536 41.9 212 2 US-08-531-525-18 Sequence 18, 536 41.9 212 2 US-08-718-2708-18	508 39.7 210 2 US-08-531-525-16 Sequence 16, 508 39.7 210 2 US-08-718-270A-16 Sequence 16, 492.5 38.5 208 2 US-08-531-525-17 Sequence 17,	492.5 38.5 208 2 US-08-718-270A-17 490 38.3 208 2 US-08-531-525-15 443 34.6 214 2 US-08-531-525-52	443 34.6 214 2 US-08-718-270A-52 Sequence 52, 425.5 33.2 213 2 US-08-713-423-8 Sequence 14, 423 33.0 202 2 US-08-531-525-14 Sequence 14, 423 33.0 202 2 US-08-718-270A-14 Sequence 14,	421.5 32.9 217 2 US-08-773-423-3 Sequence 3, 417.5 32.6 201 2 US-08-916-901-3 Sequence 3, 417.3 32.6 201 2 US-08-916-901-8 Sequence 8, 417 32.6 201 2 US-08-916-901-8 Sequence 8,	21 417 32.6 2014 4 03-09-154-6022-8 Sequence 8, Appl. 22 414 32.3 213 2 05-08-718-2708-11 Sequence 11, Appl. 23 414 32.3 213 2 05-08-718-2708-11 Sequence 11, Appl. 24 410.5 32.1 201 2 05-08-718-255-13 Sequence 13, Appl. 25 410.5 32.1 201 2 05-08-718-2708-13 Sequence 13, Appl. 26 408 31.9 203 2 05-08-766-551-8

Length 208;

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185 IKIG 188
    Query Match
Best Local Sim
Matches 174;
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                                                                                                                                                             DPEREVTFLEASRFAQENELMFLETSALIGENVEEAFLKCARTILNKIDSGELDPERMGS 220
                                                                                                                                                                                  Gaps
                                 DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTA 100
                                                                                              GOERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
                                                 17; Indels
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VENTION: Peptidomimetics Inhibiting
VENTION: the Oncogenic Action of P21 Ras
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5370 Manhattan Circle, Suite 201
   Mismatches
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/531,525
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         GIQYGDASLRQLRQPRSAQAVAPQPCGC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,270A
FILING DATE: 20-SEP-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/08718270A Patent No. 5910478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                No. 59104781e, John F
Abajian, Henry B.
                                                                                                                                                                                                                                                                                                                                                                                                   incus, Matthew R
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TELEFAX; (303), 499-8089
INFORMATION; FOR SEQ ID NO; 20
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REFERENCE/DOCKET NUMBER:
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208 amino acids
amino acid
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Matches 174; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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41 DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTA 100
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                                                                                                             5 YLFKYIIIGDTGVGKSCLLLQFTDKRFQPVHDLTIGVEFGARMITIDGKQIKLQIWDTAG 64
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APPLICANT: An, Wengian
TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
  Length 208;
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                                            Indels
67.9%; Score 869.5; DB 2;
83.7%; Pred. No. 1.1e-91;
11ve 12; Mismatches 17;
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ER APPLICATION NUMBER: USSN 60/110,277
ER FILING DATE: 1998-11-30
ER PILING DATE: 1998-11-25
ER APPLICATION NUMBER: USSN 60/110,033
ER APPLICATION NUMBER: USSN 60/109,333
ER PILING DATE: 1998-11-20
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APPLICATION NUMBER: USSN 09/298,731
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APPLICATION NUMBER: USSN 09/350,614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: MNI-070CP2
CURRENT APPLICATION NUMBER: US/09/399,913
                                                                                                                                                                                                                                                                                                                                                                      221 GIQYGDASLRQLRQPRSAQAVAPQPCGC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 67, Application US/09399913 Patent No. 6361971
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Conservative 3
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APPLICANT: Betty, Maria
                      Similarity
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US-09-399-913-67
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Kende, Andrew S.
VENTION: Peptidomimetics Inhibiting
VENTION: the Oncogenic Action of P21 Ras
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/531,525
FILING DATE: 21.5EP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,091
FILING DATE: 21.5EP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/718,270A FILING DATE: 20-SEP-1996 CLASSIFICATION: 514
, Application US/08718270A
                                                                 Hlavka, Joseph J.
Pincus, Matthew R.
No. 5910478le, John F.
Abajian, Henry B.
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REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
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TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
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linear
7: protein
NO
                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                         Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 11n
MOLECULE TYPE:
HYPOTHETICAL: N
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APPLICANT:
APPLICANT:
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                 Sequence 18,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 PEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 SRREVKKEEGEAFAREHGLIFMETSAKTASNVEEAFINTAKEIYEKIQEGVFDINNEANG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides Inhibiting the Oncogenic Action of P21 Ras
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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55.4%; Pred. No. 2.1e-53;
tive 31; Mismatches 51.
                                                                                                                                                                                                                                                                                                                               5: Greenlee and Winner, P.C.
5370 Manhattan Circle, Suite 201
                                                                                                           APPLICANT: Pincus, Matthew R.
APPLICANT: No. 58406831e, John F.
APPLICANT: Abajian, Henry B.
TITLE OF INVENTION: PEPTIGES Inhibiting FILLE OF INVENTION: Of P21 Rs.
NUMBER OF SEQUENCES: 52
CORRESPONDENCE APPLIANT ADDRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/531,525
FILING DATE: 21-SEP-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                         Sequence 18, Application US/08531525
Patent No. 5840683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 37-9
TELECONMUNICATION INFORMATION:
TELEPHONE: (303,499-8080
TELEFAX: (303) 499-8081
INFORMATION FOR SEQ ID NO: 18:
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Matches 102; Conservative
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162 PEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
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                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                              Length 212;
                                                            Ouery Match
41.9%; Score 536; DB 2; Length 21
Best Local Similarity 55.4%; Pred. No. 2.1e-53;
Matches 102; Conservative 31; Mismatches 51; Indels
; ORGANISM: Rattus norvegicus US:08-718-270a-18
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RESULT 5 US-08-718-270A-18

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 210;
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                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.7%; Score 508; DB 2; 54.9%; Pred. No. 3.3e-50;
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                                                                                                                                                                                                                                   Greenlee and Winner, P.C.
5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOLIMAND.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,525
FILING DATE: 21-SEP-1995
CTASSIFICATION: 530
Sequence 16, Application US/08531525
Patent No. 5840683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VITORNEY/AGENT INFORMATION:
NAME: PERDEY, DONNA M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lymnea stagnalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEO ID NO: 16
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 amino acids
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                                                                                                                                                                                                                                                                            Boulder
: Colorado
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                                                                                                                                                                                                                                                                                                                   COUNTRY:
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162 PEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
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   Peptidomimetics Inhibiting
the Oncogenic Action of P21 Ras
                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPELICATION NUMBER: US/08/718,270A FILING DATE: 20-SEP-1996 CLASSIFICATION: 514
                                                                       E: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 508; DB 2;
Pred. No. 3.3e-50;
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APPLICATION NUMBER: US 08/531,525
FILING DATE: 21-SEP-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (303) 499-8089
ORMATION FOR SEQ ID NO:
EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 amino acids
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TITLE OF INVENTION: Per
TITLE OF INVENTION: the
NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
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Best Local Similarity
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                                                                         ADDRESSEE:
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                                                                                                                                               COUNTRY:
                                                                                          STREET:
                                                                                                                             STATE:
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RESULT 8 US-08-531-525-17

US-08-718-270A-16; Sequence 16, Application US/08718270A; Patent No. 5910478

RESULT 7

COUNTRY:

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162 PEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
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                                                  Andrew S.
. Peptidomimetics Inhibiting
. the Oncogenic Action of P21 Ras
                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OR/71
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                                                                                                                                         E: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
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APPLICATION NUMBER: US 08/531,525
FILING DATE: 21-SEP-1995
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                     E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEG ID NO: 17: SEQUENCE CHARACTERISTICS:
LENGTH: 208 am<sup>4</sup>1-1
Matthew R
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amino acid
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                                                                                                       NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                 STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 20 CLASSIFICATION:
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US-08-718-270A-17
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US-08-531-525-15
                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 492.5; DB 2; Length 208;
Pred. No. 2e-48;
                                                                                                                                                  TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action TITLE OF INVENTION: of P21 Ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30; Mismatches
                                                                                                                                                                                              STREET: 5370 Manhattan Circle, Suite 201 CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                         MBER: US/08/531,525
21-SEP-1995
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18-08-718-270A-17
Sequence 17, Application US/08718270A
Patent No. 5910478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Oryctolagus cuniculus
                                                                       Pincus, Matthew R.
No. 58406831e, John F.
Abajian, Henry B.
 Sequence 17, Application US/08531525 Patent No. 5840683
                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ferber, Donna M. REGISTRATION NUMBER: 33,878 REFRENCE/DOCKET NUMBER: 37 PLECOMMUNICATION INFORMATION:
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llarity 54.3%;
Conservative 3
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APPLICATION NUMBER: US
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                  NUMBER OF SEQUENCES:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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Length 208;

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65 QESFRSITESYTRGAAGALLVYDITERDTFNHLTTWLEDARQHSNSNMVIMLIGNKSDLE 124
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Andrew S.
Peptidomimetics Inhibiting
: the Oncogenic Action of P21 Ras
                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                  E: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
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APPLICATION NUMBER: US 08/531,525
FILING DATE: 21-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/718,270A FILING DATE: 20-SEP-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (303) 499-8080
                                                                                                                                                                                                                                          COMPUTER READABLE FORM: .
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (303) 499-8089
ORMATION FOR SEQ ID NO: 3
EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 53.8%
Matches 99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ferber, Donna M. REGISTRATION NUMBER: 3
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MOLECULE TYPE: protein
                                   TITLE OF INVENTION: Pel
TITLE OF INVENTION: th
NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
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STRANDEDNESS: si
                                                                                                                                                                               Colorado
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                                                                                                                                                          Boulder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 FLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 PEREVIFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGSG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides Inhibiting the Oncogenic Action of P21 Ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.3%; Score 490; DB 2; I
Best Local Similarity 53.8%; Pred. No. 3.8e-48;
Matches 99; Conservative 31; Mismatches 50;
                                                                                                                                                                                                  3: Greenlee and Winner, P.C.
5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/531,525
FILING DATE: 21-SEP-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/08718270A Patent No. 5910478 GENERAL INFORMATION:
                                      APPLICANT: Pincus, Matthew R.
PAPLICANT: No. 58406831e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY FLAILIN: 33.0
ATTORNEY FEEDEN: 35.0
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33.878
REFERENCE/DOCKET NUMBER: 37-9
TELEPHONE: (303) 499-8080
TELEPHONE: (303) 499-8080
INFORMATION FOR SEQ. TD NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hlavka, Joseph J. APPLICANT: Pincus, Matthew R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                  TITLE OF INVENTION: PE
TITLE OF INVENTION: Of
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                          Boulder
: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 IQYG .225
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181 IKIG 184
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Length 208;

RESULT 11

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us-09-763-902b-8.rai

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69 GQERYRAITSAYYRGAVGALLVYDIAKHLTYENVERWLKELRDHADSNIVIMLVGNKSDL 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Abalian, Henry B.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action
TITLE OF INVENTION: of P21 Ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 DPEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kende, Andrew S.
FBNTION: Peptidomimetics Inhibiting
FBNTION: the Oncogenic Action of P21 Ras
                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/531,525 FILING DATE: 21-SEP-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 34.6%; Score 443; DB 2; Best Local Similarity 54.2%; Pred. No. 9.9e-43; Matches 91; Conservative 24; Mismatches 45
                                                                                                                                                                  5: Greenlee and Winner, P.C. 5370 Manhattan Circle, Suite 201.
                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 52 3 Application US/08718270A
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O. 5910478le, John F.
Dajian, Henry B.
Pincus, Matthew R.
No. 58406831e, John F.
Abajian, Henry B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Perber, Donna M.
REGISTRATION NUMBER: 37.878
REFERENCE/DOCKET NUMBER: 37.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           relecommunication information Telephone: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (303) 499-8069
INFORMATION FOR SEQ ID NO: 52
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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GENERAL INFORMATION:
                                                                                                                                                                                                       CITY: Boulder
STATE: Colorade
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
ORGANISM: HOW
US-08-531-525-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-08-718-270A 52
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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101 GQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 RHLRAVPTDEARAFAEKNGLSFIETSALDSTNVEAAF----QTILTEI 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 DPEREVTFLEASRFAĢĒNELMFLETSALTGENVEEAFLKCARTILNKI 208
                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
S: Greenlee, Winner and Sullivan, P.C.
5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GO11, Surya K.
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,270A
FILING DATE: 20-SEP-1996
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/531,525
FILING DATE: 21-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,091
                                                                                                                                          5: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08773423
Patent No. 5869291
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hillman, Jennifer L. APPLICANT: Goli, Surya K. APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ferber, Donna M. REGISTRATION NUMBER: 43,878
REFERENCE/DOCKET NUMBER: 7
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 21-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 214 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-718-270A-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                       OMPUTER READABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Palo Alto
                                                           Colorado
                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
  ADDRESSEE:
                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-773-423-8
                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                            CITY:
STATE:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 GQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 GLERYRAITSAYYRGAVGALLVFDLTKHQTYAVVERWLKELYDHAEATIVVMLVGNKSDL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 NFVFKVVLIGESGVGKTNLLSRFTRNEFSHDSRTIGVEFSTRTVLLGTAAVKAQIMDTA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: No. 58406831e, John F.
APPLICANT: Rende Henry B.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action
TITLE OF INVENTION: of P21 Ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 1e-40;
                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/773,423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Greenlee and Winner, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08531525
Patent No. 5840683
                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: B11110Gs, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-OTELECOMMUNICATION INFORMATION:
TELECHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 AIALGSAQAGQEPGPGRRA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 GIQYGDASLRQLRQPRSAQA 240
                                                                   COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     NFORMATION FOR SEQ ID NO:
                                                                                                                                                                    Herewith
                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-845-4166
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee
                                                                                                                                                                                         CLASSIFICATION: 514 RIOR APPLICATION NUMBER:
                       COMPUTER READABLE FORM MEDIUM TYPE: Disket
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11near:
| IMMEDIATE SOURCE:
| LIBRARY: Genbank
| CLONE: 43601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boulder
Colorado
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                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-531-525-14
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93 KLQIWDTAGQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVI 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 LCGNKKDLDPEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 202
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                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: March .4, 2003, 15:06:28 Job time : 9.59761 secs
                                                                        APPLICATION NUMBER: US/08/531,525
FILING DATE: 21-SEP-1995
CLASSIFICATION: 530
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 37-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Lymnea stagnalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 47.2%;
Matches 83; Conservative 3
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LENGTH: 202 amino acids
TYPE: amino acid
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ORGANISM: Lyn
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Sequence 1112, Application US/09764868

Patent No. US20020168711A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT 232
CURRENT APPLICATION NUMBER: US/09/764,868

CURRENT FILING DATE: 2001-01-17
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US-09-764-868-1112
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Sequence 692, App
Sequence 1100, Ap
Sequence 783, App
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1 MSVSLPLIVWVNERDWIGIH......LRQLRQPRSAQAVAPQPCGC 248
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2/pubpaa/PCT_NEW_PUB.pep:*
2/pubpaa/USO6_NEW_PUB.pep:*
2/pubpaa/USO6_PUBCOMB.pep:*
2/pubpaa/USO7_NEW_PUB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-255-30-783
US-09-350-874-67
US-09-988-974-8
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US-09-925-301-1077
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Maximum Match 100%
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Sequence 1106, Ap
Sequence 4, Appli
Sequence 6, Appli
Sequence 701, Appl
Sequence 14, Appli
Sequence 14, Appli
Sequence 1101, Ap
Sequence 1101, Ap
Sequence 1101, Ap
Sequence 1120, Ap
Sequence 1120, Appli
Sequence 1164, Appli
Sequence 10, Appli
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US-09-817-199A-3

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US-09-817-198A-5

US-09-817-198A-5

US-09-817-198A-5

US-09-764-868-1101

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### ALIGNMENTS

PNIVVILCGNKKDLDPEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILN 206 87 VGGKTVKLQIWDTAGQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLAS 146 27 SLPVGIPDFGSIMSDFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVN 86 1 SLPVGIPDFGSIWSDFLFRFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVN 60 Gaps ö Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1112
LENGTH: 222 Length 222; Indels KIDSGELDPERMGSGIQYGDASLRQLRQPRSAQAVAPQPCGC 248 Score 1147; DB 9; L; Pred. No. 1.4e-108; 0; Mismatches 0; 89.6%; Scur. 100.0%; Pre Conservative

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                                                                                                                                           Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510 SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEO ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
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                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT22 CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                     0; Indels
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58.0%; Pred. No. 1.4e-57;
tive 33; Mismatches 45
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Mismatches
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Sequence 692, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
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Similarity 100.0%; P.
12; Conservative 0;
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Best Local Similarity 58.0%
Matches 123; Conservative
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US-09-764-868-692
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LENGTH: 307
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TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS.
FILE REFERENCE: MNI-069
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                                                                                                                                                                       TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUCLEIC Acids, Proteins and Antibodies

CURRENT APPLICATION NUCLE:

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR PTLING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 896

SOFTWARE: Patentin Ver. 2.0

SEQ IN 0783

LENGTON
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CURRENT FILING DATE: 1999-07-09
EARLIER APPLICATION WUMBER: USSN 60/110,277
EARLIER TLING DATE: 1998-11-30
EARLIER FILING DATE: 1998-11-25
EARLIER FILING DATE: 1998-11-25
EARLIER FILING DATE: 1998-11-20
EARLIER FILING DATE: 1998-11-20
EARLIER FILING DATE: 1998-11-20
EARLIER FILING DATE: 1998-04-23
--CGC 248
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                                         --PQGGRLTSEPQPQREGCGC 307
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Patent No. US20020019020A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 67
LENGTH: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rhodes, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo saptens
US-09-925-302-783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Rattus sp
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                                     282 VQHKPSA-
                                                                                                                                US-09-925-302-783
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Best Local Similarity 46.5%; Pred. No. 1.7e-35;
Matches 93; Conservative 28; Mismatches 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
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US-09-988-974-3
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                                                                                                     42 FLFKFLVIGSAGTGKSCLLHOFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTAG 101
                                                                                                                                                                        102 QERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDLD 161
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                                 Length 212;
                                                                    Indels
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/988,974
FILING DATE: 19-No. US20020090712A1-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Incyte Pharmaceuticals, Inc.
                                                    ; Pred. No. 5.3e-30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 425.5;
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TITLE OF INVENTION: NOVEL RAB PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-988-974-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. US20020090712A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS
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                                    42.1%;
56.0%;
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                                   Query Match
Best Local Similarity 56.0%
Matches 103; Conservative
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185 IKIG 188
                                                                                                                                                                                                                                                                                                                  222 IQYG 225
     US-09-350-874-67
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-09-988-974-8
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Query Match

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APPLICANT: MERKULOV, Gennady et al.

TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REPERENCE: CL001196
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                                                                                                                                               26 DYLFKLLLIGDSGVGKSCLLLRPADDTYTESYISTIGVDFKIRTIELDGKTIKLQIMDTA 85
41 DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTA 100
                                                                                                               101 GQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
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                                        10 NFVFKVVLIGESGVGKTNLLSRFTRNEFSHDSRTTIGVEFSTRTVLLGTAAVKAQIMDTA 69
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Pred. No. 2.5e-35;
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ADDRESSEE: Incyte Pharmaceuticals,
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TITLE OF INVENTION: NOVEL RAB PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/820,003A CURRENT FILING DATE: 2001-03-29 NUMBER OF SEQ ID NOS: 39 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4
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Patent No. US20020090712A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09820003A
Patent No. US20020142382Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
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45.58;
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CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-301-1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 GLERYRAITSAYYRGAVGALLVFDLTKHQTYAVVERWLKELYDHAEATIVVMLVGNKSDL 155
                                                                                                                                                                                                                                                                                                                        41 DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIMDTA 100
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SOFTWARE: FastSEQ for Windows Version 2.
                                                                                                                                                                                                                                   32.9%; Score 421.5; DB 10;
46.5%; Pred. No. 5e-35;
Live 27; Mismatches 79;
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TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 28-Sep-2001 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corley, Nell C.
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                                                                                                                                                                                                                                                                Best Local Similarity
Matches 93; Conserv
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                                                                 TYPE: PRT
ORGANISM: Homo
                                                                                                                              NAME/KEY: SITE
LOCATION: (25)
SOFTWARE: Pate
SEQ ID NO 1077
LENGTH: 239
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                                                                                                              FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 217;
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IITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/988,974
FILING DATE: 19-No. US20020090712A1-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PF-0183 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: Consensus ; SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-09-988-974-3
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/215,887
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Patent No. U620020052308A1
                                                                                                                                                                                                                                                                                                 ICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 217 amino acids TYPE: amino acid.
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                                                                                                                     JTER READABLE FORM
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                                Palo Alto
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                                                                           COUNTRY: USA
                                                                                                ZIP: 94304
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176 GAASG 180
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                                                                                                                                                                                                                                                    101 GQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
                                                                                                                                                                                   41 DFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIWDTA 100
                                                                                                                                                                                                                                                                                                                     .61 DPEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELDPERMGS 220
                                                                                                                                                                                                        6 DYLFKLILIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQIMDTA 65
                                                                                                               Score 417.5; DB 10; Length 201; Pred. No. 1e-34;
                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                             70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                    32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/967,736 FILING DATE: 28-Sep-2001 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF-0367
                                                                                                                 Score 417.5;
                                                                                                                                                                                                                                                                                                                                                                                                                        176 GAASGG-----ERPNLKIDSTPVKPAGGGC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/154,602
             LIBRARY: LIVRTUT04
CLONE: 2514506
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-967-736-3
                                                                                                                                                                                                                                                                                                                                                                                         221 GIQYGDASLRQLRQPR---SAQAVAPQPCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09967736
Patent No. US20020103340A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 201 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lal, Preeti
Corley, Neil C.
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STRANDEDNESS: single
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                                                                                                                   32.6%;
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shah, Purvi
TOPOLOGY: linear
                                                                                                                                    Best_Local Similarity 42.78
Matches 90; Conservative
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APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 32705, 23224, 27423, 32700, 32712, No. US20020009804Alel
TITLE OF INVENTION: Human G-Proteins
FILE REFERENCE: 35800/209285
CURRENT APPLICATION NUMBER: US/09/794,257
CURRENT FILING DATE: 2001-02-27
PRIOR PAPLICATION NUMBER: 60/185,606
PRIOR PILING DATE: 2000-02-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. US20020009804Alel
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                                                                                                                                                                                                                                                  101 GQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASPNIVVILCGNKKDL 160
                                                                                                                                                                                                                                                                               --KKRMGP 175
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                                                                                                                   Gaps
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                                                                      Length 201;
                                                                                                                   Indels
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Patent No. US20020009804A1
GENERAL INPORMATION:
APPLICANT: MAYOFES, Rachel
TITLE OF INVENTION: 32705, 23224, 27423, 32700, 32712,
                                                                                                                                                                                                                                                                                                                                                                                126 TTKKVVDNTTAKEFADSLGVPFLETSAKNATNVEQAFMTMAAEI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                   Score 417; DB 10;
Pred. No. 1.1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 414.5; DB 1
Pred. No. 2.1e-34;
6; Mismatches 68
                                                          NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
; SEQUENCE DESCRIPTION: SEQ ID NO: 8: US-09-967-736-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09794257 Patent No. US20020009804A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 32.4%;
Best Local Similarity 40.9%;
Matches 81; Conservative 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 GIQYGDASLRQLRQPRSA 238
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                                                                 Ouery Match
Best Local Similarity 46.5%
Matches 86; Conservative
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41 DFLIRKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNVGGKTVKLQIMDTA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 IMDTAGQERFRSVTRSYYRGAAGALLVYDITSRETYNSLAAWLTDARTLASP-NIVVILC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                    155 GNKKDLDPEREVTFLEASRFAQENELMFLETSALTGENVEEAFLKCARTILNKIDSGELD 214
                                                                                                                                                                                                                                                                                                                    37 SIWSDFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGSRVVNV-GGKTVKLQ 95
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                                                                                                                                                                                                                                                                 Indels
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FITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; DB 10;
1,5e-33;
les 57; 1
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Pred. No. 2.8e-34;
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Pred. No. 3.5e-
18; Mismatches
                                                                                                                                                                                                                                 Query Match 32.3%; Score 413.5; 1
Best Local Similarity 44.0%; Pred. No. 2.8e
Matches 84; Conservative 40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
FILE REFERENCE: 35800/209285
CURRENT APPLICATION NUMBER: US/09/794,257
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 60/185,606
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. US200200449111
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nilarity 44.8%; 1
Conservative 38;
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US-09-925-302-534
                                                                                                                                                                            ; ORGANISM: homo sapiens
US-09-794-257-5
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Best Local Similarity
Matches 81; Conserv
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US-09-925-302-534
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SEQ ID NO 534
LENGTH: 246
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                                                                                                                                                                  TYPE: PRT
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Matches
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APPLICANT: ZHU, Shiaoping et al.

TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLOO1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ore 400; DB 10; Length 1
ed. No. 5.5e-33;
Mismatches .53; Indels
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/822,860
CURRENT FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                              Sequence 5, Application US/09822860 Patent No. US20020146795A1
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Best Local Similarity 45.09
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Discopyge ommata US-09-822-860-5
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ORGANT
                                                                                          RESULT 15
US-09-822-860-5
                                  224 G 224
221 G 221
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